

94 183

From: Parkin, Jeffrey  
Sent: Thursday, May 15, 2003 6:41 PM  
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MAY 16 2003

Please search **SEQ ID NOS.: 1, 3, 4, 5, 117, 118, 119, 534, 535, 536, 537, 538, 540, and 541** from the aforementioned application (09/623,533) v. all relevant databases including interference. Please note that these sequences are all close variations of the same parent peptide.

Place results on both paper and disk.

Thanks!

JSP  
AU 1648  
CM01-8E15  
308-2227

ck

Point of Contact:  
Toby Port  
Technical Info. Specialist  
CM1 6A04  
703-308-3534

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 5/16  
Date Completed: 5/19  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

## TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

## VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 25.512 Seconds

(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-117

Perfect score: 188

Sequence: 1 TSLIHSLIEESQNOQEKNEOELLELDKWSLWNMF 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	645	15	0993A6 human immun
2	188	100.0	747	15	070607 human immun
3	188	100.0	748	15	070606 human immun
4	188	100.0	752	15	070604 human immun
5	188	100.0	752	15	070605 human immun
6	188	100.0	752	15	070608 human immun
7	188	100.0	851	15	078243 human immun
8	188	100.0	852	15	089797 human immun
9	188	100.0	854	15	085582 human immun
10	188	100.0	854	15	072502 human immun
11	188	100.0	856	15	092877 human immun
12	188	100.0	856	15	074599 human immun
13	188	100.0	856	15	074090 human immun
14	184	97.9	854	15	090178 human immun
15	184	97.9	854	15	078705 human immun
16	183	97.3	856	15	0905M7 human immun

17	182	96.8	616	15	0993B0 human immun
18	182	96.8	618	15	0993B2 human immun
19	182	96.8	757	15	090722 human immun
20	182	96.8	848	15	069990 human immun
21	180	95.7	838	15	003806 human immun
22	180	95.7	854	15	078225 human immun
23	180	95.7	855	15	003805 human immun
24	179	95.2	42	15	069910 human immun
25	179	95.2	443	15	080023 human immun
26	179	95.2	841	15	041556 human immun
27	179	95.2	849	15	077368 human immun
28	179	95.2	849	15	080851 human immun
29	179	95.2	851	15	056110 human immun
30	179	95.2	851	15	080852 human immun
31	179	95.2	856	15	072993 human immun
32	179	95.2	856	15	041539 human immun
33	179	95.2	857	15	080170 human immun
34	179	95.2	858	15	080190 human immun
35	179	95.2	858	15	080188 human immun
36	179	95.2	859	15	080185 human immun
37	179	95.2	859	15	080180 human immun
38	179	95.2	859	15	080179 human immun
39	179	95.2	859	15	080177 human immun
40	179	95.2	859	15	080173 human immun
41	179	95.2	859	15	080850 human immun
42	179	95.2	862	15	080184 human immun
43	179	95.2	862	15	080183 human immun
44	179	95.2	862	15	080182 human immun
45	179	95.2	862	15	080178 human immun

# ALIGNMENTS

RESULT 1  
ID 0993A6 PRELIMINARY: PRT; 645 AA.  
AC 0993A6;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (fragment).  
ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
DR EMBL: AF321563; AK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;  
KW Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;

Query Match 100.0%; Score 188; DB 15; Length 645;  
Best Local Similarity 100.0%; Pred. No. 8.8e-15;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSLIEESQNOQEKNEOELLELDKWSLWNMF 35  
DB 608 TSLIHSLIEESQNOQEKNEOELLELDKWSLWNMF 642

## RESULT 2

070607 PRELIMINARY: PRT: 747 AA.  
 AC 070607;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RA MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Vital variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12034; AAA76669.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 RA AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 747 747  
 SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245F14 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 747;  
 Best local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESQNOQEKNEDELLELDKWSLWNMF 35  
 DB 634 TSLIHSLEESQNOQEKNEDELLELDKWSLWNMF 668

## RESULT 3

070606 PRELIMINARY: PRT: 748 AA.  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RA MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Vital variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12032; AAA76668.1;

DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 748 748  
 SQ SEQUENCE 748 AA: 84224 MW: 56BEDF186C67994B CRC64;

Query Match 100.0%; Score 188; DB 15; Length 748;  
 Best local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESQNOQEKNEDELLELDKWSLWNMF 35  
 DB 635 TSLIHSLEESQNOQEKNEDELLELDKWSLWNMF 669

## RESULT 4

070604 PRELIMINARY: PRT: 752 AA.  
 AC 070604;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RA MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Vital variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12030; AAA76666.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 752 752  
 SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 188; DB 15; Length 752;  
 Best local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESQNOQEKNEDELLELDKWSLWNMF 35  
 DB 639 TSLIHSLEESQNOQEKNEDELLELDKWSLWNMF 673

## RESULT 5

070605 PRELIMINARY: PRT: 752 AA.  
 AC 070605;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM852;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12031; AAA76667.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 RA AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 188; DB 15; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 35  
 |||||  
 DB 639 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 673

RESULT 6  
 ID 070608 PRELIMINARY; PRT; 752 AA.  
 AC 070608;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM87-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 RA AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 35  
 |||||

DB 639 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 673

RESULT 7  
 ID 078243 PRELIMINARY; PRT; 851 AA.  
 AC 078243;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env polypeptide.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
 RA Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 chronically infected HUT-78 cellular clone.";  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federic M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Macchi B., Mangano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 producer clones from HUT-78 infected with a patient HIV isolate.";  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Borselli A., Saggio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 productive clone.";  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL: 211530; CAA77628.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 RA AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 SQ SEQUENCE 851 AA; 96630 MW; 1A3767B987E98027 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 851;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 35  
 |||||  
 DB 634 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 668

RESULT 8  
 ID 089797 PRELIMINARY; PRT; 852 AA.  
 AC 089797;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker

infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM90-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 RA AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 NON\_TER 851  
 SEQUENCE 851 AA; 96630 MW; 1A3767B987E98027 CRC64;

RT Infected with HIV type 1 (HTLV type IIIB)."  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [12]  
RC SEQUENCE FROM N.A.  
RA STRAIN-LW90-2;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12053; AAA76685.1;  
DR EMBL: U12036; AAA76671.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;  
KW Transmembrane.  
SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF CRC64;  
  
Query Match 100.0%; Score 188; DB 15; Length 852;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 TSLIHSLEESONQOEKNEQLELDKWSLWNMF 35  
635 TSLIHSLEESONQOEKNEQLELDKWSLWNMF 669  
  
RESULT 9  
ID 085582 PRELIMINARY; PRT: 854 AA.  
AC 085582;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Envelope polypeptide.  
CN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
"Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone."  
RT J. Virol. 59:284-291(1986).  
RN [2]  
RN SEQUENCE FROM N.A.  
RL Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Buckler C.E.;  
RN Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92219406; PubMed=1373204;  
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;  
"Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T  
lymphocytes."  
RT J. Virol. 66:3151-3154(1992).  
DR EMBL: M19921; AAA44992.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;  
  
Query Match 100.0%; Score 188; DB 15; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 TSLIHSLEESONQOEKNEQLELDKWSLWNMF 35  
637 TSLIHSLEESONQOEKNEQLELDKWSLWNMF 671  
  
RESULT 10  
ID 072502 PRELIMINARY; PRT: 854 AA.  
AC 072502;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ENV polypeptide.  
CN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN-NLA-3;  
RX MEDLINE=96036482; PubMed=7483282;  
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
"Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
from primary virus cultures using the polymerase chain reaction."  
RT Virology 213:80-86(1995).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN-NLA-3;  
RX MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
"Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone."  
RT J. Virol. 59:284-291(1986).  
DR EMBL: U26942; AAB60578.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
FT CONFLICT 214 H -> L (IN REF. 2).  
FT CONFLICT 530 A -> S (IN REF. 2).  
FT CONFLICT 739 G -> D (IN REF. 2).  
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;  
  
Query Match 100.0%; Score 188; DB 15; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 TSLIHSLEESONQOEKNEQLELDKWSLWNMF 35  
637 TSLIHSLEESONQOEKNEQLELDKWSLWNMF 671  
  
RESULT 11  
ID 092877 PRELIMINARY; PRT: 856 AA.  
AC 092877;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Envelope glycoprotein.  
CN ENV.  
OS Simian-Human immunodeficiency virus.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=57667;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99098984; PubMed=9882298;

RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodroski J.G.;  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 RT responsible for the pathogenicity of a multiply passaged simian-human  
 RT immunodeficiency virus (SHIV-HXB2).";  
 RL J. Virol. 73:976-984(1999).

RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF041850, AAD12142.1; -;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97151 MW; C50BE038FB73659 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLESONQOEKNEOELLELDKWSLWNMF 35  
 DB 639 TSLIHSLESONQOEKNEOELLELDKWSLWNMF 673

## RESULT 12.

O74599 PRELIMINARY; PRT; 856 AA.  
 AC O74599;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCKI;  
 RX MEDLINE-90101366; PubMed-1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates.";  
 RL Virology 174:103-116(1990).

[2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCKI;  
 RA Iwatani Y.;  
 RN Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86068, BAA12995.1; -;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLESONQOEKNEOELLELDKWSLWNMF 35  
 DB 639 TSLIHSLESONQOEKNEOELLELDKWSLWNMF 673

## RESULT 13

O74090

ID 074090 PRELIMINARY; PRT; 856 AA.  
 AC 074090;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RX MEDLINE-90101366; PubMed-1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates.";  
 RL Virology 174:103-116(1990).

[2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RA Iwatani Y.;  
 RN Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86069, BAA13003.1; -;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 100.0%; Score 188; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLESONQOEKNEOELLELDKWSLWNMF 35  
 DB 639 TSLIHSLESONQOEKNEOELLELDKWSLWNMF 673

## RESULT 14

O90178 PRELIMINARY; PRT; 854 AA.  
 AC O90178;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95074930; PubMed-7983770;  
 RA Fang H., Pincus S.H.;  
 RT "Unique insertion sequence and pattern of CD4 expression in variants  
 RT selected with immunotoxins from human immunodeficiency virus type 1-  
 RT infected T cells.";  
 RL J. Virol. 69:75-81(1995).

[2]  
 RP SEQUENCE FROM N.A.  
 RA Fang H., Pincus S.H.;  
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
 RT immunotoxin-resistant variant T cell line.";  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF070521, AAC28452.1; -;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 854 AA; 96885 MW; 0808F3AE027C693B CRC64;

Query Match 97.9%; Score 184; DB 15; Length 854;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-14;  
 Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESQNOQENQELLELDKWSLWNWF 35  
 ||||||||||||||||||||||||||||||||  
 DB 637 TSLIHSLEESQNOQENQELLELDKWSLWNWF 671

## RESULT 15

Q78705 PRELIMINARY; PRT; 854 AA.  
 AC Q78705;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Envelope glycoprotein gp120.  
 GN ENV.  
 GN Human immunodeficiency virus type 1.  
 Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96013815; PubMed-7474132;  
 RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 RT resistant cell lines chronically infected with human immunodeficiency  
 RT virus type 1.";  
 RL J. Virol. 69:7122-7131(1995).  
 DR EMBL; LA2371; AAA86326.1;  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 854 AA; 97199 MW; 5B9512216533E256 CRC64;

Query Match 97.9%; Score 184; DB 15; Length 854;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-14;  
 Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESQNOQENQELLELDKWSLWNWF 35.  
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 DB 637 TSLIHSLEESQNOQENQELLELDKWSLWNWF 671

Search completed: May 16, 2003, 11:19:45  
 time : 26.5835 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 9.90964 Seconds  
(Without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-117  
Perfect score: 188  
Sequence: 1 TSLIHSLEESONOQEKNEOELLEDKWASLWNWF 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCBUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	35	1 US-08-073-028-74	Sequence 74, App1
2	188	100.0	35	3 US-08-484-223B-234	Sequence 234, App
3	188	100.0	35	4 US-08-554-616-74	Sequence 74, App1
4	188	100.0	35	4 US-09-082-279B-638	Sequence 638, App
5	188	100.0	35	4 US-09-082-279B-799	Sequence 799, App
6	188	100.0	35	4 US-08-474-349A-416	Sequence 416, App
7	188	100.0	35	4 US-09-315-304B-638	Sequence 638, App
8	188	100.0	35	4 US-09-315-304B-799	Sequence 799, App
9	188	100.0	36	1 US-08-073-028-1	Sequence 1, App1
10	188	100.0	36	3 US-08-486-099-1	Sequence 1, App1
11	188	100.0	36	3 US-09-071-877-1	Sequence 1, App1
12	188	100.0	36	3 US-08-360-107A-1	Sequence 1, App1
13	188	100.0	36	3 US-08-484-223B-1	Sequence 1, App1
14	188	100.0	36	3 US-08-484-223B-231	Sequence 231, App
15	188	100.0	36	3 US-08-919-597-1	Sequence 1, App1
16	188	100.0	36	3 US-08-475-668A-1	Sequence 1, App1
17	188	100.0	36	3 US-08-485-551A-1	Sequence 1, App1
18	188	100.0	36	3 US-08-471-913A-1	Sequence 1, App1
19	188	100.0	36	4 US-08-554-616-1	Sequence 1, App1
20	188	100.0	36	4 US-08-485-264A-1	Sequence 1, App1
21	188	100.0	36	4 US-09-082-279B-15	Sequence 15, App1
22	188	100.0	36	4 US-08-082-279B-497	Sequence 497, App
23	188	100.0	36	4 US-09-082-279B-498	Sequence 498, App
24	188	100.0	36	4 US-09-082-279B-561	Sequence 561, App
25	188	100.0	36	4 US-09-082-279B-603	Sequence 603, App
26	188	100.0	36	4 US-09-082-279B-630	Sequence 630, App
27	188	100.0	36	4 US-09-082-279B-631	Sequence 631, App

28	188	100.0	36	4 US-09-082-279B-705	Sequence 705, App
29	188	100.0	36	4 US-09-082-279B-834	Sequence 834, App
30	188	100.0	36	4 US-09-082-279B-1076	Sequence 1076, App
31	188	100.0	36	4 US-09-082-279B-1121	Sequence 1121, App
32	188	100.0	36	4 US-09-082-279B-1161	Sequence 1161, App
33	188	100.0	36	4 US-08-965-056-1	Sequence 1, App1
34	188	100.0	36	4 US-08-965-056-108	Sequence 108, App
35	188	100.0	36	4 US-09-045-920-1	Sequence 1, App1
36	188	100.0	36	4 US-08-474-349A-1	Sequence 399, App
37	188	100.0	36	4 US-08-474-349A-399	Sequence 400, App
38	188	100.0	36	4 US-08-474-349A-400	Sequence 413, App
39	188	100.0	36	4 US-08-474-349A-413	Sequence 413, App
40	188	100.0	36	4 US-09-315-304B-15	Sequence 15, App
41	188	100.0	36	4 US-09-315-304B-497	Sequence 497, App
42	188	100.0	36	4 US-09-315-304B-498	Sequence 498, App
43	188	100.0	36	4 US-09-315-304B-561	Sequence 561, App
44	188	100.0	36	4 US-09-315-304B-603	Sequence 603, App
45	188	100.0	36	4 US-09-315-304B-630	Sequence 630, App

## ALIGNMENTS

```
RESULT 1
US-08-073-028-74
: Sequence 74, Application US/08073028
: Patent No. 5464933
: GENERAL INFORMATION:
: APPLICANT: Bolognesi, Dani P.
: APPLICANT: Matthews, Thomas J.
: TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
: TITLE OF INVENTION: TRANSMISSION
: NUMBER OF SEQUENCES: 74
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/073,028
: FILING DATE: 07-JUN-1993
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7872-004-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 74:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 35 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: US-08-073-028-74

Query Match 100.0%; Score 188; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.3e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 TSLIHSLEESONOQEKNEOELLEDKWASLWNWF 35  
DB 1 TSLIHSLEESONOQEKNEOELLEDKWASLWNWF 35

RESULT 2  
US-08-484-223B-234  
Sequence 234, Application US/08484223B  
Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 234:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
8-484-223B-234

Query Match 100.0%; Score 188; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.3e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
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DB 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35

RESULT 3  
US-08-554-616-74  
Sequence 74, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-74

Query Match 100.0%; Score 188; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.3e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
|||||  
DB 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35

RESULT 4  
US-09-082-279B-638  
Sequence 638, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 638  
LENGTH: 35  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-638

Query Match 100.0%; Score 188; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.3e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
|||||



Db 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35

RESULT 5

US-09-082-279B-799

Sequence 799, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 799

LENGTH: 35

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-799

Query Match

Best Local Similarity 100.0%; Score 188; DB 4; Length 35;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35

Db 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35-

RESULT 6

US-08-474-349A-416

Sequence 416, Application US/08474349A

Patent No. 6333395

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA

NUMBER OF SEQUENCES: 517

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,349A

FILING DATE: 07-JUN-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-024

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 416:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-474-349A-416

Query Match

Best Local Similarity 100.0%; Score 188; DB 4; Length 35;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35

Db 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35

RESULT 7

US-09-315-304B-638

Sequence 638, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 638

LENGTH: 35

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-638

Query Match

Best Local Similarity 100.0%; Score 188; DB 4; Length 35;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35

Db 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35

RESULT 8

US-09-315-304B-799

Sequence 799, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: PastSeq for Windows Version 3.0  
SEQ ID NO 799  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-799

Query Match 100.0%; Score 188; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.3e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESONQOEKNEQLLELDKMSLWNMF 35  
DB 1 TSLHSLIEESONQOEKNEQLLELDKMSLWNMF 35

US-08-073-028-1  
Sequence 1, Application US/08073028  
Patent No. 5464933

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-1

Query Match 100.0%; Score 188; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESONQOEKNEQLLELDKMSLWNMF 35  
DB 2 TSLHSLIEESONQOEKNEQLLELDKMSLWNMF 36

RESULT 10  
US-08-486-099-1  
Sequence 1, Application US/08486099  
Patent No. 6013263

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Retaway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
TITLE OF INVENTION: B VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,099  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-099-1

Query Match 100.0%; Score 188; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESONQOEKNEQLLELDKMSLWNMF 35  
DB 2 TSLHSLIEESONQOEKNEQLLELDKMSLWNMF 36

RESULT 11  
US-09-071-877-1  
Sequence 1, Application US/09071877  
Patent No. 6015881  
GENERAL INFORMATION:  
APPLICANT: Kang, Myung-Chol  
APPLICANT: Bray, Brian  
APPLICANT: Lichty, Maynard  
APPLICANT: Wader, Catherine  
APPLICANT: Merutka, Gene  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS  
FILE REFERENCE: 7872-050  
CURRENT APPLICATION NUMBER: US/09/071,877  
CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus  
 US-09-071-877-1

Query Match  
 Best Local Similarity 100.0%; Score 188; DB 3; Length 36;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 35  
 Db 2 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 36

RESULT 12

US-08-360-107A-1  
 Sequence 1, Application US/08360107A  
 Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Petteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
 OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
 TITLE OF INVENTION: TRANSMISSION  
 NUMBER OF SEQUENCES: 149  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/360,107A  
 FILING DATE: 20-DEC-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-013  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-360-107A-1

Query Match  
 Best Local Similarity 100.0%; Score 188; DB 3; Length 36;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 35  
 Db 2 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 36

RESULT 13

US-08-484-223B-1  
 Sequence 1, Application US/08484223B  
 Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Petteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
 TITLE OF INVENTION: TRANSMISSION  
 NUMBER OF SEQUENCES: 245  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/484,223B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-029  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-484-223B-1

Query Match  
 Best Local Similarity 100.0%; Score 188; DB 3; Length 36;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 35  
 Db 2 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 36

RESULT 14

US-08-484-223B-231  
 Sequence 231, Application US/08484223B  
 Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Petteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 231:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-231

Query Match 100.0%; Score 188; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESQNOEKNEQELLELDKKNASLWNMF 35  
|||||  
DB 1 TSLHSLIEESQNOEKNEQELLELDKKNASLWNMF 35

RESULT 15  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dant P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 100.0%; Score 188; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESQNOEKNEQELLELDKKNASLWNMF 35  
|||||  
DB 2 TSLHSLIEESQNOEKNEQELLELDKKNASLWNMF 36

Search completed: May 16, 2003, 11:22:11  
Job time : 9.90964 secs

GenCore version 5.1.4.p5\_4578  
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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15:3213 Seconds  
(Without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-117  
Perfect score: 188  
Sequence: 1 TSLIHSLEESQNOEKNEQELLELDKWSLWNV 35

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 362568 seqs, 96450795 residues  
1 number of hits satisfying chosen parameters: 362568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCF\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCFUS\_PUBCOMB pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	36	9	US-09-874-475-16
2	188	100.0	36	9	US-10-116-797-1
3	188	100.0	36	9	US-09-493-346-1
4	188	100.0	36	10	US-09-796-202-10
5	188	100.0	36	10	US-09-779-451-5
6	188	100.0	36	10	US-09-834-628-1
7	188	100.0	36	10	US-09-854-816-1
8	188	100.0	36	10	US-09-854-816-108
9	188	100.0	37	9	US-09-848-616-176
10	188	100.0	46	10	US-09-779-451-41
11	188	100.0	56	10	US-09-779-451-4
12	188	100.0	177	9	US-10-040-349B-2
13	188	100.0	221	9	US-10-059-271-84
14	188	100.0	232	9	US-10-059-271-81
15	188	100.0	254	9	US-10-059-271-82
16	188	100.0	256	9	US-10-059-271-97
17	188	100.0	268	10	US-09-854-816-16
18	188	100.0	268	10	US-09-854-816-17
19	188	100.0	268	10	US-09-854-816-18

20	188	100.0	344	9	US-10-040-349B-1	Sequence 1, Appl1
21	188	100.0	345	9	US-10-026-741-49	Sequence 49, Appl1
22	188	100.0	345	10	US-09-779-451-8	Sequence 8, Appl1
23	188	100.0	391	9	US-10-059-271-93	Sequence 93, Appl1
24	188	100.0	519	9	US-09-756-551A-8	Sequence 8, Appl1
25	188	100.0	853	9	US-10-003-035-33	Sequence 33, Appl1
26	188	100.0	856	9	US-09-476-242-1	Sequence 1, Appl1
27	188	100.0	861	9	US-10-026-741-103	Sequence 103, Appl1
28	188	100.0	1101	9	US-10-003-035-53	Sequence 53, Appl1
29	188	100.0	1186	9	US-10-003-035-55	Sequence 55, Appl1
30	185	98.4	36	10	US-09-912-824-1	Sequence 1, Appl1
31	185	98.4	268	10	US-09-854-816-19	Sequence 19, Appl1
32	182	96.8	1231	9	US-10-059-271-94	Sequence 94, Appl1
33	180	95.7	268	10	US-09-854-816-13	Sequence 13, Appl1
34	179	95.2	233	10	US-09-854-816-50	Sequence 50, Appl1
35	179	95.2	268	10	US-09-854-816-9	Sequence 9, Appl1
36	179	95.2	269	10	US-09-854-816-12	Sequence 12, Appl1
37	178	94.7	269	10	US-09-854-816-46	Sequence 46, Appl1
38	177	94.1	269	10	US-09-854-816-28	Sequence 28, Appl1
39	176	93.6	268	10	US-09-854-816-26	Sequence 26, Appl1
40	176	93.6	619	10	US-09-891-609-4	Sequence 4, Appl1
41	176	93.6	646	10	US-09-891-609-2	Sequence 2, Appl1
42	176	93.6	847	10	US-09-476-242-2	Sequence 2, Appl1
43	175	93.1	46	10	US-09-854-816-109	Sequence 109, Appl1
44	175	93.1	267	10	US-09-854-816-38	Sequence 38, Appl1
45	175	93.1	268	10	US-09-854-816-41	Sequence 41, Appl1

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
: Sequence 16, Application US/09874475  
: Publication NO. US20020182592A1  
: GENERAL INFORMATION:  
: APPLICANT: Petropoulos, Christos J.  
: APPLICANT: Parkin, Neil T.  
: APPLICANT: Whitcomb, Jeanette  
: APPLICANT: Huang, Wei  
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
: FILE REFERENCE: 2793/65166  
: CURRENT APPLICATION NUMBER: US/09/874,475  
: CURRENT FILING DATE: 2001-06-04  
: NUMBER OF SEQ ID NOS: 16  
: SOFTWARE: PatentIn version 3.1  
: SEQ ID NO 16  
: LENGTH: 36  
: TYPE: PRT  
: ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16

Query Match 100.0%; Score 188; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6; 2e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESQNOEKNEQELLELDKWSLWNV 35  
Db 2 TSLIHSLEESQNOEKNEQELLELDKWSLWNV 36

RESULT 2  
US-10-116-797-1  
: Sequence 1, Application US/10116797  
: Publication No. US2003004411A1  
: GENERAL INFORMATION:  
: APPLICANT: Olsen, William C.  
: APPLICANT: Maddon, Paul J.  
: TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
: FILE REFERENCE: 64672-A  
: CURRENT APPLICATION NUMBER: US/10/116,797  
: CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match  
Best Local Similarity 100.0%; Score 188; DB 9; Length 36;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:  
APPLICANT: Madison, William C  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match  
Best Local Similarity 100.0%; Score 188; DB 9; Length 36;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

HT 4  
US-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)-(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match  
Best Local Similarity 100.0%; Score 188; DB 10; Length 36;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match  
Best Local Similarity 100.0%; Score 188; DB 10; Length 36;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

RESULT 6  
US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US20020119922A1  
GENERAL INFORMATION:  
APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DPL78  
US-09-834-628-1

Query Match  
Best Local Similarity 100.0%; Score 188; DB 10; Length 36;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

```

1      RESULT 7
2      US-09-854-816-1
3      Sequence 1, Application US/09854816
4      Patent No. US20020151473A1
5      GENERAL INFORMATION:
6      APPLICANT: Andrew C. Braisted
7      J. Kevin Judice
8      Robert S. McDowell
9      J. Christopher Pheilan
10     Melissa A. Starovasnik
11     James A. Wells
12     TITLE OF INVENTION: Constrained Helical Peptides and Methods of
13     Making Same
14     NUMBER OF SEQUENCES: 113
15     CORRESPONDENCE ADDRESSES:
16     ADDRESSEE: Genentech, Inc.
17     STREET: 1 DNA Way
18     CITY: South San Francisco
19     STATE: California
20     COUNTRY: USA
21     ZIP: 94080
22     COMPUTER READABLE FORM:
23     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
24     COMPUTER: IBM PC compatible
25     OPERATING SYSTEM: PC-DOS/MS-DOS
26     SOFTWARE: Winpatin (Genentech)
27     CURRENT APPLICATION DATA:
28     APPLICATION NUMBER: US/09/854,816
29     FILING DATE: 15-May-2001
30     CLASSIFICATION: <Unknown>
31     PRIOR APPLICATION DATA:
32     APPLICATION NUMBER: 08/965,056
33     FILING DATE: <Unknown>
34     ATTORNEY/AGENT INFORMATION:
35     NAME: Torchia, PhD., Timothy E.
36     REGISTRATION NUMBER: 36,700
37     REFERENCE/DOCKET NUMBER: P1005R2
38     TELECOMMUNICATION INFORMATION:
39     TELEPHONE: 650/425-8674
40     TELEFAX: 650/952-9881
41     INFORMATION FOR SEQ ID NO: 1:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 36 amino acids
44     TYPE: amino acid
45     TOPOLOGY: linear
46     MOLECULE TYPE: DP178
47     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
48     09-854-816-1
49
50     Query Match      100.0%; Score 188; DB 10; Length 36;
51     Best Local Similarity 100.0%; Pred. No. 6.2e-16;
52     Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0
53
54     1  TSLIHSLEESQNOEKNEQELLLEDKWASLNNWF 35
55     |||||||
56     2  TSLIHSLEESQNOEKNEQELLLEDKWASLNNWF 36
57
58     RESULT 8
59     US-09-854-816-108
60     Sequence 108, Application US/09854816
61     Patent No. US20020151473A1
62     GENERAL INFORMATION:
63     APPLICANT: Andrew C. Braisted
64     J. Kevin Judice
65     Robert S. McDowell
66     J. Christopher Pheilan
67     Melissa A. Starovasnik
68     James A. Wells
69     TITLE OF INVENTION: Constrained Helical Peptides and Methods of
70     Making Same
71     NUMBER OF SEQUENCES: 113

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854, 816
FILING DATE: 15-May-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965, 056
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-09-854-816-108

Query Match 100.0%; Score 188; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 6,2e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 TSLIHSLIEESQNOEQEKNEQLLELDKNASLWNWF 35
|||||
2 TSLIHSLIEESQNOEQEKNEQLLELDKNASLWNWF 36

RESULT 9
US-09-848-616-176
Sequence 176, Application US/09848616
Publication No. US20030054010A1
GENERAL INFORMATION:
APPLICANT: Seibel, Peter
APPLICANT: Dunant, Nicolas
APPLICANT: Bachmann, Martin
APPLICANT: Tisot, Alain
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0180002
CURRENT APPLICATION NUMBER: US/09/848,616
CURRENT FILING DATE: 2001-05-05
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 176
LENGTH: 37
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DP178c peptide
US-09-848-616-176

Query Match 100.0%; Score 188; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 6,4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 TSLIHSLIEESQNOEQEKNEQLLELDKNASLWNWF 35
|||||

```

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DB      3  TSLHSLIESONQOEKNEOELLELDKWSLWNMF 37
RESULT 10
US-09-779-451-41
; Sequence 41, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-41
Query Match      100.0%; Score 188; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 8e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TSLHSLIESONQOEKNEOELLELDKWSLWNMF 35
DB      12 TSLHSLIESONQOEKNEOELLELDKWSLWNMF 46
RESULT 11
US-09-779-451-4
; Sequence 4, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-4
Query Match      100.0%; Score 188; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 9.9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TSLHSLIESONQOEKNEOELLELDKWSLWNMF 35
DB      17 TSLHSLIESONQOEKNEOELLELDKWSLWNMF 51
RESULT 12
US-10-040-349B-2
; Sequence 2, Application US/10040349B
; Publication No. US20030082521A1
; GENERAL INFORMATION:
; APPLICANT: Brasseur, Robert
```

```
; APPLICANT: Charloreaux, Benoit
; APPLICANT: Chevalier, Michel
; APPLICANT: El Habib, Raphaelle
; APPLICANT: Krell, Tino
; TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
; FILE REFERENCE: 01-078-A
; CURRENT APPLICATION NUMBER: US/10/040,349B
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(177)
; OTHER INFORMATION: polypeptide derived from gp41 LAI
US-10-040-349B-2
Query Match      100.0%; Score 188; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.3e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TSLHSLIESONQOEKNEOELLELDKWSLWNMF 35
DB      105 TSLHSLIESONQOEKNEOELLELDKWSLWNMF 139
RESULT 13
US-10-059-271-84
; Sequence 84, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STERAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-84
Query Match      100.0%; Score 188; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TSLHSLIESONQOEKNEOELLELDKWSLWNMF 35
DB      132 TSLHSLIESONQOEKNEOELLELDKWSLWNMF 166
RESULT 14
US-10-059-271-81
; Sequence 81, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STERAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
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; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-81

```

```

Query Match          100.0%; Score 188; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TSLIHSLEESQNOQEKNEQELLELDKWSLWME 35
|||||
DB 145 TSLIHSLEESQNOQEKNEQELLELDKWSLWME 179

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RESULT 15
US-10-059-271-82
; Sequence 82, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

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```

Query Match          100.0%; Score 188; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSLEESQNOQEKNEQELLELDKWSLWME 35
|||||
DB 167 TSLIHSLEESQNOQEKNEQELLELDKWSLWME 201

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Search completed: May 16, 2003, 12:10:23  
Job time : 15.3213 secs

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XX	RESULT 1	
XX	AAAR64396	
XX	AAAR64396 standard; Peptide; 34 AA.	
XX	AAAR64396;	
XX	25-AUG-1995 (first entry)	
XX	DP-178 homologue 65 derived from HIV-1 has antiviral activity.	
XX	antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;	
XX	human immunodeficiency virus; transmembrane protein; gp41;	
XX	alpha helix; leucine zipper; DP-185.	
XX	Synthetic.	
XX	Key	Location/Qualifiers
XX	Modified-site	1
XX	/note= "optionally has an amino, acetyl-	
XX	9-Fluorenylmethoxy-carbonyl, hydrophobic or	
XX	macromolecular carrier gp. attached"	
XX	Modified-site	34
XX	/note= "optionally has a carboxyl, amide, hydrophobic	
XX	or macromolecular carrier gp. attached"	
XX	PN	WD9428920-A.
XX	PD	22-DEC-1994.
XX	PF	07-JUN-1994; 94WO-US05739.
XX	PR	07-JUN-1993; 93US-0073028.

PA (UYDU-) UNIV DUKE.  
 XX  
 PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Petterway SR, Wild CT;  
 DR WPI: 1995-036105/05.  
 XX  
 PT Computer search generated synthetic peptides - are inhibitors of  
 PT HIV transmission  
 XX  
 PS Claim 11; Page 133; 182pp; English.  
 CC AAR64365-97 are peptide derivs. of DP-178 (AAR64364) which have been  
 CC truncated at the amino terminus. DP-178 corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. The peptide derivs. were identified by a computer assisted  
 CC peptide sequence search. The peptides inhibit transmission to  
 CC uninfected cells, and can also be used as type and/or subtype  
 CC specific diagnostic tools.  
 XX  
 SQ Sequence 34 AA:  
 XX  
 Query Match 100.0%; Score 183; DB 16; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 SLIHSLIESONQOEKNEQELLELDKWSLWMWF 34  
 DB 1 SLIHSLIESONQOEKNEQELLELDKWSLWMWF 34  
 XX  
 RESULT 2  
 AAB52686  
 ID AAB52686 standard; Peptide: 34 AA.  
 XX  
 AC AAB52686;  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DE T20/DP178 peptide fragment #64.  
 XX  
 KW Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemottractant.  
 XX  
 PT Human immunodeficiency virus type 1.  
 XX  
 PN WO200066622-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PE 05-MAY-2000; 2000WO-US12371.  
 XX  
 PR 05-MAY-1999; 99US-0132686.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 XX  
 DR WPI: 2000-656493/63.  
 XX  
 PT Administration of peptide agents with a sequence corresponding to a  
 PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
 PT antagonist is used to modulate inflammation -  
 XX  
 PS Claim 12; Page 25; 148pp; English.  
 CC The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
 CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is

CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
 CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
 CC interacts with members of the formyl peptide receptor (FPR) family and  
 CC thereby up-regulates an inflammatory response, and acts as a potent  
 CC chemottractant and activator of human peripheral blood phagocytes  
 CC (but not T cells). The present peptide can be used to modulate an  
 CC inflammatory response in a subject.  
 XX  
 SQ Sequence 34 AA:  
 XX  
 Query Match 100.0%; Score 183; DB 21; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 SLIHSLIESONQOEKNEQELLELDKWSLWMWF 34  
 DB 1 SLIHSLIESONQOEKNEQELLELDKWSLWMWF 34  
 XX  
 RESULT 3  
 AAB14669  
 ID AAB14669 standard; peptide: 34 AA.  
 XX  
 AC AAB14669;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE HIV-1 isolate LAI gp41 C-helical domain peptide P-18, fragment #63.  
 XX  
 KW HIV-1; gp41 C-helical domain;  
 KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KW core 6-helix bundle; viral entry inhibition; immunogenic;  
 KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;  
 KW isolate LAI.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200040616-A1.  
 XX  
 PD 13-JUL-2000.  
 XX  
 PE 10-JAN-2000; 2000WO-US00456.  
 XX  
 PR 08-JAN-1999; 99US-0115404.  
 XX  
 PR 07-JAN-2000; 2000US-0480336.  
 XX  
 PA (WILD/) WILD C T.  
 PA (WEIS/) WEISS C D.  
 XX  
 PI Wild CT, Weiss CD;  
 XX  
 DR WPI: 2000-465959/40.  
 XX  
 PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -  
 XX  
 PS Disclosure; Page 33; 97pp; English.  
 XX  
 XX Sequences AAB14604-B14606 and AAB14607-B14670 represent peptides derived  
 XX from the C-helical domain of the gp41 envelope glycoprotein from  
 XX HIV-1 group M, subtype B, isolate LAI. The invention relates to raising  
 XX a neutralizing antibody response to a broad spectrum of HIV (human  
 XX immunodeficiency virus) strains and isolates, comprising the  
 XX administration of a peptide which corresponds to or mimics highly  
 XX conserved portions of gp41 which are important in mediating the  
 XX process of viral entry into host cells. Such peptides can correspond  
 XX to or mimic the coiled coil solution structure of the N-helical domain  
 XX (the heptad repeat region), or can correspond or mimic the C-helical  
 XX domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 XX or the gp41 core 6-helix bundle, which is formed by the interaction  
 XX of the N- and C-helical domains of three gp41 proteins. The peptides

CC can be administered either singly or as a combination (particularly  
CC a combination of N-helical and C-helical peptides), and can be  
CC multimerised. For example, N- and C-helical domain peptides can be  
CC alternately linked together to form a peptide which mimics the core  
CC 6-helix bundle. Administration of the peptide(s) generates a humoral  
CC response, with the production of antibodies against gp41 structures  
CC involved in viral entry. As these portions of gp41 are well conserved,  
CC such antibodies may be effective against a broad range of HIV strains  
CC and isolates. The peptide compositions may be administered as a  
CC prophylactic or therapeutic vaccine to generate antibodies which reduce  
CC or inhibit the ability of HIV to infect uninfected cells. A composition  
CC comprising polyclonal or monoclonal antibodies can be administered to  
CC reduce HIV infection of uninfected cells. Antibodies raised against  
CC entry-relevant gp41 structures may also be used therapeutically and as  
CC tools to further elucidate the mechanism of HIV cell entry.

SQ Sequence 34 AA:

Query Match 100.0%; Score 183; DB 21; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEOELELDKWSLMMWF 34  
|||||  
Db 1 SLIHSLEESQNOQEKNEOELELDKWSLMMWF 34

RESULT 4  
AAV89389  
ID AAV89389 standard; peptide; 34 AA.  
XX AAV89389;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Core polypeptide fragment T No. 924.  
XX  
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KM anti-fusogenic; differentiation factor; interleukin; interferon;  
KM colony stimulating factor; hormone; angiogenic factor.  
XX  
XX Unidentified.  
OS  
XX WO959615-A1.  
XX  
XX 25-NOV-1999.  
PD  
XX 20-MAY-1999; 99WO-US11219.  
XX  
PR 20-MAY-1998; 98US-0082279.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
XX WPI; 2000-136792/12.  
DR  
XX  
XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence -  
XX  
XX Disclosure: Page 35; 124pp; English.  
PS  
XX The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AAV8651-V90055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.

SQ Sequence 34 AA:

Query Match 100.0%; Score 183; DB 21; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY -1 SLIHSLEESQNOQEKNEOELELDKWSLMMWF 34  
|||||  
Db 1 SLIHSLEESQNOQEKNEOELELDKWSLMMWF 34

RESULT 5  
ABB00797  
ID ABB00797 standard; Peptide; 34 AA.  
XX  
XX ABB00797;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
DE Viral DP178/107-like region peptide T924.  
XX  
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
KM virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
KM infection.  
XX  
XX Virididae.  
OS  
XX  
FH Key Location/Qualifiers  
FT Modified-site 34 /note="C-terminal amide"  
FT  
XX  
XX MO200164013-A2.  
XX  
XX 07-SEP-2001.  
PD  
XX  
XX 07-FEB-2001; 2001WO-US03988.  
XX  
XX 29-FEB-2000; 2000US-0515965.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
XX  
XX WPI; 2001-514829/56.  
DR  
XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory syncytial virus  
PT infection -  
XX  
XX  
PS Disclosure: Page 49; 587pp; English.  
XX  
XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1/tat transmembrane protein gp41. The HRI  
CC and HR2 regions of proteins interact non-covalently with each other  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.

SQ Sequence 34 AA:

Query Match 100.0%; Score 183; DB 22; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOEKNEOELELDKWSLWNF 34  
 ||||||||||||||||||||||||||||||||  
 DB 1 SLIHSLSIESQNOEKNEOELELDKWSLWNF 34

RESULT 6  
 ABB02273  
 ID ABB02273 standard; Peptide; 34 AA.  
 AC ABB02273;  
 DT 03-JAN-2002 (first entry)  
 DE Viral core polypeptide, SEQ ID NO: 800.  
 XX  
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 XX virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 XX infection.  
 OS Viridiae.  
 XX  
 XX WO200164013-A2.  
 XX  
 XX 07-SEP-2001.  
 XX  
 XX 07-FEB-2001; 2001WO-US03988.  
 XX  
 XX 29-FEB-2000; 2000US-0515965.  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 XX  
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.  
 XX  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 XX fusion, useful for treating HIV and Respiratory Syncytial Virus  
 XX infection -  
 XX  
 XX Disclosure; Page 380; 587pp; English.  
 XX  
 XX The invention relates to isolated analogues of the heptad repeat region  
 XX peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 XX 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 XX HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 XX and HR2 regions of proteins interact non-covalently with each other  
 XX and/or with peptides derived from them. This interaction is required for  
 XX normal infectivity of viruses such as RSV and HIV. The heptad  
 XX repeat region peptide analogues may be used to inhibit respiratory  
 XX syncytial virus (RSV) infection in a cell. They may also be used to  
 XX inhibit HIV infection. The present sequence is a peptide provided in  
 XX the specification.  
 XX  
 XX Sequence 34 AA:  
 XX  
 XX Query Match 100.0%; Score 183; DB 22; Length 34;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOEKNEOELELDKWSLWNF 34  
 ||||||||||||||||||||||||||||||||  
 DB 1 SLIHSLSIESQNOEKNEOELELDKWSLWNF 34

RESULT 7  
 AAU13343  
 ID AAU13343 standard; Peptide; 34 AA.  
 XX  
 XX AAU13343;

XX 21-NOV-2001 (first entry)  
 DT  
 XX  
 XX DP178-1like/DP107-1like peptide T-924.  
 DE  
 XX  
 XX Anti-retroviral; DP178-1like; DP107-1like; transmembrane protein gp41;  
 XX antifusogenic; antiviral; HIV transmission; mutant; mutain.  
 XX  
 XX Human immunodeficiency virus 1 isolate LAI.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX FT Modified-site 34 /note="C-terminal amide"  
 XX  
 XX WO200151673-A2.  
 XX  
 XX 19-JUL-2001.  
 XX  
 XX 05-JUL-2000; 2000WO-US35727.  
 XX  
 XX 09-JUL-1999; 99US-0350841.  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 XX  
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
 XX WPI; 2001-442157/47.  
 XX  
 XX Identifying a compound that inhibits the formation of or disrupts a  
 XX DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
 XX or intracellular modulatory activity, by detecting the formation of a  
 XX DP107/DP178 complex -  
 XX  
 XX Disclosure; Page 68; 259pp; English.  
 XX  
 XX The present invention relates to peptides which exhibit anti-retroviral  
 XX activity. The peptides of the invention (AAU12559-AAU14009) comprise  
 XX DP178-1like and DP107-1like peptides. The DP178 peptide corresponds  
 XX to amino acids 639-673 of the transmembrane protein gp41 from human  
 XX immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
 XX corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
 XX also relates to a method of identifying compounds that inhibit the  
 XX formation of or disrupts a DP107/DP178 complex. The method comprises  
 XX detecting the formation of a DP107/DP178 complex, both in the presence  
 XX or absence of a test compound, in a reaction mixture containing DP107  
 XX and DP178 peptides. The method is useful for identifying compounds,  
 XX including small molecule compounds, which may themselves exhibit  
 XX antifusogenic, antiviral or intracellular modulatory activity. The  
 XX DP178-1like/DP107-1like peptides are useful to inhibit human and non-human  
 XX retroviral, particularly HIV, transmission to uninfected cells. The  
 XX present sequence represents one of the DP178-1like/DP107-1like peptides  
 XX of the invention.  
 XX  
 XX Sequence 34 AA:  
 XX  
 XX Query Match 100.0%; Score 183; DB 22; Length 34;  
 XX Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
 XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOEKNEOELELDKWSLWNF 34  
 ||||||||||||||||||||||||||||||||  
 DB 1 SLIHSLSIESQNOEKNEOELELDKWSLWNF 34

RESULT 8  
 AAB77790  
 ID AAB77790 standard; Peptide; 34 AA.  
 AC AAB77790;  
 XX  
 XX 19-APR-2001 (first entry)  
 DT  
 XX

KW	slmian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;
KM	human respiratory syncytial virus; human immunodeficiency virus; HIV.
XX	
OS	Human immunodeficiency virus type 1.
XX	
PN	WO20069902-A1.
XX	
PD	23-NOV-2000.
XX	
PE	17-MAY-2000; 2000WO-US13651.
XX	
PR	17-MAY-1999; 99US-0134406.
PR	10-SEP-1999; 99US-0153406.
XX	
PA	(CONJ-) CONJUCHEM INC.
XX	
PI	Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;
XX	
DR	WPI; 2001-007496/01.
XX	
PT	A modified peptide and a reactive group which is reactive with amino
PT	groups, hydroxyl groups, or thiol groups on blood components to form
PT	stable covalent bonds useful for treatment of viral infections, e.g.
PT	human immunodeficiency virus
XX	
PS	Disclosure; Page 135; 211pp; English.
XX	
CC	The present invention describes a modified anti-viral peptide (I)
CC	comprising a peptide that exhibits anti-viral activity and a reactive
CC	group which is reactive with amino groups, hydroxyl groups, or thiol
CC	groups on blood components to form stable covalent bonds. (I) has
CC	anti-viral and anti-fusogenic activities. (I) inhibits viral infection
CC	of cells by inhibiting cell-cell fusion or free virus infection or to
CC	reduce the level of membrane fusion events between two or more entities,
CC	e.g., virus-cell or cell-cell, relative to the level of membrane fusion
CC	that occurs in the absence of the peptide. (I) is useful in the
CC	treatment of patients who are suffering from viral infection, e.g. HIV,
CC	RSV, HPIV, MeV, and SIV. (I) may be administered prophylactically to
CC	previously uninfected individuals. This is useful in cases where an
CC	individual has been subjected to a high risk of exposure to a virus.
CC	By bonding of long-lived components of the blood, such as immunoglobulin,
CC	serum albumin, red blood cells and platelets the activity is extended
CC	for days to weeks. This is due to improved stability in vivo and a
CC	reduced susceptibility to peptidase or protease degradation. This
CC	minimises the need for more frequent, or even continual, administration
CC	of the peptides. AAB54784 to AAB55431 represent peptides used in the
CC	exemplification of the present invention.
XX	
SO	Sequence 34 AA:
	Query Match 100.0%; Score 183; DB 22; Length 34;
	Best Local Similarity 100.0%; Pred. No. 1.1e-15;
	Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 SLIHSLEESONQOEKNEOELLELPKMSLWMPF 34
DB	1 SLIHSLEESONQOEKNEOELLELPKMSLWMPF 34
RESULT 10	
AA64397	
ID	AA64397 standard; Peptide; 35 AA.
XX	
AC	AA64397;
XX	
DT	25-AUG-1995 (first entry)
XX	
DE	DP-178 homologue 66 derived from HIV-1 has antiviral activity.
XX	
KW	antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;
KW	human immunodeficiency virus; transmembrane protein; gp41;
KW	alpha helix; leucine zipper; DP-185.
XX	

OS Synthetic. Location/Qualifiers  
XX Key 1  
FH Modified-site /note= "optionally has an amino- acetyl,  
FT 9-fluorenylmethoxy-carbonyl, hydrophobic or  
FT macromolecular carrier gp. attached"  
FT Modified-site 35  
FT /note= "optionally has a carboxyl, amido, hydrophobic  
FT or macromolecular carrier gp. attached"  
XX WO9428920-A.  
XX 22-DEC-1994.  
XX PD  
XX 07-JUN-1994; 94WO-US05739.  
XX PF  
XX 07-JUN-1993; 93US-0073028.  
XX PR  
XX (UYDU-) UNIV DUKE.  
PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
PI Petterway SR, Wild CT;  
DR WPI; 1995-036105/05.  
XX Computer search generated synthetic peptides - are inhibitors of  
PT HIV transmission  
XX Claim 11; Page 133; 182pp; English.  
XX AAR64365-97 are peptide derivs. of DP-178 (AAR64364) which have been  
CC truncated at the amino terminus. DP-178 corresponds to amino acids  
CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
CC forms a putative alpha helix at the C-terminal end of the gp41  
CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
CC 558-595) which contains a leucine zipper motif. The peptides complex  
CC via non-covalent protein-protein interactions, and possess anti-viral  
CC activity. The peptide derivs. were identified by a computer assisted  
CC peptide sequence search. The peptides inhibit transmission to  
CC uninfected cells, and can also be used as type and/or subtype  
CC specific diagnostic tools.  
XX SQ  
XX Sequence 35 AA:  
Query Match 100.0%; Score 183; DB 16; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 SLIHSLSIESQNOQEKNEDELLELDKWSLWMNF 34  
|||||  
2 SLIHSLSIESQNOQEKNEDELLELDKWSLWMNF 35  
RESULT 11  
AAB52687  
ID AAB52687 standard; Peptide; 35 AA.  
XX AC.  
XX AAB52687;  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/DP178 peptide fragment #65.  
XX ANtlinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
KW chemottractant.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO20006622-A1.  
XX PD 09-NOV-2000.

XX 05-MAY-2000; 2000WO-US12371.  
PF 05-MAY-1999; 99US-0132686.  
PR (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
PI WPI; 2000-656493/63.  
XX Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX Claim 12; Page 25; 148pp; English.  
XX The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemottractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX SQ  
XX Sequence 35 AA:  
Query Match 100.0%; Score 183; DB 21; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 SLIHSLSIESQNOQEKNEDELLELDKWSLWMNF 34  
|||||  
2 SLIHSLSIESQNOQEKNEDELLELDKWSLWMNF 35  
RESULT 12  
AAB14670  
ID AAB14670 standard; peptide; 35 AA.  
XX AC.  
XX AAB14670;  
XX DT 24-NOV-2000 (first entry)  
XX DE HIV-1 isolate LAI gp41 C-helical domain peptide P-18, fragment #64.  
XX HIV-1; gp41 C-helical domain;  
KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
KW core 6-helix bundle; viral entry inhibition; immunogenic;  
KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;  
KW isolate LAI.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO200040616-A1.  
XX 13-JUL-2000.  
XX PF 10-JAN-2000; 2000WO-US00456.  
XX PR 08-JAN-1999; 99US-0115404.  
PR 07-JAN-2000; 2000US-0480336.  
XX (WILD/) WILD C T.  
PA (WEISS/) WEISS C D.  
XX WILD CT, Weiss CD;  
PI WPI; 2000-465959/40.  
XX DR



PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -

Disclosure: Page 34; 97pp; English.

CC Sequences AAB14604-B14606 and AAB14607-B14670 represent peptides derived  
 CC from the C-helical domain of the gp41 envelope glycoprotein from  
 CC HIV-1 group M, subtype B, isolate LAI. The invention relates to raising  
 CC a neutralising antibody response to a broad spectrum of HIV (human  
 CC immunodeficiency virus) strains and isolates, comprising the  
 CC administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the  
 CC process of viral entry into host cells. Such peptides can correspond  
 CC to or mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane/proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly  
 CC a combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can be  
 CC alternately linked together to form a peptide which mimics the core  
 CC 6-helix bundle. Administration of the peptide(s) generates a humoral  
 CC response, with the production of antibodies against gp41 structures  
 CC involved in viral entry. As these portions of gp41 are well conserved,  
 CC such antibodies may be effective against a broad range of HIV strains  
 CC and isolates. The peptide compositions may be administered as a  
 CC prophylactic or therapeutic vaccine to generate antibodies which reduce  
 CC or inhibit the ability of HIV to infect uninfected cells. A composition  
 CC comprising polyclonal or monoclonal antibodies can be administered to  
 CC reduce HIV infection of uninfected cells. Antibodies raised against  
 CC entry-relevant gp41 structures may also be used therapeutically and as  
 CC tools to further elucidate the mechanism of HIV cell entry.

SO Sequence 35 AA:

Query Match 100.0%; Score 183; DB 21; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSIIESNQOEKNEDELLEDKWASLWVNF 34  
 ||||||||||||||||||||||||||||||||  
 DB 2 SLIHSIIESNQOEKNEDELLEDKWASLWVNF 35

RESULT 13

AA893388  
 AAY893388 standard; peptide; 35 AA.

AC AAY893388;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 923.

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

PN WO959615-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US11219.

PR 20-MAY-1998; 98US-0082279.

PA (TRIM-) TRIMERIS INC.

XX

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

PS Disclosure: Page 35; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

SO Sequence 35 AA:

Query Match 100.0%; Score 183; DB 21; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSIIESNQOEKNEDELLEDKWASLWVNF 34  
 ||||||||||||||||||||||||||||||||  
 DB 2 SLIHSIIESNQOEKNEDELLEDKWASLWVNF 35

RESULT 14

ABB00634  
 ABB00634 standard; peptide; 35 AA.

AC ABB00634;

DT 03-JAN-2002 (first entry)

DE Viral DP178/107-like region peptide T715.

KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HRL; HR2;  
 KW infection.

OS Virididae.

FT Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal is substituted by Ac"

FT Modified-site 35 /note= "C-terminal amide"

PN WO200164013-A2.

PD 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US03988.

PR 29-FEB-2000; 2000US-0515965.

PA (TRIM-) TRIMERIS INC.

PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

DR WPI; 2001-514829/56.

XX



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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 11.4699 Seconds

(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-118

Perfect score: 183

Sequence: 1 SLIHSLEESQNOQEKNEQELLELDKWSLWNV 34

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183	100.0	851	2 S33985	env polypeptide - huma
2	183	100.0	854	2 S13288	env polypeptide - huma
3	183	100.0	856	1 VCLJH3	env polypeptide pr
4	183	100.0	861	1 VCLJH3	env polypeptide pr
5	174	95.1	443	2 C41621	env polypeptide pr
6	174	95.1	856	1 VCLJH3	env polypeptide pr
7	174	95.1	856	1 VCLJH3	env polypeptide pr
8	174	95.1	861	1 VCLJH3	env polypeptide pr
9	171	93.4	358	2 S21998	env polypeptide pr
10	171	93.4	358	2 S21998	env polypeptide pr
11	170	92.9	347	2 S21996	env polypeptide pr
12	167	91.3	847	2 T09448	env polypeptide pr
13	167	91.3	847	2 S13289	env polypeptide pr
14	166	90.7	445	2 A41621	env polypeptide pr
15	165	90.2	358	2 S22002	env polypeptide pr
16	165	90.2	358	2 S22002	env polypeptide pr
17	165	90.2	358	2 S22002	env polypeptide pr
18	165	90.2	852	2 S70417	env polypeptide pr
19	165	90.2	852	2 T12016	env polypeptide pr
20	164	89.6	357	2 S22004	env polypeptide pr
21	164	89.6	855	1 VCLJH3	env polypeptide pr
22	162	88.5	843	1 H44001	env polypeptide pr
23	162	88.5	855	1 S54384	env polypeptide pr
24	162	88.5	855	1 S54384	env polypeptide pr
25	161	88.0	357	2 S22006	env polypeptide pr
26	160	87.4	846	1 VCLJH3	env polypeptide pr
27	158	86.3	357	2 S21992	env polypeptide pr
28	158	86.3	852	1 VCLJH3	env polypeptide pr
29	156	85.2	729	1 VCLJH3	env polypeptide pr

30	156	85.2	861	1 VCLJH3	env polypeptide pr
31	155	84.7	859	2 T01672	env polypeptide pr
32	154	84.2	454	2 B41621	env polypeptide pr
33	152	83.1	868	1 VCLJH3	env polypeptide pr
34	148	80.9	136	2 J00266	env polypeptide pr
35	148	80.9	136	2 J00266	env polypeptide pr
36	141	77.0	854	1 VCLJH3	env polypeptide pr
37	137	74.9	856	1 A44963	env polypeptide pr
38	135	73.8	357	2 S21990	env polypeptide pr
39	135	73.8	877	2 S49197	env polypeptide pr
40	118	64.5	863	2 A53034	env polypeptide pr
41	86	47.0	881	1 VCLJH3	env polypeptide pr
42	86	47.0	881	2 S03068	env polypeptide pr
43	86	47.0	889	1 VCLJH3	env polypeptide pr
44	85	46.4	151	2 S30448	env polypeptide pr
45	85	46.4	151	2 S30452	env polypeptide pr

## ALIGNMENTS

Result 1  
S33985  
env polypeptide - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-References: EMBL:211530; NID:960192; PIDN:CAA7628.1; PID:960199  
C:Superfamily: type E retrovirus env polypeptide

Query Match  
Best Local Similarity 100.0%; Score 183; DB 2; Length 851;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLIHSLEESQNOQEKNEQELLELDKWSLWNV 34  
Db 635 SLIHSLEESQNOQEKNEQELLELDKWSLWNV 668

Result 2  
S13288  
env polypeptide - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polypeptide

Query Match  
Best Local Similarity 100.0%; Score 183; DB 2; Length 854;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLIHSLEESQNOQEKNEQELLELDKWSLWNV 34  
Db 638 SLIHSLEESQNOQEKNEQELLELDKWSLWNV 671

Result 3  
VCLJH3

env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03973  
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora-  
nberger, J.A.; Papas, T.S.; Chareyb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A93353; MUID:85111123; PMID:2578615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAAA442  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:1-316/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status predic  
Query Match 100.0%; Score 183; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 4,1e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEDELLELDKASLWNF 34  
DB 640 SLIHSLEESQNOEKNEDELLELDKASLWNF 673

VCJLV  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; MUID:85093333; PMID:2981635  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <MAI>  
A:Cross-references: GB:K02013; NID:9326417; PIDN:AAB59751.1; PID:9326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:1-316/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (asn) (covalent) #status predic  
Query Match 100.0%; Score 183; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 4,1e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEDELLELDKASLWNF 34  
DB 645 SLIHSLEESQNOEKNEDELLELDKASLWNF 678

RESULT 5  
env polypeptide precursor - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polypeptide

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Gull, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity.  
A:Reference number: A41621; MUID:92107924; PMID:1765038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015  
A:Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:424-443/Domain: transmembrane #status predicted <TM>  
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:  
Query Match 95.1%; Score 174; DB 2; Length 443;  
Best Local Similarity 94.1%; Pred. No. 2,4e-13;  
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEDELLELDKASLWNF 34  
DB 380 SLIHSLEESQNOEKNEDELLELDKASLWNF 413

VCJLV  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LV)  
N:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03974  
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A:Title: Nucleotide structure and expression of the human AIDS/lymphadenopathy retr  
A:Reference number: A93355; MUID:85111157; PMID:2982104  
A:Accession: A03974  
A:Molecule type: DNA  
A:Residues: 1-856 <MUE>  
A:Cross-references: GB:K02083; NID:9555008; PIDN:AAB59873.1; PID:9328559  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:1-316/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status pre  
Query Match 95.1%; Score 174; DB 1; Length 856;  
Best Local Similarity 97.0%; Pred. No. 4,9e-13;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEDELLELDKASLWNF 33  
DB 640 SLIHSLEESQNOEKNEDELLELDKASLWNF 672

VCJLV  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997

C:Accession: A24774  
 R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; MUID:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STA>  
 A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
 C:Genetics: env  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 95.1%; Score 174; DB 1; Length 856;  
 Best Local Similarity 94.1%; Pred. No. 4,9e-13;  
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSILIESONOEKNEOELELDKWSLWNMF 34  
 DB 640 SLIYTLIESONOEKNEOELELDKWSLWNMF 673

RESULT 8  
 VCLJSC  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
 virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics: env  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-861/Product: env polyprotein #status predicted <EP>  
 F:7,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 95.1%; Score 174; DB 1; Length 861;  
 Best Local Similarity 94.1%; Pred. No. 5e-13;  
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSILIESONOEKNEOELELDKWSLWNMF 34  
 DB 645 SLIYTLIESONOEKNEOELELDKWSLWNMF 678

RESULT 9  
 S21994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 27B  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21990  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STEL>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140,'X',142-312,'X',314-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:g60179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 93.4%; Score 171; DB 2; Length 357;  
 Best Local Similarity 91.2%; Pred. No. 4,3e-13;  
 Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSILIESONOEKNEOELELDKWSLWNMF 34  
 DB 141 SLIYTLIESONOEKNEOELELDKWSLWNMF 174

RESULT 10  
 S21998  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 28  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21998; S70425  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21998  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STEL>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70425  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222,'X',224-358 <STE2>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 93.4%; Score 171; DB 2; Length 358;  
 Best Local Similarity 91.2%; Pred. No. 4,3e-13;  
 Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSILIESONOEKNEOELELDKWSLWNMF 34  
 DB 142 SLIYTLIESONOEKNEOELELDKWSLWNMF 175

RESULT 11  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S70422; S21996  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <ST2>  
 A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129  
 A:Experimental source: patient 27L  
 A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polypeptide

Query Match 92.9%; Score 170; DB 2; Length 357;  
Best Local Similarity 93.9%; Pred. No. 5,6e-13;  
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLHSLIESQNOQEKNEDELLELDKWSLWNF 34  
DB 142 LLYTLIESQNOQEKNEDELLELDKWSLWNF 174

RESULT 12

envelope glycoprotein - human immunodeficiency virus type 1 (strain JFRL)

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
C:Accession: T09448  
R:Rang, S.; Vinters, H.V.; Akashli, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,  
submitted to the EMBL Data Library, July 1996  
Reference number: Z1673  
Accession: T09448  
Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAM>

A:Cross-references: EMBL:U63632; NID:q1465777; PID:q1465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

Query Match 91.3%; Score 167; DB 2; Length 847;  
Best Local Similarity 91.2%; Pred. No. 3,4e-12;  
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLHSLIESQNOQEKNEDELLELDKWSLWNF 34  
DB 631 SEIYTLIESQNOQEKNEDELLELDKWSLWNF 664

RESULT 13

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13289  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Disigne, A.; Idler, K.; Zack, J.A.  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13289; MUID:91043044; PMID:2172833  
Accession: S13289  
Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-847 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 91.3%; Score 167; DB 2; Length 847;  
Best Local Similarity 91.2%; Pred. No. 3,4e-12;  
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLHSLIESQNOQEKNEDELLELDKWSLWNF 34  
DB 631 SEIYTLIESQNOQEKNEDELLELDKWSLWNF 664

RESULT 14

env polypeptide M - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypeptide

M:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

C:Accession: A41621

R:Burger, H.; Weisner, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: A41621

A:Molecule type: DNA

A:Residues: 1-445 <BUB>

A:Cross-references: GB:M77228; NID:9328627; PID:NAB03790.1; PID:9555013

A:Note: this virus was isolated from the mother

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:426-445/Domain: transmembrane #status predicted <TM>

F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding si

Query Match 90.7%; Score 166; DB 2; Length 445;  
Best Local Similarity 88.2%; Pred. No. 2,2e-12;  
Matches 30; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLHSLIESQNOQEKNEDELLELDKWSLWNF 34  
DB 382 SLIYTLIESQNOQEKNEDELLELDKWSLWNF 415

RESULT 15

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 3L  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S22002; S70418  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as de

A:Reference number: S21990

A:Accession: S22002

A:Molecule type: DNA

A:Residues: 1-358 <STEL>

A:Cross-references: EMBL:X61352; NID:960186; PID:CAA43616.1; PID:960187

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333, 'X', 335-358 <STRE2>

A:Cross-references: EMBL:X61352; NID:960186

C:Superfamily: type E retrovirus env polypeptide

Query Match 90.2%; Score 165; DB 2; Length 358;  
Best Local Similarity 88.2%; Pred. No. 2,2e-12;  
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLHSLIESQNOQEKNEDELLELDKWSLWNF 34  
DB 142 SLIYTLIESQNOQEKNEDELLELDKWSLWNF 175

Search completed: May 16, 2003, 11:25:08

Job time: 12.4699 secs

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 5.73494 Seconds  
(without alignments)  
245.895 Million cell updates/sec

Title: us-09-623-533a-118  
Perfect score: 183  
Sequence: 1 SLIHSLESONOQEKNEELLELDKWSLMMNF 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues  
al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	100.0	851	1 ENV_HV1B8	P04582 human immun
2	183	100.0	856	1 ENV_HV1B1	P03375 human immun
3	183	100.0	856	1 ENV_HV1H2	P04578 human immun
4	183	100.0	856	1 ENV_HV1H3	P04624 human immun
5	183	100.0	856	1 ENV_HV1LW	O70626 human immun
6	183	100.0	861	1 ENV_HV1BR	P03377 human immun
7	180	98.4	853	1 ENV_HV1MF	P15551 human immun
8	174	95.1	856	1 ENV_HV1PV	P03376 human immun
9	174	95.1	856	1 ENV_HV1SC	P03878 human immun
10	174	95.1	856	1 ENV_HV1W1	P13872 human immun
11	172	94.0	852	1 ENV_HV1S3	P15549 human immun
12	171	93.4	847	1 ENV_HV1S1	P15550 human immun
13	168	91.8	847	1 ENV_HV1W2	P05880 human immun
14	167	91.3	867	1 ENV_HV1J3	P12489 human immun
15	165	90.2	856	1 ENV_HV1M2	P05877 human immun
16	164	89.6	855	1 ENV_HV1A2	P03378 human immun
17	163	89.1	853	1 ENV_HV1E1	P04581 human immun
18	163	89.1	865	1 ENV_HV1RH	P04579 human immun
19	162	88.5	843	1 ENV_HV1Y2	P35961 human immun
20	162	88.5	853	1 ENV_HV1Z2	P12487 human immun
21	162	88.5	855	1 ENV_HV1Z6	P04580 human immun
22	161	88.0	855	1 ENV_HV1OY	P20888 human immun
23	160	87.4	846	1 ENV_HV1ND	P18799 human immun
24	158	86.3	852	1 ENV_HV1BN	P12488 human immun
25	157	85.8	848	1 ENV_HV1JR	P20871 human immun
26	156	85.2	861	1 ENV_HV1KB	P31819 human immun
27	155	84.7	859	1 ENV_HV1MA	P04583 human immun
28	152	83.1	868	1 ENV_HV1C4	P05879 human immun
29	150	82.0	863	1 ENV_HV1Z8	P05882 human immun
30	141	77.0	854	1 ENV_HV1CZ	P17281 chimpanzee
31	137	74.9	856	1 ENV_HV1ZH	P05881 human immun
32	90	49.2	854	1 ENV_HV1AI	O05837 simian immun
33	86	47.0	881	1 ENV_STVMK	P05884 simian immun

ALIGNMENTS

RESULT 1	34	86	47.0	882	1	ENV_STVM1	P05885 simian immun
ENV_HV1B8	35	85	46.4	885	1	ENV_STVS4	P12492 simian immun
ID ENV_HV1B8	36	84	45.9	859	1	ENV_HV2D2	P15831 human immun
AC P04582;	37	84	45.9	860	1	ENV_HV2BE	P18094 human immun
DT 13-AUG-1987 (rel. 05, Last sequence update)	38	82	44.8	880	1	ENV_STVM1	P11267 simian immun
DT 15-JUL-1999 (rel. 38, Last annotation update)	39	80	43.7	859	1	ENV_HV2CA	P24105 human immun
DE Envelope glycoprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].	40	80	43.7	889	1	ENV_STVSP	P19503 simian immun
GN ENV.	41	77	42.1	846	1	ENV_HV2SB	P12449 human immun
OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).	42	77	42.1	851	1	ENV_HV2D1	P17755 human immun
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.	43	77	42.1	851	1	ENV_HV2G1	P18040 human immun
OX NCBI_TaxID=11684;	44	77	42.1	858	1	ENV_HV2RO	P04577 human immun
RP MEDLINE=8511123; PubMed=2578615;	45	77	42.1	859	1	ENV_HV2ST	P20872 human immun
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Peteway S.R. Jr., Pearson M.D., Lautenberger J.A., Papas T.S., Ghayab J., Chang N.T., Gallo R.C., Wong-Staal F.;							
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.;"							
RL Nature 313:277-284(1985).							
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CC EMBL, K02011; AAA44661.1; -							
CC HIV, K02011; ENVSBR8.							
DR GLYCOSULEDB: P04582; -							
DR InterPro: IPR000328; ENV_GP41.							
DR Pfam: PF00516; GP120; 1.							
DR Pfam: PF00517; GP41; 1.							
KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.							
KW SIGNAL.	1	30					
FT CHAIN	31	506					EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN	507	851					TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID	54	74					BY SIMILARITY.
FT DISULFID	119	205					BY SIMILARITY.
FT DISULFID	126	196					BY SIMILARITY.
FT DISULFID	131	157					BY SIMILARITY.
FT DISULFID	218	247					BY SIMILARITY.
FT DISULFID	228	239					BY SIMILARITY.
FT DISULFID	296	331					BY SIMILARITY.
FT DISULFID	378	440					BY SIMILARITY.
FT DISULFID	385	413					BY SIMILARITY.
FT CARBOHD	88	88					N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	136	136					N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD	141	141					N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 851 AA: 96644 MW: D16A3C90857785F1 CRC64:

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Query Match 100.0%; Score 183; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 6.5e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 SLIHSLSIESQNOEKNEDELLELDKWSLWVNF 34
DB 635 SLIHSLSIESQNOEKNEDELLELDKWSLWVNF 668

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RESULT 2
ENV_HV1B1 STANDARD: PRT: 856 AA.
ID ENV_HV1B1
AC P03375;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV
RA Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
RA Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RA NCBI_TaxID=11678;

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RN SEQUENCE FROM N.A.
RP MEDLINE=8511123; PubMed=2578615;
RX Ratter L., Haseltine W., Palanca R., Livak K.J., Starcich B.R.,
RA Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumesler K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Pappas T.S., Grayed J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RA Nature 313:277-284(1985).
RN [2]
RN DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RP MEDLINE=90285159; PubMed=2355006;
RX Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RA "Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells."
RT J. Biol. Chem. 265:10373-10382(1990).
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CC EMBL: M15654; AAA44205.1;
DR PIR: A03973; VCLJH3.
DR HIV: M15654; ENV5BH102.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coal protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
KW CHAIN 1
KW CHAIN 30
FT CHAIN 512 856
FT CHAIN 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
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FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 366 366
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA: 97224 MW: 0BF6B1A18531BB27 CRC64:

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Query Match 100.0%; Score 183; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 6.5e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 SLIHSLSIESQNOEKNEDELLELDKWSLWVNF 34
DB 640 SLIHSLSIESQNOEKNEDELLELDKWSLWVNF 673

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RESULT 3
ENV_HV1B2 STANDARD: PRT: 856 AA.
AC P04578; 009779;

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DT 13-AUG-1987 (Rel. 05, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11706;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8729196; PubMed=3040055;  
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,  
 RA Gallo R.C., Wong-Staal F.;  
 RT "Complete nucleotide sequences of functional clones of the AIDS  
 virus ";  
 RL AIDS Res. Hum. Retroviruses 3:57-69(1987).  
 RN [2]  
 RP REVISIONS.  
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,  
 RA Gallo R.C., Wong-Staal F.;  
 CC Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 CC EMBL; K03455; AAB50262.1; -;  
 DR EMBL; AF038399; AAB99976.1; -;  
 DR EMBL; AF038119; AAC82596.1; -;  
 DR HTV; K03455; ENVSHXB2.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00517; GP41; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT 1 30  
 FT CHAIN 511 856  
 FT DISULEID 54 74  
 FT DISULEID 119 205  
 FT DISULEID 126 196  
 FT DISULEID 131 157  
 FT DISULEID 131 247  
 FT DISULEID 218 239  
 FT DISULEID 228 331  
 FT DISULEID 296 378  
 FT DISULEID 378 445  
 FT DISULEID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
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 FT CARBOHYD 230 230  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
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 FT CARBOHYD 295 295  
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 FT CARBOHYD 332 332  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AR85107PE0 CRC64;  
 Query Match 100.0%; Score 183; DB 1; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SLHSLIEESQNOQEKNEDELLDKWASLWNP 34  
 Db 640 SLHSLIEESQNOQEKNEDELLDKWASLWNP 673  
 |||||  
 ID ENV\_HV1H3 STANDARD; PRT; 856 AA.  
 AC P04624;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85228248; PubMed=2988795;  
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,  
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;  
 RT "HIV-III env gene products synthesized in E. coli are recognized by  
 RT antibodies present in the sera of AIDS patients.";  
 RL Cell 41:979-986(1985).  
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 CC -----  
 CC EMBL; M14100; AAA44679.1; -;  
 DR HTV; M14100; ENVSHXB3.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT 1 30  
 FT CHAIN 511 856  
 FT DISULEID 119 205  
 FT DISULEID 126 196  
 FT DISULEID 131 157  
 FT DISULEID 131 247  
 FT DISULEID 218 239  
 FT DISULEID 228 239  
 FT DISULEID 296 331  
 FT DISULEID 378 445  
 FT DISULEID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 856 AA; 97188 MW; 3373C688B84C1AFC CRC64;

Query Match 100.0%; Score 183; DB 1; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 6,5e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESONOEKNEOLLELDKASLWNMF 34  
 DB 640 SLIHSLEESONOEKNEOLLELDKASLWNMF 673

RESULT 5  
 ENV\_HV1LW STANDARD; PRT; 856 AA.  
 AC Q70626;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DT Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 ENV.

OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).  
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.  
 NC NCI\_TaxID=82834;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93127297; PubMed=7826699;  
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.J.  
 RT "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB)".  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
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 CC -----  
 DR EMBL: U12055; AAA76690.1; -  
 DR GlycoSuiteDB: Q70626; -  
 DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.  
 FT CHAIN 1 30  
 FT CHAIN 511 511  
 FT CHAIN 512 512  
 FT CHAIN 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 131 247  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 289 289  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392  
 FT CARBOHYD 397 397  
 FT CARBOHYD 406 406  
 FT CARBOHYD 448 448  
 FT CARBOHYD 463 463  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 624 624  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

Query Match 100.0%; Score 183; DB 1; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 6,5e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESONOEKNEOLLELDKASLWNMF 34  
 DB 640 SLIHSLEESONOEKNEOLLELDKASLWNMF 673

RESULT 6  
 ENV\_HV1BR STANDARD; PRT; 861 AA.  
 ID ENV\_HV1BR  
 AC P03377;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DT Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 ENV.  
 OS Human immunodeficiency virus type 1 (BR isolate) (HIV-1).  
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.  
 NC NCI\_TaxID=11686;  
 RN [1]



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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA: 96912 MW: 3377B93B6F22ABA CRC64.

Query Match
Best Local Similarity 98.4% Score 180; DB 1; Length 853;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 SLIHSLSIESQNOQEKNEQELLELDKWSLWMWF 34
|||||:|||||:|||||:|||||:|||||:
638 SLIHSLSIESQNOQEKNEQELLELDKWSLWMWF 671

RESULT 8
ENV_HV1PV STANDARD: PRT: 856 AA.
ID ENV_HV1PV
AC P03376:
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/Lymphadenopathy retrovirus."
RC Nature 313:450-458(1985).
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: K02083; AAB59873.1;
DR EMBL: X01762; CA25903.1; ALT_SEQ.
DR PIR: A03974; VCLJVL.
DR HIV: K02083; ENVSPV22.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
DR AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
KW SIGNAL.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 511 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.

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FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA: 97339 MW: 5FCDB1DC3C1209B3 CRC64.

Query Match
Best Local Similarity 95.1% Score 174; DB 1; Length 856;
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 SLIHSLSIESQNOQEKNEQELLELDKWSLWMWF 33
|||||:|||||:|||||:|||||:|||||:
640 SLIHSLSIESQNOQEKNEQELLELDKWSLWMWF 672

RESULT 9
ENV_HV1SC STANDARD: PRT: 856 AA.
ID ENV_HV1SC
AC P05878:
DT 01-NOV-1988 (rel. 09, Created)
DT 01-NOV-1988 (rel. 09, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates."
RT Virology 164:531-536(1988).
CC MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ANC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC -----

DR EMBL: M17450; -; NOT\_ANNOTATED\_CDS.

DR PIR: B28922; VCLJSC.

DR HIV: M17450; ENV5SC.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Glycoprotein; Transmembrane; Signal.

KW Signal.

FT CHAIN 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT SITE 760 760

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 160

FT DISULFID 219 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 439

FT DISULFID 383 412

FT CARBOHYD 87 129

FT CARBOHYD 129 135

FT CARBOHYD 135 135

FT CARBOHYD 140 140

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 295 295

FT CARBOHYD 301 301

FT CARBOHYD 302 302

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 384 384

FT CARBOHYD 394 394

FT CARBOHYD 400 400

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

FT CARBOHYD 674 674

FT CARBOHYD 816 816

SO SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match 95.1%; Score 174; DB 1; Length 856;

Best Local Similarity 94.1%; Pred. No. 8.3e-14;

Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIEESQNOOEKNEOLELIDKWSLWNMF 34

DB 640 SLIYTLIEESQNOOEKNEOLELIDKWSLWNMF 673

RESULT 10

ENV\_HV1M1 STANDARD; PRT: 856 AA.

AC P31872;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=31678;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86218077; PubMed=2423250;

RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

RT Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";

RT AIDS.";

RL Cell 45:637-648(1986).

CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Glycoprotein; Transmembrane; Signal.

KW Signal.

FT CHAIN 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT SITE 760 760

FT DISULFID 53 73

FT DISULFID 118 205

FT DISULFID 125 196

FT DISULFID 130 152

FT DISULFID 218 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 444

FT DISULFID 383 417

FT CARBOHYD 87 87

FT CARBOHYD 134 134

FT CARBOHYD 140 140

FT CARBOHYD 151 151

FT CARBOHYD 155 155

FT CARBOHYD 183 183

FT CARBOHYD 197 197

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 289 289

FT CARBOHYD 295 295

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 390 390

FT CARBOHYD 394 394

FT CARBOHYD 404 404

FT CARBOHYD 447 447

FT CARBOHYD 459 459

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

SO SEQUENCE 856 AA; 97526 MW; DB68D1E49C404D59 CRC64;

Query Match 95.1%; Score 174; DB 1; Length 856;

Best Local Similarity 94.1%; Pred. No. 8.3e-14;

Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIEESQNOOEKNEOLELIDKWSLWNMF 34

Db 640 SLIYNLEESONQOEKNEOELLELDKASLWMMF 673

RESULT 11

ID	ENV_HV153	STANDARD	PRT	852 AA
AC	P19549			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
DE	ENV.			
OS	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).			
OS	Viruses; Retroviral viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11690;			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=90317906; PubMed=2370688;			
	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;			
	"Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";			
RL	J. Virol. 64:4016-4020(1990).			
CC	-----			
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CC	-----			
DR	EMBL: M38427; AAA45067.1; -			
DR	HIV: M38427; ENVSEF33.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	31	BY SIMILARITY.
FT	CHAIN	32	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	852	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	156	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	331	BY SIMILARITY.
FT	DISULFID	377	439	BY SIMILARITY.
FT	DISULFID	384	412	BY SIMILARITY.
FT	CARBOHYD	87	129	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	129	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	159	159	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	189	189	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	277	277	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	339	339	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	385	385	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	391	391	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQ SEQUENCE 852 AA; 96663 MW; EE7BFB8D23C9910D CRC64.

Query Match 94.0%; Score 172; DB 1; Length 852;

Best Local Similarity 91.2%; Pred. No. 1.5e-13;

Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESONQOEKNEOELLELDKASLWMMF 34

Db 636 SLIYNLEESONQOEKNEOELLELDKASLWMMF 669

RESULT 12

ID	ENV_HV151	STANDARD	PRT	847 AA
AC	P19550;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
DE	ENV.			
OS	Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).			
OS	Viruses; Retroviral viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11691;			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=90347835; PubMed=2384920;			
RA	Cheng-Mayer C., Quitoza M., Tung J.W., Dina D., Levy J.;			
RT	"Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";			
RL	J. Virol. 64:4390-4398(1990).			
CC	-----			
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CC	-----			
DR	EMBL: M65024; AAA45072.1; -			
DR	HIV: M38428; ENVSEF162.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	29	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	30	502	TRANSMEMBRANE GLYCOPROTEIN.
FT	CHAIN	503	847	BY SIMILARITY.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	203	BY SIMILARITY.
FT	DISULFID	125	194	BY SIMILARITY.
FT	DISULFID	130	155	BY SIMILARITY.
FT	DISULFID	216	245	BY SIMILARITY.
FT	DISULFID	226	237	BY SIMILARITY.
FT	DISULFID	294	328	BY SIMILARITY.
FT	DISULFID	374	435	BY SIMILARITY.
FT	DISULFID	381	408	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 847 AA: 96135 MW: 0A901317FD7FF2AB CRC64:

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Query Match 93.4%; Score 171; DB 1; Length 847;
Best Local Similarity 91.2%; Pred. No. 1,9e-13;
Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SLHSLSIESQNOQKNEQLELDKWSLWME 34
Db 631 NLYTLESQNOQKNEQLELDKWSLWME 664

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RESULT 13
ENV_HV1W2 STANDARD; PRT: 847 AA.
ID ENV_HV1W2
AC P05880.01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP MEDLINE=86235450; PubMed=3012778;
Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
"Genetic variation in HIV-1/LAV over time in patients with AIDS or
at risk for AIDS."
Science 233:1548-1553(1986).

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CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAIRIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.

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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).

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DR EMBL: M12507; AAB12990.1; -
DR HIV: M12507; ENV:WMJ2.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KM Signal.

```

```

FT SIGNAL 1 29
FT CHAIN 30 501
FT CHAIN 847 73
FT DISULFID 502 53
FT DISULFID 118 202
FT DISULFID 125 193
FT DISULFID 130 152
FT DISULFID 150 244
FT DISULFID 225 236
FT DISULFID 293 326
FT DISULFID 372 435
FT DISULFID 379 408
FT DISULFID 87 87
FT CARBOHYD 134 134
FT CARBOHYD 140 140
FT CARBOHYD 151 151
FT CARBOHYD 155 155
FT CARBOHYD 183 183
FT CARBOHYD 184 184
FT CARBOHYD 194 194
FT CARBOHYD 231 231
FT CARBOHYD 238 238
FT CARBOHYD 259 259
FT CARBOHYD 273 273
FT CARBOHYD 286 286
FT CARBOHYD 292 292
FT CARBOHYD 327 327
FT CARBOHYD 334 334
FT CARBOHYD 350 350
FT CARBOHYD 356 356
FT CARBOHYD 380 380
FT CARBOHYD 386 386
FT CARBOHYD 390 390
FT CARBOHYD 400 400
FT CARBOHYD 438 438
FT CARBOHYD 450 450
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SEQUENCE 847 AA: 96466 MW: CDIE33D73A5BCAE CRC64:

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Query Match 91.8%; Score 168; DB 1; Length 847;
Best Local Similarity 91.2%; Pred. No. 4.5e-13;
Matches 31; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 SLHSLSIESQNOQKNEQLELDKWSLWME 34
Db 631 SLHSLSIESQNOQKNEQLELDKWSLWME 664

```

```

RESULT 14
ENV_HV1J3 STANDARD; PRT: 867 AA.
ID ENV_HV1J3
AC P12489.01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RP MEDLINE=89352108; PubMed=2669897;
Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
"Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria."
AIDS Res. Hum. Retroviruses 5:411-419(1989).

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FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 626 626 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 97140 MM; D197D809940BE732 CRC64;

Query Match 90.2%; Score 165; DB 1; Length 856;  
 Best Local Similarity 88.2%; Pred. No. 1,1e-12;  
 Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLIHSLEBSNQOEKNEOELLELDKWSLWNWF 34  
 |||:||||:|||||  
 Db 641 SLIYSLEKSKTOOEKNEOELLELDKWSLWNWF 674

Search completed: May 16, 2003, 11:13:33  
 Job time : 5.73494 secs

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GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 24.7831 Seconds

(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-118

Perfect score: 183  
Sequence: 1 SLIHSLEESQNOOEKNEDELLELDKMASLWNMF 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183	100.0	645	15	Q993A6 human immun
2	183	100.0	747	15	Q70607 human immun
3	183	100.0	748	15	Q70606 human immun
4	183	100.0	752	15	Q70604 human immun
5	183	100.0	752	15	Q70605 human immun
6	183	100.0	752	15	Q70608 human immun
7	183	100.0	851	15	Q78243 human immun
8	183	100.0	852	15	Q89797 human immun
9	183	100.0	854	15	Q85582 human immun
10	183	100.0	854	15	Q72502 human immun
11	183	100.0	856	15	Q92877 simian-huma
12	183	100.0	856	15	Q74599 human immun
13	183	100.0	856	15	Q74090 human immun
14	179	97.8	854	15	Q90178 human immun
15	179	97.8	854	15	Q78705 human immun
16	178	97.3	856	15	Q905M7 human immun

17	177	96.7	616	15	Q993B0 human immun
18	177	96.7	718	15	Q993B2 human immun
19	177	96.7	757	15	Q90722 human immun
20	177	96.7	848	15	Q69990 human immun
21	175	95.6	838	15	Q03806 human immun
22	175	95.6	854	15	Q78225 human immun
23	175	95.6	855	15	Q03805 human immun
24	174	95.1	42	15	Q69910 human immun
25	174	95.1	443	15	Q80023 human immun
26	174	95.1	841	15	Q41556 human immun
27	174	95.1	849	15	Q77368 human immun
28	174	95.1	849	15	Q8Q851 human immun
29	174	95.1	851	15	Q61110 human immun
30	174	95.1	851	15	Q8Q852 human immun
31	174	95.1	856	15	Q72993 human immun
32	174	95.1	856	15	Q41539 human immun
33	174	95.1	857	15	Q8UL70 human immun
34	174	95.1	858	15	Q8UL90 human immun
35	174	95.1	858	15	Q8UL88 human immun
36	174	95.1	859	15	Q8UL85 human immun
37	174	95.1	859	15	Q8UL80 human immun
38	174	95.1	859	15	Q8UL79 human immun
39	174	95.1	859	15	Q8UL77 human immun
40	174	95.1	859	15	Q8UL73 human immun
41	174	95.1	859	15	Q8Q850 human immun
42	174	95.1	862	15	Q8UL84 human immun
43	174	95.1	862	15	Q8UL83 human immun
44	174	95.1	862	15	Q8UL82 human immun
45	174	95.1	862	15	Q8UL78 human immun

## ALIGNMENTS

RESULT 1  
Q993A6 PRELIMINARY; PRT; 645 AA.  
AC Q993A6;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (fragment).  
ENF.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Suman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
RL EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env-GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW Aids; Coat protein; Envelope protein; Glycoprotein; Polypotein;  
KW Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 645 AA: 72485 MW: B076514BE93362EC CRC64;  
Query Match 100.0%; Score 183; DB 15; Length 645;  
Best Local Similarity 100.0%; Pred. No. 3.3e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLIHSLEESQNOOEKNEDELLELDKMASLWNMF 34  
DB 609 SLIHSLEESQNOOEKNEDELLELDKMASLWNMF 642

```

RESULT 2
ID 070607 PRELIMINARY: PRT: 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM87-1;
RX MEDLINE=95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)".
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12034; AAA76669.1;
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00516; GP120. 1.
DR Pfam: PF00517; GP41. 1.
KM AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747 AA; 84250 MW; 732836A52245F14 CRC64;
SQ SEQUENCE

Query Match 100.0%; Score 183; DB 15; Length 747;
Best Local Similarity 100.0%; Pred. No. 3.8e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOEKNEQELLELDKWSIWNMF 34
DB 635 SLIHSLSIESQNOEKNEQELLELDKWSIWNMF 668

RESULT 3
ID 070606 PRELIMINARY: PRT: 748 AA.
AC 070606;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM881;
RX MEDLINE=95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)".
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12032; AAA76668.1;
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00516; GP120. 1.
DR Pfam: PF00517; GP41. 1.
KM AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747 AA; 84250 MW; 732836A52245F14 CRC64;
SQ SEQUENCE

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DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120. 1.
DR Pfam: PF00517; GP41. 1.
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748 AA; 84224 MW; 56BEDF186C67694B CRC64;
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 100.0%; Score 183; DB 15; Length 748;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOEKNEQELLELDKWSIWNMF 34
DB 636 SLIHSLSIESQNOEKNEQELLELDKWSIWNMF 669

RESULT 4
ID 070604 PRELIMINARY: PRT: 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM851;
RX MEDLINE=95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)".
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12030; AAA76666.1;
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120. 1.
DR Pfam: PF00517; GP41. 1.
KM AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752 AA; 84894 MW; 8B30AE894013B45A CRC64;
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 183; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOEKNEQELLELDKWSIWNMF 34
DB 640 SLIHSLSIESQNOEKNEQELLELDKWSIWNMF 673

RESULT 5
ID 070605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12031; AAA76667.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON_TER 752
SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 183; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLHSLIESONQOEKNEDELLELDKMASLWNMF 34
Db 640 SLHSLIESONQOEKNEDELLELDKMASLWNMF 673

RESULT 6
ID 070608 PRELIMINARY; PRT; 752 AA.
AC 070608;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-2;
RL MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12035; AAA76670.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON_TER 752
SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 100.0%; Score 183; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLHSLIESONQOEKNEDELLELDKMASLWNMF 34
Db 640 SLHSLIESONQOEKNEDELLELDKMASLWNMF 673
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Db 640 SLHSLIESONQOEKNEDELLELDKMASLWNMF 673

RESULT 7
ID 078243 PRELIMINARY; PRT; 851 AA.
AC 078243;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Env polyprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai O.,
  Verani P., Rossi G.B.;
RT "Sequence analysis of HIV-1 proviral DNA from a non producer
  chronically infected HUT-78 cellular clone.";
RL J. Viral Diseases 1:40-55(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352106; PubMed=2765297;
RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
  Macchi B., Mangiano N., Verani P., Rossi G.;
RT "Biological and molecular characterization of producer and non
  producer clones from HUT-78 infected with a patient HIV isolate.";
RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,
  Borselli A., Saggio I., Verani P., Rossi G.;
RT "Variability of HIV-1 virus: characteristics of an infected but not
  productive clone.";
RL Int. J. Immunopharmacol. 3:17-23(1990).
DR EMBL: Z11530; CAA7628.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON_TER 851
SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 100.0%; Score 183; DB 15; Length 851;
Best Local Similarity 100.0%; Pred. No. 4.4e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLHSLIESONQOEKNEDELLELDKMASLWNMF 34
Db 635 SLHSLIESONQOEKNEDELLELDKMASLWNMF 668

RESULT 8
ID 089797 PRELIMINARY; PRT; 852 AA.
AC 089797;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM90-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
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RT Infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN-IM90-2.
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12053; AAA76685.1; -.
DR EMBL: U12036; AAA76671.1; -.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: Coat protein; Envelope protein; Glycoprotein; Polypotein;
KW Transmembrane.
SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4E833CF CRC64;

Query Match 100.0%; Score 183; DB 15; Length 852;
Best Local Similarity 100.0%; Pred. No. 4.4e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SLIHSLEESONQOEKNEQELLELDKASLWMNF 34
636 SLIHSLEESONQOEKNEQELLELDKASLWMNF 669

RESULT 9
085582 PRELIMINARY: PRT; 854 AA.
AC 085582;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope polypeptide.
GN ENV.
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone."
RL J. Virol. 59:284-291(1986).
RN [2]
RC SEQUENCE FROM N.A.
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RA Buckler C.E.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [4]
RC SEQUENCE FROM N.A.
RX MEDLINE-92219406; PubMed-1373204;
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
RT gp1 results in loss of killing by CD8+ A24-restricted cytotoxic T
RT lymphocytes."
RL J. Virol. 66:3151-3154(1992).
DR EMBL: M19921; AAA44992.1; -.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR Pfam: Coat protein; Glycoprotein; Polypotein; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;

Query Match 100.0%; Score 183; DB 15; Length 854;
Best Local Similarity 100.0%; Pred. No. 4.4e-14;

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Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESONQOEKNEQELLELDKASLWMNF 34
DB 638 SLIHSLEESONQOEKNEQELLELDKASLWMNF 671

RESULT 10
072502 PRELIMINARY: PRT; 854 AA.
AC 072502;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENV polypeptide.
GN ENV.
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone."
RL J. Virol. 59:284-291(1986).
DR EMBL: U26942; AAB60578.1; -.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT CONFLICT 214 H -> L (IN REF. 2).
FT CONFLICT 530 A -> S (IN REF. 2).
FT CONFLICT 739 G -> D (IN REF. 2).
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match 100.0%; Score 183; DB 15; Length 854;
Best Local Similarity 100.0%; Pred. No. 4.4e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESONQOEKNEQELLELDKASLWMNF 34
DB 638 SLIHSLEESONQOEKNEQELLELDKASLWMNF 671

RESULT 11
092877 PRELIMINARY: PRT; 856 AA.
AC 092877;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Simian-human immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=57667;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE-99098984; PubMed-9882298;

```

RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,  
RA Steenbeke T., Halloran M., Fenton J.W., Axthelm M.K., Letvin N.L.,  
RA Sodroski J.G.;  
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
RT responsible for the pathogenicity of a multiply passaged simian-human  
RT immunodeficiency virus (SHIV-HXBc2).";  
RL J. Virol. 73:976-984(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,  
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF041850; AAD12142.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;

Query Match 100.0%; Score 183; DB 15; Length 856;  
Best Local Similarity 100.0%; Pred. No. 4,4e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESNQOEKNEQELLELDKWSLWMNF 34  
Db 640 SLIHSLSIESNQOEKNEQELLELDKWSLWMNF 673

RESULT 12  
O74599 PRELIMINARY; PRT; 856 AA.  
AC O74599;

DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MCK1;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.;  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates";  
RL J. Virol. 73:976-984(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MCK1;  
RX Iwatani Y.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: D86068; BAA12995.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 100.0%; Score 183; DB 15; Length 856;  
Best Local Similarity 100.0%; Pred. No. 4,4e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESNQOEKNEQELLELDKWSLWMNF 34  
Db 640 SLIHSLSIESNQOEKNEQELLELDKWSLWMNF 673

RESULT 13  
O74090

ID O74090 PRELIMINARY; PRT; 856 AA.  
AC O74090;

DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM213;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.;  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates";  
RL J. Virol. 73:976-984(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM213;  
RX Iwatani Y.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: D86069; BAA13003.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 100.0%; Score 183; DB 15; Length 856;  
Best Local Similarity 100.0%; Pred. No. 4,4e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESNQOEKNEQELLELDKWSLWMNF 34  
Db 640 SLIHSLSIESNQOEKNEQELLELDKWSLWMNF 673

RESULT 14  
O90178 PRELIMINARY; PRT; 854 AA.  
AC O90178;

DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95074930; PubMed=7983770;  
RA Fang H., Pincus S.H.;  
RT "Unique insertion sequence and pattern of CD4 expression in variants  
RT selected with immunotoxins from human immunodeficiency virus type 1-  
RT infected T cells";  
RL J. Virol. 69:75-81(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Fang H., Pincus S.H.;

RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
RT immunotoxin-resistant variant T cell line.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF070521; AAC28452.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 97.8%; Score 179; DB 15; Length 854;  
 Best Local Similarity 97.1%; Pred. No. 1.3e-13;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOQENQELLEDKMSLWNF 34  
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 Db 638 SLIHSLSIESQNOQENQELLEDKMSLWNF 671

## RESULT 15

078705 PRELIMINARY; PRT; 854 AA.  
 AC 078705;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Envelope glycoprotein gp120.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96013815; PubMed-7474132;  
 RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 RT resistant cell lines chronically infected with human immunodeficiency  
 RT virus type 1."  
 RL J. Virol. 69:7122-7131(1995).  
 DR EMBL; L42371; AA696326.1; -  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 854 AA; 97199 MW; 589512216533E256 CRC64;

Query Match 97.8%; Score 179; DB 15; Length 854;  
 Best Local Similarity 97.1%; Pred. No. 1.3e-13;  
 Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOQENQELLEDKMSLWNF 34  
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 Db 638 SLIHSLSIESQNOQENQELLEDKMSLWNF 671

Search completed: May 16, 2003, 11:19:45  
 Time : 24.8546 secs



GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 9.62651 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-118

Perfect score: 183

Sequence: 1 SLHSLIESQNOQEKNEOELLELDKWSLWNF 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : issued\_patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the record being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183	100.0	34	1	US-08-073-028-73
2	183	100.0	34	4	US-08-554-616-73
3	183	100.0	34	4	US-09-082-279B-800
4	183	100.0	34	4	US-09-315-304B-800
5	183	100.0	35	1	US-08-073-028-74
6	183	100.0	35	4	US-08-484-223B-234
7	183	100.0	35	4	US-08-554-616-74
8	183	100.0	35	4	US-09-082-279B-638
9	183	100.0	35	4	US-09-082-279B-799
10	183	100.0	35	4	US-08-471-913A-116
11	183	100.0	35	4	US-09-315-304B-638
12	183	100.0	35	4	US-09-315-304B-799
13	183	100.0	36	1	US-08-073-028-1
14	183	100.0	36	1	US-08-486-029-1
15	183	100.0	36	3	US-09-071-877-1
16	183	100.0	36	3	US-08-360-107A-1
17	183	100.0	36	3	US-08-484-223B-1
18	183	100.0	36	3	US-08-484-223B-231
19	183	100.0	36	3	US-08-484-223B-232
20	183	100.0	36	3	US-08-919-597-1
21	183	100.0	36	3	US-08-475-668A-1
22	183	100.0	36	3	US-08-485-551A-1
23	183	100.0	36	3	US-08-471-913A-1
24	183	100.0	36	4	US-08-554-616-1
25	183	100.0	36	4	US-08-485-264A-1
26	183	100.0	36	4	US-09-082-279B-15
27	183	100.0	36	4	US-09-082-279B-497

28	183	100.0	36	4	US-09-082-279B-498	Sequence 498, App
29	183	100.0	36	4	US-09-082-279B-560	Sequence 560, App
30	183	100.0	36	4	US-09-082-279B-561	Sequence 561, App
31	183	100.0	36	4	US-09-082-279B-603	Sequence 603, App
32	183	100.0	36	4	US-09-082-279B-630	Sequence 630, App
33	183	100.0	36	4	US-09-082-279B-631	Sequence 631, App
34	183	100.0	36	4	US-09-082-279B-705	Sequence 705, App
35	183	100.0	36	4	US-09-082-279B-834	Sequence 834, App
36	183	100.0	36	4	US-09-082-279B-11076	Sequence 11076, App
37	183	100.0	36	4	US-09-082-279B-11121	Sequence 11121, App
38	183	100.0	36	4	US-09-082-279B-11161	Sequence 11161, App
39	183	100.0	36	4	US-08-965-056-1	Sequence 1108, App
40	183	100.0	36	4	US-08-965-056-108	Sequence 108, App
41	183	100.0	36	4	US-09-045-920-1	Sequence 1, Appli
42	183	100.0	36	4	US-08-474-349A-1	Sequence 1, Appli
43	183	100.0	36	4	US-08-474-349A-399	Sequence 399, App
44	183	100.0	36	4	US-08-474-349A-400	Sequence 400, App
45	183	100.0	36	4	US-08-474-349A-401	Sequence 401, App

## ALIGNMENTS

RESULT 1  
US-08-073-028-73  
Sequence 73, Application US/08073028  
Patent No. 5464933  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-73

Query Match 100.0%; Score 183; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLHSLIESQNOQEKNEOELLELDKWSLWNF 34  
DB 1 SLHSLIESQNOQEKNEOELLELDKWSLWNF 34

RESULT 2  
US-08-554-616-73  
Sequence 73, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-73  
Query Match 100.0%; Score 183; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEQELLELDKWSLWNMF 34  
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DB 1 SLIHSLEESQNOEKNEQELLELDKWSLWNMF 34

RESULT 3  
US-09-082-279B-800  
Sequence 800, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
COMPUTER READABLE FORM:

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 800  
LENGTH: 34  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-800  
Query Match 100.0%; Score 183; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEQELLELDKWSLWNMF 34  
|||||  
DB 1 SLIHSLEESQNOEKNEQELLELDKWSLWNMF 34

RESULT 4  
US-09-315-304B-800  
Sequence 800, Application US/09315304B  
Patent No. 6348568  
GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.  
APPLICANT: Anwer, M.  
APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
TITLE OF INVENTION: PROPERTIES  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 800  
LENGTH: 34  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-800  
Query Match 100.0%; Score 183; DB 4; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEQELLELDKWSLWNMF 34  
|||||  
DB 1 SLIHSLEESQNOEKNEQELLELDKWSLWNMF 34

RESULT 5  
US-08-073-028-74  
Sequence 74, Application US/08073028  
Patent No. 546933  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073.028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-74

Query Match 100.0%; Score 183; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESONQOEKNEDELLELDKMASLWNWF 34  
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Db 2 SLIHSLSIESONQOEKNEDELLELDKMASLWNWF 35

RESULT 6  
US-08-484-223B-234  
Sequence 234, Application US/08484223B  
Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 234:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-234

Query Match 100.0%; Score 183; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESONQOEKNEDELLELDKMASLWNWF 34  
|||||  
Db 2 SLIHSLSIESONQOEKNEDELLELDKMASLWNWF 35

RESULT 7  
US-08-554-616-74  
Sequence 74, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-74

Query Match 100.0%; Score 183; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESONQOEKNEDELLELDKMASLWNWF 34  
|||||  
Db 2 SLIHSLSIESONQOEKNEDELLELDKMASLWNWF 35

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RESULT 8
US-09-082-279B-638
; Sequence 638, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082, 279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 638
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-638

Query Match          100.0%; Score 183; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESNQOEKNEQLELLDKKASLWNWF 34
Db 2 SLIHSLSIESNQOEKNEQLELLDKKASLWNWF 35

RESULT 9
US-09-082-279B-799
; Sequence 799, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082, 279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 799
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-799

Query Match          100.0%; Score 183; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESNQOEKNEQLELLDKKASLWNWF 34
Db 2 SLIHSLSIESNQOEKNEQLELLDKKASLWNWF 35

RESULT 10
US-08-474-349A-416
; Sequence 416, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
```

```
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474, 349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 416:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-416

Query Match          100.0%; Score 183; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESNQOEKNEQLELLDKKASLWNWF 34
Db 2 SLIHSLSIESNQOEKNEQLELLDKKASLWNWF 35

RESULT 11
US-09-315-304B-638
; Sequence 638, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315, 304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082, 279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 638
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LENGTH: 35  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Core polypeptide  
 US-09-315-304B-638

Query Match 100.0%; Score 183; DB 4; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESONQOEKNEQELLELDKWSIWMNF 34  
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 DB 2 SLIHSLEESONQOEKNEQELLELDKWSIWMNF 35

RESULT 12  
 US-09-315-304B-799  
 Sequence 799, Application US/09315304B  
 Patent No. 6348568  
 GENERAL INFORMATION:  
 APPLICANT: Barney, S.  
 APPLICANT: Guthrie, K.  
 APPLICANT: Merutka, G.  
 APPLICANT: Anwer, M.  
 APPLICANT: Lambert, D.  
 TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
 FILE REFERENCE: 7872-052  
 CURRENT APPLICATION NUMBER: US/09/315,304B  
 CURRENT FILING DATE: 1999-05-20  
 PRIOR APPLICATION NUMBER: 09/082,279  
 NUMBER OF SEQ ID NOS: 1667  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 799  
 LENGTH: 35  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Core polypeptide  
 US-09-315-304B-799

Query Match 100.0%; Score 183; DB 4; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESONQOEKNEQELLELDKWSIWMNF 34  
 |||||  
 DB 2 SLIHSLEESONQOEKNEQELLELDKWSIWMNF 35

RESULT 13  
 US-08-073-028-1  
 Sequence 1, Application US/08073028  
 Patent No. 5464933  
 GENERAL INFORMATION:  
 APPLICANT: Bolognesi, Daniel P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
 NUMBER OF SEQUENCES: 74  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/073,028  
 FILING DATE: 07-JUN-1993  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-004-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-073-028-1

Query Match 100.0%; Score 183; DB 1; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-16;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESONQOEKNEQELLELDKWSIWMNF 34  
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 DB 3 SLIHSLEESONQOEKNEQELLELDKWSIWMNF 36

RESULT 14  
 US-08-486-099-1  
 Sequence 1, Application US/08486099  
 Patent No. 6013263  
 GENERAL INFORMATION:  
 APPLICANT: Bolognesi, Daniel P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Petteway, Stephen R.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
 NUMBER OF SEQUENCES: 209  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,099  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-031  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELE: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-099-1

Query Match 100.0%; Score 183; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,8e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEQELLELDKWSIWMNF 34  
|||||  
DB 3 SLIHSLEESQNOEKNEQELLELDKWSIWMNF 36

## RESULT 15

US-09-071-877-1  
Sequence 1, Application US/09071877  
Patent No. 6015881

## GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol  
APPLICANT: Bray, Brian  
APPLICANT: Lichey, Maynard  
APPLICANT: Mader, Catherine  
APPLICANT: Merutka, Gene  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS  
FILE REFERENCE: 7872-050  
CURRENT APPLICATION NUMBER: US/09/071,877  
CURRENT FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus  
US-09-071-877-1

Query Match 100.0%; Score 183; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,8e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEQELLELDKWSIWMNF 34  
|||||  
DB 3 SLIHSLEESQNOEKNEQELLELDKWSIWMNF 36

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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 14,8835 Seconds  
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Title: US-09-623-533A-118

Perfect score: 183  
Sequence: 1 SLIHSLEESONQOEKNEQLLELDKWSLWMPF 34

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Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	183	100.0	36	US-09-874-475-16	Sequence 16, Appl
2	183	100.0	36	US-10-116-797-1	Sequence 1, Appl
3	183	100.0	36	US-09-493-346-1	Sequence 1, Appl
4	183	100.0	36	US-09-796-202-10	Sequence 10, Appl
5	183	100.0	36	US-09-779-451-5	Sequence 5, Appl
6	183	100.0	36	US-09-834-628-1	Sequence 1, Appl
7	183	100.0	36	US-09-854-816-1	Sequence 1, Appl
8	183	100.0	36	US-09-854-816-108	Sequence 108, App
9	183	100.0	37	US-09-848-616-176	Sequence 176, App
10	183	100.0	46	US-09-779-451-41	Sequence 41, Appl
11	183	100.0	56	US-09-779-451-41	Sequence 4, Appl
12	183	100.0	177	US-10-040-349B-2	Sequence 2, Appl
13	183	100.0	221	US-10-059-271-84	Sequence 84, Appl
14	183	100.0	232	US-10-059-271-84	Sequence 84, Appl
15	183	100.0	254	US-10-059-271-82	Sequence 82, Appl
16	183	100.0	256	US-10-059-271-97	Sequence 97, Appl
17	183	100.0	268	US-09-854-816-16	Sequence 16, Appl
18	183	100.0	268	US-09-854-816-17	Sequence 17, Appl
19	183	100.0	268	US-09-854-816-18	Sequence 18, Appl

20	183	100.0	344	9	US-10-040-349B-1	Sequence 1, Appl
21	183	100.0	345	9	US-10-026-741-49	Sequence 49, Appl
22	183	100.0	345	10	US-09-779-451-8	Sequence 8, Appl
23	183	100.0	391	9	US-10-059-271-93	Sequence 93, Appl
24	183	100.0	519	10	US-09-756-551A-8	Sequence 8, Appl
25	183	100.0	853	9	US-10-003-035-33	Sequence 33, Appl
26	183	100.0	856	10	US-09-476-242-1	Sequence 1, Appl
27	183	100.0	861	9	US-10-026-741-103	Sequence 103, App
28	183	100.0	1101	9	US-10-003-035-53	Sequence 53, Appl
29	183	100.0	1186	9	US-10-003-035-55	Sequence 55, Appl
30	180	98.4	36	10	US-09-912-824-1	Sequence 1, Appl
31	180	98.4	268	10	US-09-854-816-19	Sequence 19, Appl
32	177	96.7	1231	9	US-10-059-271-94	Sequence 94, Appl
33	175	95.6	268	10	US-09-854-816-13	Sequence 13, Appl
34	174	95.1	233	10	US-09-854-816-50	Sequence 50, Appl
35	174	95.1	268	10	US-09-854-816-9	Sequence 9, Appl
36	174	95.1	268	10	US-09-854-816-12	Sequence 12, Appl
37	173	94.5	269	10	US-09-854-816-46	Sequence 46, Appl
38	172	94.0	269	10	US-09-854-816-28	Sequence 28, Appl
39	171	93.4	268	10	US-09-854-816-26	Sequence 26, Appl
40	171	93.4	619	10	US-09-891-609-4	Sequence 4, Appl
41	171	93.4	646	10	US-09-891-609-2	Sequence 2, Appl
42	171	93.4	847	10	US-09-476-242-2	Sequence 2, Appl
43	170	92.9	46	10	US-09-854-816-109	Sequence 109, App
44	170	92.9	267	10	US-09-854-816-38	Sequence 38, Appl
45	170	92.9	268	10	US-09-854-816-41	Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
; Sequence 16, Application US/09874475  
; Publication No. US20020182592A1  
; GENERAL INFORMATION:  
; APPLICANT: Petropoulos, Christos J.  
; APPLICANT: Parkin, Neil T.  
; APPLICANT: Whitcomb, Jeanette  
; APPLICANT: Huang, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
; FILE REFERENCE: 2793/65166  
; CURRENT APPLICATION NUMBER: US/09/874,475  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16  
  
Query Match 100.0%; Score 183; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SLIHSLEESONQOEKNEQLLELDKWSLWMPF 34  
DB 3 SLIHSLEESONQOEKNEQLLELDKWSLWMPF 36  
  
RESULT 2  
US-10-116-797-1  
; Sequence 1, Application US/10116797  
; Publication No. US20030044411A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen, William C.  
; APPLICANT: Maddon, Paul J.  
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
; FILE REFERENCE: 64672-A  
; CURRENT APPLICATION NUMBER: US/10/116,797  
; CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 100.0%; Score 183; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 34  
|||||  
DB 3 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Patent No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Olson, William C  
APPLICANT: Maddon, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
TITLE OF INVENTION: Infection  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 100.0%; Score 183; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 34  
|||||  
DB 3 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 36

PUT 4

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SOLIDATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPM/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 100.0%; Score 183; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 34  
|||||  
DB 3 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.030003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 100.0%; Score 183; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 34  
|||||  
DB 3 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 36

RESULT 6  
US-09-834-628-1

Sequence 1, Application US/09834628  
Patent No. US2002011922A1  
GENERAL INFORMATION:  
APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: pep178  
US-09-834-628-1

Query Match 100.0%; Score 183; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 34  
|||||  
DB 3 SLIHSLIEESQNOQEKNEQELLELDKWSLWMWF 36



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US-09-854-816-1
Sequence 1, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: DP178
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
9-854-816-1
Query Match 100.0%; Score 183; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 2,7e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
1 SLIHSLIESSQNOQEKNEDELLIDKWSLWMMF 34
|||||
3 SLIHSLIESSQNOQEKNEDELLIDKWSLWMMF 36
RESULT 8
US-09-854-816-108
Sequence 108, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: DP178
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
9-854-816-1
Query Match 100.0%; Score 183; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 2,7e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
1 SLIHSLIESSQNOQEKNEDELLIDKWSLWMMF 34
|||||
3 SLIHSLIESSQNOQEKNEDELLIDKWSLWMMF 36

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Query	DB	Score	Length	Indels	Gaps
1 SLIHSLSIESQNOQEKNEQELLEDKWSLWME	34	100.0%	36	0	0
3 SLIHSLSIESQNOQEKNEQELLEDKWSLWME	36	100.0%	36	0	0
US-09-848-616-176					
Sequence 176, Application US/09848616					
Publication No. US20030054010A1					
GENERAL INFORMATION:					
APPLICANT: Sebbel, Peter					
APPLICANT: Dumant, Nicolas					
APPLICANT: Bachmann, Martin					
APPLICANT: Tissot, Alain					
APPLICANT: Lechner, Franziska					
TITLE OF INVENTION: Molecular Antigen Array					
FILE REFERENCE: 1700.0180002					
CURRENT APPLICATION NUMBER: US/09/848,616					
CURRENT FILING DATE: 2001-05-05					
NUMBER OF SEQ ID NOS: 186					
SOFTWARE: PatentIn Ver. 2.1					
SEQ ID NO 176					
LENGTH: 37					
TYPE: PRT					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: DP178c peptide					
US-09-848-616-176					
Query Match		100.0%	Score 183;	DB 10:	Length 36;
Best Local Similarity		100.0%;	Pred. No. 2.7e-15;		
Matches 34;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1 SLIHSLSIESQNOQEKNEQELLEDKWSLWME	34	100.0%	Score 183;	DB 10:	Length 36;
3 SLIHSLSIESQNOQEKNEQELLEDKWSLWME	36	100.0%	Score 183;	DB 10:	Length 36;
US-09-848-616-176					
Sequence 176, Application US/09848616					
Publication No. US20030054010A1					
GENERAL INFORMATION:					
APPLICANT: Sebbel, Peter					
APPLICANT: Dumant, Nicolas					
APPLICANT: Bachmann, Martin					
APPLICANT: Tissot, Alain					
APPLICANT: Lechner, Franziska					
TITLE OF INVENTION: Molecular Antigen Array					
FILE REFERENCE: 1700.0180002					
CURRENT APPLICATION NUMBER: US/09/848,616					
CURRENT FILING DATE: 2001-05-05					
NUMBER OF SEQ ID NOS: 186					
SOFTWARE: PatentIn Ver. 2.1					
SEQ ID NO 176					
LENGTH: 37					
TYPE: PRT					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: DP178c peptide					
US-09-848-616-176					
Query Match		100.0%	Score 183;	DB 10:	Length 36;
Best Local Similarity		100.0%;	Pred. No. 2.7e-15;		
Matches 34;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1 SLIHSLSIESQNOQEKNEQELLEDKWSLWME	34	100.0%	Score 183;	DB 10:	Length 36;
3 SLIHSLSIESQNOQEKNEQELLEDKWSLWME	36	100.0%	Score 183;	DB 10:	Length 36;
US-09-848-616-176					
Sequence 176, Application US/09848616					
Publication No. US20030054010A1					
GENERAL INFORMATION:					
APPLICANT: Sebbel, Peter					
APPLICANT: Dumant, Nicolas					
APPLICANT: Bachmann, Martin					
APPLICANT: Tissot, Alain					
APPLICANT: Lechner, Franziska					
TITLE OF INVENTION: Molecular Antigen Array					
FILE REFERENCE: 1700.0180002					
CURRENT APPLICATION NUMBER: US/09/848,616					
CURRENT FILING DATE: 2001-05-05					
NUMBER OF SEQ ID NOS: 186					
SOFTWARE: PatentIn Ver. 2.1					
SEQ ID NO 176					
LENGTH: 37					
TYPE: PRT					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: DP178c peptide					
US-09-848-616-176					
Query Match		100.0%	Score 183;	DB 10:	Length 36;
Best Local Similarity		100.0%;	Pred. No. 2.7e-15;		
Matches 34;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1 SLIHSLSIESQNOQEKNEQELLEDKWSLWME	34	100.0%	Score 183;	DB 10:	Length 36;
3 SLIHSLSIESQNOQEKNEQELLEDKWSLWME	36	100.0%	Score 183;	DB 10:	Length 36;
US-09-848-616-176					
Sequence 176, Application US/09848616					
Publication No. US20030054010A1					
GENERAL INFORMATION:					
APPLICANT: Sebbel, Peter					
APPLICANT: Dumant, Nicolas					

Db 4 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 37

RESULT 10  
US-09-779-451-41  
; Sequence 41, Application US/09779451  
; Patent No. US20020094521A1  
; GENERAL INFORMATION:  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Allaway, Graham P.  
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
; FILE REFERENCE: 1900.0300003  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/235,901  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/181,543  
; PRIOR FILING DATE: 2000-02-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 41  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-41

Query Match 100.0%; Score 183; DB 10; Length 46;  
Best Local Similarity 100.0%; Pred. No. 3.5e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 34  
Db 13 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 46

RESULT 11  
US-09-779-451-4  
; Sequence 4, Application US/09779451  
; Patent No. US20020094521A1  
; GENERAL INFORMATION:  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Allaway, Graham P.  
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
; FILE REFERENCE: 1900.0300003  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/235,901  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/181,543  
; PRIOR FILING DATE: 2000-02-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 56  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-4

Query Match 100.0%; Score 183; DB 10; Length 56;  
Best Local Similarity 100.0%; Pred. No. 4.3e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 34  
Db 18 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 51

RESULT 12  
US-10-040-349B-2  
; Sequence 2, Application US/10040349B  
; Publication No. US20030082521A1  
; GENERAL INFORMATION:  
; APPLICANT: Brasseur, Robert

APPLICANT: Charlotiaux, Benoit  
APPLICANT: Chevalier, Michel  
APPLICANT: El Habib, Raphaelle  
APPLICANT: Krell, Tino  
TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV  
FILE REFERENCE: 01-078-A  
CURRENT APPLICATION NUMBER: US/10/040.349B  
CURRENT FILING DATE: 2002-07-09  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: (1)...(177)  
OTHER INFORMATION: polypeptide derived from gp41 LAI  
US-10-040-349B-2

Query Match 100.0%; Score 183; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 34  
Db 106 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 139

RESULT 13  
US-10-059-271-84  
; Sequence 84, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPE, HEINRICH  
; APPLICANT: BUDE, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
; TITLE OF INVENTION: BEING IMMOBILIZED  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 84  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-059-271-84

Query Match 100.0%; Score 183; DB 9; Length 221;  
Best Local Similarity 100.0%; Pred. No. 1.8e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 34  
Db 133 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 166

RESULT 14  
US-10-059-271-81  
; Sequence 81, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPE, HEINRICH  
; APPLICANT: BUDE, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

;; TITLE OF INVENTION: BEING IMMOBILIZED  
;; FILE REFERENCE: ALBRE-22  
;; CURRENT APPLICATION NUMBER: US/10/059,271  
;; CURRENT FILING DATE: 2002-01-31  
;; PRIOR APPLICATION NUMBER: DE 101 06 295  
;; PRIOR FILING DATE: 2001-02-02  
;; NUMBER OF SEQ ID NOS: 97  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 81  
;; LENGTH: 232  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
US-10-059-271-81

Query Match 100.0%; Score 183; DB 9; Length 232;  
Best Local Similarity 100.0%; Pred. No. 1.9e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SLIHSLEESQNOQEKNEQELLELDKWSLWNMF 34  
DB 146 SLIHSLEESQNOQEKNEQELLELDKWSLWNMF 179

RESULT 15  
US-10-059-271-82  
; Sequence 82, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPKKE, HEINRICH  
; APPLICANT: BUDDER, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-82

Query Match 100.0%; Score 183; DB 9; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.1e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOQEKNEQELLELDKWSLWNMF 34  
DB 168 SLIHSLEESQNOQEKNEQELLELDKWSLWNMF 201

Search completed: May 16, 2003, 12:10:23  
Job time : 14.8835 secs

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C:Genetics: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polypotein; transmembrane protei  
F:1-29/Domains: signal sequence #status predicted <SIG>  
F:30-861/Product: env polyprotein #status predicted <EPP>  
F:87,129,139,140,143,159,163,167,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match Best Local Similarity 89.5%, Score 179; DB 1; Length 861;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YTGIIYNLEESONQEKNEDELLEDKANIMNMF 36  
Db 643 YTSLITLIESONQEKNEDELLEDKANIMNMF 678  
||.:|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.

RESULT 8 S22004  
Holo protein gp120/gp41 - human immunodeficiency virus type 1  
Accession: S22004  
Species: human immunodeficiency virus type 1, HIV-1  
Variety: isolate 4B  
Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
Accession: S22004  
R.Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
Submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR  
A:Reference number: S21990  
A:Accession: S22004  
A:Molecule type: DNA  
A:Residues: 1-357 <STE1>  
A:Cross-references: EMBL:X61353; NID:G60188; PIDN:CA43618.1; PID:G60189  
R.Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70419  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-292,'X',294-357 <STE2>  
A:Cross-references: EMBL:X61353; NID:G60188  
C:Superfamily: type E retrovirus env polyprotein

Query Match Best Local Similarity 89.0%, Score 178; DB 2; Length 357;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

1 YTGIIYNLEESONQEKNEDELLEDKANIMNMF 36  
||.:|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.  
139 YTDLITYLIESONQEKNEDELLALDRKANIMNMF 174

RESULT 9 VCLJMJ2  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Nucleotide: host Homo sapiens (man)  
C>Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
Accession: A03976  
R.Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Stickney,  
Science 227, 484-492, 1985  
A>Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453; PMID:2578227  
A:Accession: A03976  
A:Molecule type: DNA  
A:Residues: 1-855 <SAN>  
A:Cross-references: GB:K02007; NID:gj328658; PIDN:AAB59882.1; PID:gj328666  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypotein  
F:1-30/Domains: signal sequence #status predicted <SIG>

```

F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  

F:510-855/Product: transmembrane glycoprotein #status predicted <TM>  

E:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,  

F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted  

Query Match      89.0%; Score 178; DB 1; Length 855;  

Best Local Similarity    86.1%; Pred. No. 1,3e-13;  

Matches   32; Conservative     1; Mismatches     3; Indels       0; Gaps       0;  

QY          1 YTGIIYNLEESQNQEKNEDLLELDKWNALWMMNF 36  

           || | | | | | | | | | | | | | | | | | |  

Db         637 YTNITVTLLESQNQEKNEDLLELDKWNALWMMNF 672  

RESULT 10  

S2200f  

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4U)  

C:Species: human immunodeficiency virus type 1, HIV-1  

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999  

A:Accession: S70420; S22006  

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  

AIDS Res. Hum. Retroviruses 8, 53-59, 1992  

A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  

A:Reference number: S70417; MUID:92144209; PMID:11756940  

A:Accession: S70420  

A>Status: Preliminary  

A:Molecule type: DNA  

A:Residues: 1-357 <STR2>  

A:Cross-references: EMBL:X61354; NID:960190; PIDN:CAA43620.1; PID:960191  

A:Experimental source: patient L  

A>Note: Submitted to the EmbI Data Library, July 1991  

C:Superfamily: type E retrovirus env polyprotein  

Query Match      88.5%; Score 177; DB 2; Length 357;  

Best Local Similarity    86.1%; Pred. No. 1,3e-13;  

Matches   31; Conservative     2; Mismatches     3; Indels       0; Gaps       0;  

QY          1 YTGIIYNLEESQNQEKNEDLLELDKWNALWMMNF 36  

           || | | | | | | | | | | | | | | | | | |  

Db        139 YTDLIVTLLIESQNQEKNEDLLELDKWNALWMMNF 174  

RESULT 11  

S2199f  

envelope protein gp120/gp41 - human immunodeficiency virus type 1  

C:Species: human immunodeficiency virus type 1, HIV-1  

A:Variety: isolate 27B  

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000  

A:Accession: S21994; S70421  

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  

submitted to the EMBL Data Library, July 1991  

A>Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  

A:Reference number: S21990  

A:Accession: S21994  

A:Molecule type: DNA  

A:Residues: 1-357 <STE1>  

A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:960180  

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  

AIDS Res. Hum. Retroviruses 8, 53-59, 1992  

A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  

A:Reference number: S70417; MUID:92144209; PMID:11756940  

A:Accession: S70421  

A>Status: Preliminary  

A:Molecule type: DNA  

A:Residues: 1-140,'X','142-312','X','314-357<STE2>  

A:Cross-references: EMBL:X61355; NID:960179  

C:Superfamily: type E retrovirus env polyprotein  

Query Match      88.5%; Score 177; DB 2; Length 357;  

Best Local Similarity    86.1%; Pred. No. 1,3e-13;  

Matches   31; Conservative     3; Mismatches     2; Indels       0; Gaps       0;  

QY          1 YTGIIYNLEESQNQEKNEDLLELDKWNALWMMNF 36
```

```
Db      139 YTLIYTLIEESQÑQEKNEQELLELDKNASLWNWF 174
```

RESULT 12

env polyprotein: MW - human immunodeficiency virus type 1 (fragment)  
N: Alternate names: coat polyprotein  
N: Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C: Species: human immunodeficiency virus type 1, HIV-1  
A: Note: host Homo sapiens (man)  
C: Date: 11-Feb-1993 #sequence: revision 31-Dec-1993 #text\_change 26-Aug-1999  
C: Accession: A41621  
R: Burger, H.; Weisler, B.; Flaherty, K.; Gullia, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A: Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A: Reference number: A41621; MUID: 92107924; PMID: 1765038  
A: Accession: A41621  
A: Molecule type: DNA  
A: Residues: 1-445 <BPUR>  
A: Cross-references: GB: M77228; NID: g338627; PIDN: AAB03790.1; PID: g555013  
Note: this virus was isolated from the mother  
C: Genetics:

Query Match	88.58;	Score 177;	DB 2;	Length 445;
Best Local Similarity	83.38;	Pred. No. 1.7e-13;		

```
Oy      1 YTGIIYNLLEESQNOEKNQEOLLELDKWANLWMEF   36
          || :|||:|||:|||:|||:|||:|||:|||:|||
Db     380 YTSLIYNLLEESQNOEKNQEODLLELDKWSLWSWF  415
```

## RESULT 13

envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variate: isolate 28  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21998 S70425  
R:Seiwerter, H., Storch-Hagenlocher, B., Wildemann, B.; Hacke, W.  
Submitted to the EMBL Data Library, July 1991  
Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by polymerase chain reaction (PCR) and sequence analysis  
Reference number: S21990

Query Match	88.0%;	Score 176;	DB 2;	Length 358;
Best Local Similarity	83.3%;	Pred. No. 1.7e-13;		
Matches	30;	Conservative	4;	Mismatches 2;
			Indels	0;
			Gaps	0;

```

Oy      1 YTGIIYNLLEESQNOQEKNEQELLEEDKWANLWNMF 36
         ||::||:|||||:|||||:|||||:|||||:|||||:
Db     140 YTSLIYTLIEQSQNOQEKNEQELLEEDKWASLWNMF 175

```

RESULT 14  
C32005

env polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1997  
C:Accession: S33985  
R:Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-references: NCBI:211530; NID:g60192; PIDN:CAA77628.1; PID:g60199  
C:Superfamily: type E retrovirus env polyprotein

Query Match	87.5%	Score 175;	DB 2;	Length 851;
Best Local Similarity	83.3%	Pred. No. 6.1e-13;		
Matches 30;	Conservative 5;	Mismatches 1;	Indels 0;	Gaps 0;

```
QY      1 YTGIIIVLLLEESQNQEKNQEQLLELDKMANLWNWF 36
          || : |:|:|||||||:|||||:|||||
Db     633 YTSLIHSLIEESQNQEKNQEQLLELDKVASLWNWF 666
```

RESULT 15  
S13288

env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13288, MUID:91043044, PMID:21212833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OHR>  
C:Superfamily: Type E retrovirus env polyprotein

Query Match	87.5%	Score 175;	DB 2;	Length 854;
Best Local Similarity	83.3%	Pred. No. 6.1e-13;		
Matches 30;	Conservative 5;	Mismatches 1;	Indels 0;	Gaps 0.

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKMANLWNWF 36  
||:::|||||:|||||:|||||  
Db 636 YTSLSHSLIEESQNOQEKNEQELLELDKVASLWNWF 673

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Search completed: May 16, 2003, 11:25:06
Job time : 13.1446 secs
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FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 825 825 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCA6 CRC64;

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Query Match 100.0%; Score 200; DB 1; Length 865;
Best Local Similarity 100.0%; Pred. No. 3.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTGIIYNLLESQNOOEKNEOELLELDKMANLWNMF 36
Db 647 YTGIIYNLLESQNOOEKNEOELLELDKMANLWNMF 682

```

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RESULT 2
ENV_HV1M1 STANDARD; PRT; 856 AA.
ID ENV_HV1M1 STANDARD; PRT; 856 AA.
AC P31872.2 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=31678;
OC [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
Starch B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
"Identification and characterization of conserved and variable
regions in the envelope gene of HTLV-III/LAV, the retrovirus of
AIDS";
RT Cell 45:637-648(1986).
RL -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
WAS PERINATALLY INFECTED BY HER MOTHER.
CC PIR: A24774; VCLJ3M.
DR InterPro: IPR000777; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00517; GP120; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.

```

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FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 205 BY SIMILARITY.
FT DISULFID 125 196 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB68D1E9C404DE9 CRC64;

```

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Query Match 92.5%; Score 185; DB 1; Length 856;
Best Local Similarity 88.9%; Pred. No. 2.2e-14;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 YTGIIYNLLESQNOOEKNEOELLELDKMANLWNMF 36
Db 638 YTGIIYNLLESQNOOEKNEOELLELDKMANLWNMF 673

```

```

RESULT 3
ENV_HV1S3 STANDARD; PRT; 852 AA.
ID ENV_HV1S3 STANDARD; PRT; 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11690;
OC [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
"Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
the viral genome";
RT J. Virol. 64:4016-4020(1990).
RL
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: M38427; AAA5067.1; -  
 DR HIV: M38427; ENV5SF33.  
 DR InterPro: IPR000328; Env-GP41.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 KM AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 Signal.  
 FT SIGNAL 1 31 BY SIMILARITY.  
 FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 206 BY SIMILARITY.  
 FT DISULFID 125 197 BY SIMILARITY.  
 FT DISULFID 130 156 BY SIMILARITY.  
 FT DISULFID 219 248 BY SIMILARITY.  
 FT DISULFID 229 240 BY SIMILARITY.  
 FT DISULFID 297 331 BY SIMILARITY.  
 FT DISULFID 377 439 BY SIMILARITY.  
 FT DISULFID 384 412 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 SQ SEQUENCE 852 AA; 96663 MW; E77BBFBD23C9910D CRC64;  
 Query Match 90.5%; Score 181; DB 1; Length 852;  
 Best Local Similarity 88.9%; Pred. No. 6,6e-14;  
 Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 YTGIIYNLEESQNOEKNEQELLEDKMANLWNMF 36  
 Db 634 YTSLLTYTLLSESONOEKNEQELLEDKMASLWNMF 669  
 RESULT 4  
 ENV\_HY1MA STANDARD: PRT: 859 AA.  
 AC P04563;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
 glycoprotein (GP120), Transmembrane glycoprotein (GP41)].

GN ENV.  
 OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11697;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86245056; PubMed=2424612;  
 RA Allison M., Main-Hobson S., Montagnier L., Sonigo P.;  
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis  
 of two isolates from African patients";  
 RL Cell 46:63-74(1986).  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: X04415; CAA28016.1; -  
 DR EMBL: A07116; CAA00623.1; -  
 DR HIV: K03456; ENV5MAL.  
 DR InterPro: IPR000328; Env-GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 513  
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 FT DISULFID 53 73  
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 SQ SEQUENCE 859 AA; 97109 MW; DBCF9A5A253ABF29 CRC64;  
 Query Match 90.0%; Score 180; DB 1; Length 859;



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SO SEQUENCE 855 AA; 97043 MW; 849B0B8CBAF7008 CRC64;

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Query Match Score 179; DB 1; Length 853;  
 Best Local Similarity 86.1%; Pred. No. 1.1e-13;  
 Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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OY 1 YNGIIVNLEESONOEKNEDELLEDKRANLNMWF 36
DB 635 VTGLYRLIEESOTOEKNEDLELDKWSLNMWF 670

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## RESULT 7

ENV\_HV126

STANDARD: PRT: 855 AA.

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AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11708;

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SEQUENCE FROM N.A.

MEDLINE=87248097; PubMed=3036660;

Strilivsan A., Anand R., Ranganathan P., Feorino P.,  
 Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,  
 Sanchez-Pescador R.;

"Molecular characterization of human immunodeficiency virus from  
 Zaire: nucleotide sequence analysis identifies conserved and variable  
 domains in the envelope gene.";

Gene 52:71-82(1987).

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EMBL: K03458; AAA45380.1; -

PIR: D26192; VCLJZR.

HIV: K03458; ENV526.

InterPro: IPR000328; ENV\_GP41.

InterPro: IPR000777; GP120.

Pfam: PF00516; GP120.1.

Pfam: PF00517; GP41.1.

KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.

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FT SIGNAL 31 510 TRANSMEMBRANE GLYCOPROTEIN.
FT CHAIN 511 855
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FT DISULFID 118 207 BY SIMILARITY.
FT DISULFID 125 198 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 220 249 BY SIMILARITY.
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FT DISULFID 258 332 BY SIMILARITY.
FT DISULFID 378 444 BY SIMILARITY.
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SO SEQUENCE 855 AA; 96971 MW; 3B4D3D6E239C457 CRC64;

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Query Match Score 179; DB 1; Length 855;  
 Best Local Similarity 86.1%; Pred. No. 1.1e-13;  
 Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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OY 1 YNGIIVNLEESONOEKNEDELLEDKRANLNMWF 36
DB 637 VTGLYRLIEESOTOEKNEDLELDKWSLNMWF 672

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## RESULT 8

ENV\_HV15C

STANDARD: PRT: 856 AA.

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AC P05678;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11702;

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Human immunodeficiency virus type 1 (SC isolate) (HIV-1).  
 Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI\_Taxid=11702;

[1]

SEQUENCE FROM N.A.

MEDLINE=88219542; PubMed=3369091;

RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Colliati E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;  
 RT "Envelope sequences of two new United States HIV-1 isolates";  
 RL Virology 164:531-536(1988)  
 CC -i- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 DR EMBL: M17450; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: B28922; VCLJSC.  
 DR HIV: M17450; ENVSSC.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 KM Signal. 1 29  
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 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.  
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 Query Match 89.5%; Score 179; DB 1; Length 856;  
 Best Local Similarity 86.1%; Pred. No. 1.le-13;

Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNF 36  
 DB 638 YTSIIYTLIEESQNOEKNEQELLELDKRWASLWNF 673  
 RESULT 9  
 ENV\_HVIA2 STANDARD: PRT; 855 AA.  
 ID ENV\_HVIA2  
 AC P03378;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DE ENV.  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85090453; PubMed=2578227;  
 RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,  
 RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,  
 RA Levy J.A., Dina D., Luciw P.A.;  
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus.  
 RT (ARV-2).";  
 RT Science 227:484-492(1985).  
 CC -----  
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 CC -----  
 CC EMBL: K02007; AAB59882.1; -  
 DR PIR: A03976; VCLJAZ.  
 DR HIV: K02007; ENVSS2.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 KM Signal. 1 29  
 FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 208 BY SIMILARITY.  
 FT DISULFID 125 199 BY SIMILARITY.  
 FT DISULFID 130 155 BY SIMILARITY.  
 FT DISULFID 221 250 BY SIMILARITY.  
 FT DISULFID 231 242 BY SIMILARITY.  
 FT DISULFID 299 333 BY SIMILARITY.  
 FT DISULFID 380 442 BY SIMILARITY.  
 FT DISULFID 387 415 BY SIMILARITY.  
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 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT	DISULFID	125
FT	DISULFID	130

FT	DISULFID	125
FT	DISULFID	130

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 CC -1- MISCELLANEOUS: ISOLATES MWJ1, MWJ2, AND MWJ3 WERE OBTAINED FROM  
 CC BLOOD SAMPLES SPONTANEOUSLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO  
 CC WAS PERINATALLY INFECTED BY HER MOTHER.  
 CC -----  
 CC

FT	632	632	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	669	669	N-LINKED (GLCNAC. . .)	(POTENTIAL).











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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-4

Perfect score: 200  
Sequence: 1 YTGIIYNLEESQNOEKNEQELLEDKRWANLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organella:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	99.0	122	15	Q9QIW9 human immun
2	196	98.0	122	15	Q9QIV1 human immun
3	194	97.0	117	15	Q9YRS7 human immun
4	193	96.5	122	15	Q9YXPI human immun
5	193	96.5	123	15	Q9EAA3 human immun
6	193	96.5	854	15	Q56566 human immun
7	193	96.5	861	15	Q41560 human immun
8	192	96.0	50	15	Q69898 human immun
9	192	96.0	122	15	Q9QD37 human immun
10	191	95.5	122	15	Q9YXR1 human immun
11	191	95.5	122	15	Q9YXR1 human immun
12	191	95.5	122	15	Q9YXR1 human immun
13	190	95.0	122	15	Q9EAB9 human immun
14	189	94.5	122	15	Q9YXR2 human immun
15	189	94.5	122	15	Q9YXR2 human immun
16	188	94.0	122	15	Q9YXR6 human immun

17	188	94.0	122	15	Q9YXN0 human immun
18	188	94.0	122	15	Q9QIW0 human immun
19	188	94.0	857	15	Q92823 human immun
20	188	94.0	857	15	Q71013 human immun
21	188	94.0	857	15	Q92821 human immun
22	188	94.0	857	15	Q92821 human immun
23	187	93.5	117	15	Q9QON2 human immun
24	187	93.5	117	15	Q9QON1 human immun
25	187	93.5	122	15	Q9YXW9 human immun
26	187	93.5	122	15	Q9YXR7 human immun
27	187	93.5	122	15	Q9YXR5 human immun
28	187	93.5	852	15	Q92761 human immun
29	187	93.5	852	15	Q73303 human immun
30	187	93.5	857	15	Q8UL89 human immun
31	187	93.5	859	15	Q73307 human immun
32	186	93.0	50	15	Q69900 human immun
33	186	93.0	118	15	Q9E5R0 human immun
34	186	93.0	122	15	Q9YXR7 human immun
35	186	93.0	122	15	Q9YXR7 human immun
36	186	93.0	122	15	Q9EAA5 human immun
37	186	93.0	122	15	Q9EAA5 human immun
38	186	93.0	122	15	Q9EAA4 human immun
39	186	93.0	122	15	Q9YXR0 human immun
40	186	93.0	122	15	Q9YXR9 human immun
41	186	93.0	856	15	Q73295 human immun
42	186	93.0	861	15	Q56109 human immun
43	186	93.0	866	15	Q9E1R5 human immun
44	185	92.5	122	15	Q9YXR2 human immun
45	185	92.5	122	15	Q9YXR8 human immun

## ALIGNMENTS

RESULT 1  
Q9QIW9 PRELIMINARY; PRT; 122 AA.  
AC Q9QIW9;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GP41ERRJ02;  
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,  
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Meneses J.A.,  
RA Calzans A.R., Tanuri A.;  
RT "Genotyping and phenotyping analysis of B and non-B Human  
RT Immunodeficiency Virus type 1 subtypes from patients under HAART";  
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF165535; AAF08480.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR Pfam: PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14744 MW; 02F0BE9F79AEC75 CRC64;

Query Match Best Local Similarity 99.0%; Score 198; DB 15; Length 122;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQNOEKNEQELLEDKRWANLWNMF 36  
DB 78 YTGIIYNLEESQNOEKNEQELLEDKRWANLWNMF 113

RESULT 2

```
0901V1
ID 0901V1 PRELIMINARY; PRT; 122 AA.
AC 0901V1:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GP41ERR120;
RA Caride E., Hertogs K., Larder B., Deheretogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,
RA Calazado A.R., Tanuri A.;
RT "Genotyping and phenotyping analysis of B and non-B Human
RT immunodeficiency virus type 1 subtypes from patients under HAART.";
RT Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF165553; AAF08498.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14815 MW; 14BFEE39890812B1 CRC64;

Query Match 98.0%; Score 196; DB 15; Length 122;
Best Local Similarity 94.4%; Pred. No. 2.6e-16;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESONQOEKNEOELLELDKKNANLNMWF 36
DB 78 YTGIIYNLLEESONQOEKNEOELLELDKKNANLNMWF 113

RESULT 3
OYRS7
ID 09YRS7 PRELIMINARY; PRT; 117 AA.
AC 09YRS7:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USSN07;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Stork C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 group M."
RT Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF096339; AAD04414.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14133 MW; ECBAF66A1CDA17D CRC64;

Query Match 97.0%; Score 194; DB 15; Length 117;
Best Local Similarity 94.4%; Pred. No. 4.4e-16;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESONQOEKNEOELLELDKKNANLNMWF 36
DB 78 YTGIIYNLLEESONQOEKNEOELLELDKKNANLNMWF 113
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RESULT 4
OYXPI
ID 09YXPI PRELIMINARY; PRT; 122 AA.
AC 09YXPI:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP081;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RT Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF034062; AAC79314.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14778 MW; FD3191CE79AB819D CRC64;

Query Match 96.5%; Score 193; DB 15; Length 122;
Best Local Similarity 94.4%; Pred. No. 6.1e-16;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESONQOEKNEOELLELDKKNANLNMWF 36
DB 78 YTGIIYNLLEESONQOEKNEOELLELDKKNANLNMWF 113

RESULT 5
O9EAA3
ID 09EAA3 PRELIMINARY; PRT; 123 AA.
AC 09EAA3:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX158;
RC MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganes C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RT J. Infect. Dis. 181:470-475(2000).
DR EMBL: AF190949; AAG02311.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 123
SQ SEQUENCE 123 AA; 14790 MW; 26DFA44D922DC546 CRC64;

Query Match 96.5%; Score 193; DB 15; Length 123;
Best Local Similarity 94.4%; Pred. No. 6.1e-16;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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OY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 36  
|||||:|||||:|||||:|||||:|||||  
Db 79 YTGIIYNLLEESQNOEKNEQELLELDKRWASLNMNF 114

RESULT 6  
ID 056566 PRELIMINARY; PRT; 854 AA.  
AC 056566;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
R MEDLINE=99372987; PubMed=10445815;  
R Altman-Onal Y., Colffier C., Giraud A., Babic-Ercog A., Biron F.,  
R Verrier B.;  
RT "Comparison of complete env gene sequences from individuals with  
RT symptomatic primary HIV type 1 infection."  
RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999).  
DR EMBL: AF041132; AAC02523.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.

Query Match 96.5%; Score 193; DB 15; Length 854;  
Best Local Similarity 94.4%; Pred. No. 4.3e-15;  
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 36  
|||||:|||||:|||||:|||||:|||||  
Db 636 YTGIIYNLLEESQNOEKNEQELLELDKRWASLNMNF 671

RESULT 7  
ID 041560 PRELIMINARY; PRT; 861 AA.  
AC 041560;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE - Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
R MEDLINE=98105804; PubMed=9445059;  
R Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,  
R Walker B.D., Neumann A.U., Vermond S.H., Westleky J., Jackson S.,  
R Fenimore E., Cao Y., Gao F., Kalam S., Kunstman K.J., McDonald D.,  
R McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;  
RT "Immunological and virological analyses of persons infected by human  
RT immunodeficiency virus type 1 while participating in trials of  
RT recombinant gp120 subunit vaccines."  
RL J. Virol. 72:1552-1576(1998).  
DR EMBL: U84817; AAC58848.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.

FT NON\_TER 1 1  
SQ SEQUENCE 861 AA; 97500 MW; 98C2DFADEAC76539 CRC64;  
Query Match 96.5%; Score 193; DB 15; Length 861;  
Best Local Similarity 91.7%; Pred. No. 4.4e-15;  
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 36  
|||||:|||||:|||||:|||||:|||||  
Db 643 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 678

RESULT 8  
ID 069898 PRELIMINARY; PRT; 50 AA.  
AC 069898;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
R MEDLINE=94211861; PubMed=7512731;  
R Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,  
R Keller P.M., Shaw A.R., Emami E.A.;  
RT "Neutralization of divergent human immunodeficiency virus type 1  
RT variants and primary isolates by IAW-41-2F5, an anti-gp41 human  
RT monoclonal antibody."  
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).  
DR EMBL: U06728; AAA19141.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR Pfam: PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
SQ SEQUENCE 50 AA; 6358 MW; EABA093A1CGC79E1 CRC64;

Query Match 96.0%; Score 192; DB 15; Length 50;  
Best Local Similarity 94.4%; Pred. No. 3.3e-16;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 36  
|||||:|||||:|||||:|||||:|||||  
Db 15 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 50

RESULT 9  
ID 090DJ7 PRELIMINARY; PRT; 122 AA.  
AC 090DJ7;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
R STRAIN=UG;  
R Hu D.J., Bages J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
R Bityawaho B., Sempa S.D.K., Rayfield M.A., Dondero T.J., Lai R.;  
RT "Similar distribution and continued predominance of HIV-1 subtypes A  
RT and D infections in Uganda."  
RL submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF307734; AAL08795.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR Pfam: PF00517; GP41; 1.

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KW Transmembrane.
FT NON_TER 1
KW NON_TER 122
SQ SEQUENCE 122 AA: 14743 MW: FBB3D55A1B1482A2 CRC64;

Query Match
Best Local Similarity 96.0%; Score 192; DB 15; Length 122;
Pred. No. 8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGIIYNLIESONOEKNEQELLELDKKNALMNMF 36
   |||:|||||:|||||:|||||:|||||:|||||:
DB 78 YTRITYNLIESONOEKNEQELLELDKKNALMNMF 113

RESULT 10
O9YXR1 PRELIMINARY: PRT: 122 AA.
AC O9YXR1:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP019;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF034042; AAC79294.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA: 14835 MW: 396EA258E3BAABD5 CRC64;

Query Match
Best Local Similarity 95.5%; Score 191; DB 15; Length 122;
Pred. No. 1.1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGIIYNLIESONOEKNEQELLELDKKNALMNMF 36
   |||:|||||:|||||:|||||:|||||:|||||
DB 78 YTGIIYNLIESONOEKNEQELLELDKKNALMNMF 113

RESULT 11
O9IJRO PRELIMINARY: PRT: 122 AA.
AC O9IJRO:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ARI;
RA MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggis J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL: AF220672; AAF74224.1; -

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DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA: 14808 MW: ADDACE746A9C757 CRC64;

Query Match
Best Local Similarity 95.5%; Score 191; DB 15; Length 122;
Pred. No. 1.1e-15;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLIESONOEKNEQELLELDKKNALMNMF 36
   |||:|||||:|||||:|||||:|||||:|||||
DB 78 YTGIIYNLIESONOEKNEQELLELDKKNALMNMF 113

RESULT 12
O9IJQ3 PRELIMINARY: PRT: 122 AA.
AC O9IJQ3:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR46;
RA MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggis J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL: AF220679; AAF74231.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA: 14478 MW: A548C7BE0315D851 CRC64;

Query Match
Best Local Similarity 95.5%; Score 191; DB 15; Length 122;
Pred. No. 1.1e-15;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLIESONOEKNEQELLELDKKNALMNMF 36
   |||:|||||:|||||:|||||:|||||:|||||
DB 78 YTGIIYNLIESONOEKNEQELLELDKKNALMNMF 113

RESULT 13
O9EA89 PRELIMINARY: PRT: 122 AA.
AC O9EA89:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX774;
RA MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Canea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B

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RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic  
 RT diversity in the United States.";  
 RL J. Infect. Dis. 181:470-475(2000).  
 DR EMBL: AF190963; AAG02325.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 122 AA; 14892 MW; 8EF45DAF0E5FAFA7 CRC64;  
 Query Match 95.0%; Score 190; DB 15; Length 122;  
 Best Local Similarity 91.7%; Pred. No. 1.4e-15;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESONOQEKNEQELLELDKWNANLWNMF 36  
 DB 78 YTNLIYNLLEESONOQEKNEQELLELDKWNANLWNMF 113  
 LT 14  
 ID 09JUN3 PRELIMINARY; PRT: 122 AA.  
 AC 09JUN3;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AR48;  
 RX MEDLINE-20346416; PubMed-10890362;  
 RA Masciocla S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,  
 RA Baggs J., Lai R., Pieniazek D.;  
 RT "Evidence for a high frequency of HIV-1 subtype F infections among  
 RT heterosexual population in Buenos Aires, Argentina.";  
 RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).  
 DR EMBL: AF220699; AAF76818.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 122 AA; 14748 MW; 2B120F6B47730DFD CRC64;  
 Query Match 94.5%; Score 189; DB 15; Length 122;  
 Best Local Similarity 91.7%; Pred. No. 1.9e-15;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESONOQEKNEQELLELDKWNANLWNMF 36  
 DB 78 YTGIIYNLLEESONOQEKNEQELLELDKWNANLWNMF 113  
 RESULT 15  
 ID 09ODK9 PRELIMINARY; PRT: 122 AA.  
 AC 09ODK9;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-UG;

RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
 RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lai R.;  
 RT "Similar distribution and continued predominance of HIV-1 subtypes A  
 RT and D infections in Uganda.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF307722; AAL08783.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 SQ SEQUENCE 122 AA; 14675 MW; 2FFD0A7866F3BB37 CRC64;  
 Query Match 94.5%; Score 189; DB 15; Length 122;  
 Best Local Similarity 94.4%; Pred. No. 1.9e-15;  
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESONOQEKNEQELLELDKWNANLWNMF 36  
 DB 78 YTGIIYNLLEESONOQEKNEQELLELDKWNANLWNMF 113

Search completed: May 16, 2003, 11:19:44  
 Job time : 27.3124 secs

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-4

Perfect score: 200

Sequence: 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANIMNMF 36

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents.AA:\*  
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2: /cgn2-6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2-6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2-6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2-6/ptodata/1/1aa/PTCTUS\_COMB.pep:\*  
6: /cgn2-6/ptodata/1/1aa/Backfilltest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	100.0	36	1	US-08-073-028-4
2	200	100.0	36	3	US-08-486-099-4
3	200	100.0	36	3	US-08-360-107A-4
4	200	100.0	36	3	US-08-484-223B-4
5	200	100.0	36	3	US-08-919-597-4
6	200	100.0	36	3	US-08-475-668A-4
7	200	100.0	36	3	US-08-485-551A-4
8	200	100.0	36	3	US-08-471-913A-4
9	200	100.0	36	4	US-08-534-616-4
10	200	100.0	36	4	US-08-485-264A-4
11	200	100.0	36	4	US-09-082-279B-1358
12	200	100.0	36	4	US-09-082-279B-1359
13	200	100.0	36	4	US-08-474-349A-4
14	200	100.0	36	4	US-09-315-304B-1358
15	200	100.0	36	4	US-09-315-304B-1359
16	200	100.0	36	4	US-08-255-208A-4
17	200	100.0	36	4	US-09-570-921-18
18	200	100.0	269	4	US-08-965-056-33
19	200	100.0	865	4	US-07-956-483-13
20	200	100.0	887	4	US-08-472-240A-4
21	185	92.5	138	4	US-09-570-921-27
22	185	92.5	233	4	US-08-965-056-50
23	185	92.5	267	4	US-08-965-056-38
24	185	92.5	268	4	US-08-965-056-41
25	184	92.0	36	1	US-08-073-028-3
26	184	92.0	36	3	US-08-360-107A-3
27	184	92.0	36	4	US-08-554-616-3

28	183	91.5	269	4	US-08-965-056-43	Sequence 43, Appl
29	182	91.0	46	4	US-08-965-056-110	Sequence 110, App
30	182	91.0	268	4	US-08-965-056-13	Sequence 13, Appl
31	182	91.0	269	4	US-08-965-056-48	Sequence 48, Appl
32	182	91.0	270	4	US-08-965-056-67	Sequence 67, Appl
33	182	91.0	855	1	US-08-022-835-6	Sequence 6, Appl1
34	182	91.0	855	1	US-08-388-809-6	Sequence 6, Appl1
35	182	91.0	855	2	US-08-647-714-6	Sequence 19, Appl
36	181	90.5	138	4	US-09-570-921-19	Sequence 28, Appl
37	181	90.5	269	4	US-08-965-056-28	Sequence 28, Appl
38	180	90.0	36	4	US-09-082-279B-642	Sequence 642, App
39	180	90.0	36	4	US-09-315-304B-642	Sequence 642, App
40	180	90.0	138	4	US-09-570-921-5	Sequence 5, Appl1
41	180	90.0	613	4	US-09-257-490-14	Sequence 14, Appl
42	180	90.0	850	2	US-08-448-603A-28	Sequence 28, Appl
43	180	90.0	850	3	US-09-134-075-28	Sequence 28, Appl
44	180	90.0	850	4	US-09-492-739-28	Sequence 28, Appl
45	179	89.5	138	4	US-09-570-921-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-073-028-4  
Sequence 4, Application US/08073028

Patent No. 5464933

GENERAL INFORMATION:

APPLICANT: Biologest, Dani P.

APPLICANT: Mathews, Thomas J.

APPLICANT: Wild, Carl T.

TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/073,028

FILING DATE: 07-JUN-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO. 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-073-028-4

Query Match 100.0%; Score 200; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANIMNMF 36  
|||||

Db 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLNMNF 36

RESULT 2

US-08-486-099-4

Sequence 4, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-4

Query Match 100.0%; Score 200; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.8e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLNMNF 36

Db 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLNMNF 36

RESULT 3

US-08-360-107A-4

Sequence 4, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-4

Query Match 100.0%; Score 200; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.8e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLNMNF 36

Db 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLNMNF 36

RESULT 4

US-08-484-223B-4

Sequence 4, Application US/08484223B

Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
DB-484-223B-4

Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTGIIYNLLEESONOEKNEOELLELDKKNANLWNMF 36  
Db 1 YTGIIYNLLEESONOEKNEOELLELDKKNANLWNMF 36

RESULT 5  
US-08-919-597-4  
Sequence 4, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-4

Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTGIIYNLLEESONOEKNEOELLELDKKNANLWNMF 36  
Db 1 YTGIIYNLLEESONOEKNEOELLELDKKNANLWNMF 36

RESULT 6  
US-08-475-668A-4  
Sequence 4, Application US/08475668A  
Patent No. 606065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-4

Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTGIIYNLLEESONOEKNEOELLELDKKNANLWNMF 36  
Db 1 YTGIIYNLLEESONOEKNEOELLELDKKNANLWNMF 36

RESULT 7  
US-08-485-551A-4  
Sequence 4, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-4  
Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
DB 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
RESULT 8  
US-08-471-913A-4  
Sequence 4, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSSTEIN-BARR VIRUS  
TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-4  
Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
DB 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
RESULT 9  
US-08-554-616-4  
Sequence 4, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-004-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-554-616-4

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNF 36  
 1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNF 36

RESULT 10  
 US-08-485-264A-4  
 Sequence 4, Application US/08485264A  
 Patent No. 6228983

GENERAL INFORMATION:  
 APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Peteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
 TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
 NUMBER OF SEQUENCES: 232  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Pennile & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/485,264A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-021  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide

US-08-485-264A-4

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNF 36  
 1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNF 36

RESULT 11  
 US-09-082-279B-1358  
 Sequence 1358, Application US/09082279B  
 Patent No. 6258782

GENERAL INFORMATION:  
 APPLICANT: Barney, Shawn  
 APPLICANT: Guthrie, Kelly  
 APPLICANT: Merutka, Gene  
 APPLICANT: Anwer, Mohamed  
 APPLICANT: Lambert, Dennis  
 TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
 TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
 FILE REFERENCE: 7872-043  
 CURRENT APPLICATION NUMBER: US/09/082,279B  
 CURRENT FILING DATE: 1998-05-20  
 NUMBER OF SEQ ID NOS: 1515  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 1358  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Core polypeptide  
 US-09-082-279B-1358

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNF 36  
 1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNF 36

RESULT 12  
 US-09-082-279B-1359  
 Sequence 1359, Application US/09082279B  
 Patent No. 6258782

GENERAL INFORMATION:  
 APPLICANT: Barney, Shawn  
 APPLICANT: Guthrie, Kelly  
 APPLICANT: Merutka, Gene  
 APPLICANT: Anwer, Mohamed  
 APPLICANT: Lambert, Dennis  
 TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
 TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
 FILE REFERENCE: 7872-043  
 CURRENT APPLICATION NUMBER: US/09/082,279B  
 CURRENT FILING DATE: 1998-05-20  
 NUMBER OF SEQ ID NOS: 1515  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 1359  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Core polypeptide  
 US-09-082-279B-1359

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36

RESULT 13  
US-08-474-349A-4  
Sequence 4, Application US/08474349A  
Patent No. 6333395

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petterway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
NUMBER OF SEQUENCES: 517  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2211

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,349A  
FILING DATE: 07-JUN-1995

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-08-474-349A-4

Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36

RESULT 14  
US-09-315-304B-1358

Sequence 1358, Application US/09315304B  
Patent No. 6348568

GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.  
APPLICANT: Anwer, M.

APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
TITLE OF INVENTION: PROPERTIES  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1358  
LENGTH: 36  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1358

Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36

RESULT 15  
US-09-315-304B-1359

Sequence 1359, Application US/09315304B  
Patent No. 6348568

GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.

APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
TITLE OF INVENTION: PROPERTIES  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1359  
LENGTH: 36  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1359

Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36

Search completed: May 16, 2003, 11:22:10  
Job time : 10.1928 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-4  
Perfect score: 200  
Sequence: 1 YTGIIYNLEESQNOQEKNEQLLELDKWMANIMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

al number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA.\*  
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2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppaa/PCT05\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep.\*  
9: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep.\*  
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12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200	100.0	269	10	US-09-854-816-33
2	185	92.5	233	10	US-09-854-816-50
3	185	92.5	267	10	US-09-854-816-38
4	185	92.5	268	10	US-09-854-816-41
5	183	91.5	269	10	US-09-854-816-43
6	182	91.0	46	10	US-09-854-816-110
7	182	91.0	268	10	US-09-854-816-113
8	182	91.0	269	10	US-09-854-816-48
9	182	91.0	270	10	US-09-854-816-67
10	181	90.5	269	10	US-09-854-816-28
11	179	89.5	268	10	US-09-854-816-9
12	179	89.5	268	10	US-09-854-816-26
13	179	89.5	269	10	US-09-854-816-12
14	179	89.5	619	10	US-09-891-609-4
15	179	89.5	646	10	US-09-891-609-2
16	179	89.5	847	10	US-09-476-242-2
17	178	89.0	46	10	US-09-854-816-109
18	178	89.0	145	12	US-10-000-321-11
19	178	89.0	268	10	US-09-854-816-40

20	178	89.0	269	10	US-09-854-816-6	Sequence 6, Appl
21	178	89.0	269	10	US-09-854-816-30	Sequence 30, Appl
22	178	89.0	269	10	US-09-854-816-31	Sequence 31, Appl
23	178	89.0	269	10	US-09-854-816-42	Sequence 42, Appl
24	177	88.5	233	10	US-09-854-816-49	Sequence 49, Appl
25	176	88.0	36	10	US-09-779-451-44	Sequence 44, Appl
26	176	88.0	46	10	US-09-779-451-42	Sequence 42, Appl
27	176	88.0	268	10	US-09-854-816-68	Sequence 68, Appl
28	176	88.0	268	10	US-09-854-816-71	Sequence 71, Appl
29	176	88.0	269	10	US-09-854-816-21	Sequence 21, Appl
30	176	88.0	269	10	US-09-854-816-22	Sequence 22, Appl
31	176	88.0	269	10	US-09-854-816-44	Sequence 44, Appl
32	176	88.0	269	10	US-09-854-816-46	Sequence 46, Appl
33	175	87.5	36	9	US-09-874-475-16	Sequence 16, Appl
34	175	87.5	36	9	US-10-116-797-1	Sequence 1, Appl
35	175	87.5	36	9	US-09-493-346-1	Sequence 1, Appl
36	175	87.5	36	10	US-09-796-202-10	Sequence 10, Appl
37	175	87.5	36	10	US-09-779-451-5	Sequence 5, Appl
38	175	87.5	36	10	US-09-834-628-1	Sequence 1, Appl
39	175	87.5	36	10	US-09-854-816-1	Sequence 1, Appl
40	175	87.5	36	10	US-09-854-816-108	Sequence 108, App
41	175	87.5	37	9	US-09-848-616-176	Sequence 176, App
42	175	87.5	46	10	US-09-779-451-41	Sequence 41, Appl
43	175	87.5	56	10	US-09-779-451-4	Sequence 4, Appl
44	175	87.5	177	9	US-10-040-349B-2	Sequence 2, Appl
45	175	87.5	221	9	US-10-059-271-84	Sequence 84, Appl

## ALIGNMENTS

RESULT 1  
US-09-854-816-33  
; Sequence 33, Application US/09854816  
; Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasinik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-854-816-33

Query Match 100.0%; Score 200; DB 10; Length 269;  
Best Local Similarity 100.0%; Pred. No. 3,1e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEQELLELDKMANLNMWF 36  
|||||  
DB 169 YTGIIYNLLEESONQOEKNEQELLELDKMANLNMWF 204

RESULT 2  
US-09-854-816-50  
Sequence 50, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpactin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-854-816-50

Query Match 92.5%; Score 185; DB 10; Length 233;  
Best Local Similarity 88.9%; Pred. No. 1.6e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEQELLELDKMANLNMWF 36  
|||||  
DB 168 YTSIIYNLLEESONQOEKNEQELLELDKMANLNMWF 203

RESULT 3

US-09-854-816-38  
Sequence 38, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpactin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-854-816-38

Query Match 92.5%; Score 185; DB 10; Length 267;  
Best Local Similarity 88.9%; Pred. No. 1.8e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEQELLELDKMANLNMWF 36  
|||||  
DB 168 YTGIIYNLLEESONQOEKNEQELLELDKMANLNMWF 203

RESULT 4  
US-09-854-816-41  
Sequence 41, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way



CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-09-854-816-41  
Query Match 92.5%; Score 185; DB 10; Length 268;  
Best Local Similarity 88.9%; Pred. No. 1,8e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGIIYNLEESQNOEKNEQELLEDKWANIWMNF 36  
Db 168 YTGIIYNLEESQNOEKNEQELLEDKWASIWMNF 203  
RESULT 5  
US-09-854-816-43  
Sequence 43, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-09-854-816-43  
Query Match 91.5%; Score 183; DB 10; Length 269;  
Best Local Similarity 86.1%; Pred. No. 3.1e-14;  
Matches 31; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTGIIYNLEESQNOEKNEQELLEDKWANIWMNF 36  
Db 169 YTGIIYNLEESQNOEKNEQELLEDKWASIWMNF 204  
RESULT 6  
US-09-854-816-110  
Sequence 110, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 110:  
US-09-854-816-110  
Query Match 91.0%; Score 182; DB 10; Length 46;



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-854-816-67

Query Match 91.0%; Score 182; DB 10; Length 270;  
Best Local Similarity 88.9%; Pred. No. 4,1e-14;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEDELLEDKMANLWNMF 36  
DB 170 YTSIIYNLLEESONQOEKNEDELLEDKMANLWNMF 205

RESULT 10  
US-09-854-816-28  
Sequence 28, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-09-854-816-28

Query Match 90.5%; Score 181; DB 10; Length 269;  
Best Local Similarity 88.9%; Pred. No. 5.4e-14;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEDELLEDKMANLWNMF 36  
DB 169 YTSIIYNLLEESONQOEKNEDELLEDKMANLWNMF 204

RESULT 11  
US-09-854-816-9  
Sequence 9, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-854-816-9

Query Match 89.5%; Score 179; DB 10; Length 268;  
Best Local Similarity 86.1%; Pred. No. 9.3e-14;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEDELLEDKMANLWNMF 36  
DB 168 YTSIIYNLLEESONQOEKNEDELLEDKMANLWNMF 203

RESULT 12  
US-09-854-816-26  
Sequence 26, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovastnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-854-816-26  
Query Match 89.5%; Score 179; DB 10; Length 268;  
Best Local Similarity 86.1%; Pred. No. 9,3e-14;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YTGIIYNLEESONOEKNEDELLELDKWNANLWNMF 36  
DB 168 YTNLITLTLEESONOEKNEDELLELDKWNANLWNMF 203  
RESULT 13  
US-09-854-816-12  
Sequence 12, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovastnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-854-816-12  
Query Match 89.5%; Score 179; DB 10; Length 269;  
Best Local Similarity 86.1%; Pred. No. 9,3e-14;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YTGIIYNLEESONOEKNEDELLELDKWNANLWNMF 36  
DB 169 YTNLITLTLEESONOEKNEDELLELDKWNANLWNMF 204  
RESULT 14  
US-09-891-609-4  
Sequence 4, Application US/09891609  
Patent No. US20020127238A1  
GENERAL INFORMATION:  
APPLICANT: Stamatos, Leonidas  
TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR  
FILE REFERENCE: 2570-1-002N  
CURRENT FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: US/09/891,609  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 619  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-891-609-4  
Query Match 89.5%; Score 179; DB 10; Length 619;  
Best Local Similarity 86.1%; Pred. No. 2,2e-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YTGIIYNLEESONOEKNEDELLELDKWNANLWNMF 36  
DB 574 YTNLITLTLEESONOEKNEDELLELDKWNANLWNMF 609  
RESULT 15  
US-09-891-609-2

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: Sequence 2, Application US/09891609
: Patent No. us20020127238A1
: GENERAL INFORMATION:
: APPLICANT: Statatatos, Leonidas
: TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
: FILE REFERENCE: 2570-1-002N
: CURRENT APPLICATION NUMBER: US/09/891,609
: CURRENT FILING DATE: 2001-06-26
: PRIOR APPLICATION NUMBER: 60/214,608
: PRIOR FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 646
: TYPE: PRN
: ORGANISM: Human immunodeficiency virus type 1
US-09-891-609--2

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		89.5%;	Score 179;	DB 10;	Length 646;
Query Match		86.1%;	Pred. No. 2.3e-13;		
Best Local Similarity					
Matches 31; Conservative	3;	Mismatches . 2;	Indels 0;	Gaps 0;	
Oy	1 YTGITYNLLEESQNOOEKNEDELLDLDRKANLMNF	36			
Ds	YTNLTITLIEESQNOOEKNEDELLDLDRKANLMNF	636			

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GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
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147.792 Million cell updates/sec

Title: US-09-623-533A-5

Perfect score: 193

Sequence: 1 YNSLIYSLLEKSGTOEKNEDLELDKWSLNNMF 36

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

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Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	100.0	36	17 AAR98401	Peptide correspond
2	193	100.0	36	18 AAM17014	DP-178-like peptid
3	193	100.0	36	22 AAG67042	HIV-1 gp41 peptide
4	193	100.0	36	22 AAU14014	DP178 homologue de
5	193	100.0	36	22 AAB92247	Virus related pept
6	193	100.0	36	22 AAB54788	HIV antiviral acti
7	193	100.0	267	19 AAY22819	SEQ ID NO. 15 from
8	193	100.0	267	23 ABG68290	Envelope protein g
9	193	100.0	854	19 AAM43068	HIV-1 gp120 protei
10	193	100.0	856	12 AAR14903	HIV-1(MN) env prot

11	193	100.0	856	16 AAR79173	HIV virus-1 isolat
12	193	100.0	856	18 AAM11579	Human Immunodefici
13	193	100.0	856	19 AAM58805	HIV-1 isolate MN e
14	193	100.0	856	20 AAR88111	Predicted amino ac
15	193	100.0	1188	17 AAR94622	HIV-1 gp160-NY5 p5
16	193	100.0	36	21 AAR98940	Core polypeptide f
17	193	100.0	36	21 AAY89841	Core polypeptide f
18	193	100.0	36	22 AAU70182	HIV viral envelope
19	193	100.0	36	22 ABB01248	Viral DP178/107-11
20	193	100.0	36	22 ABB01249	Viral DP178/107-11
21	193	100.0	36	22 ABB02833	Viral core polypep
22	193	100.0	36	22 AAU13794	DP178-1-like/DP107-1
23	193	100.0	36	22 AAU13795	Core polypeptide T
24	193	100.0	36	22 AAB78241	Core polypeptide T
25	193	100.0	36	22 AAB78242	Core polypeptide T
26	193	100.0	160	21 AAB12265	HIV-1 gp41 ectodom
27	193	100.0	857	12 AAR14904	HIV-1(MN-ST1) env
28	193	100.0	857	18 AAM11580	Human Immunodefici
29	193	100.0	857	20 AAM88112	Predicted amino ac
30	193	100.0	36	22 ABB02834	Viral core polypep
31	193	100.0	36	22 ABB00638	Viral DP178/107-11
32	193	100.0	36	22 ABB02115	Viral core polypep
33	193	100.0	36	22 AAU13186	DP178-1-like/DP107-1
34	193	100.0	36	22 AAB77633	Core polypeptide T
35	193	100.0	850	16 AAB67724	Core polypeptide T
36	193	100.0	36	16 AAR67700	DP-178 homologue d
37	193	100.0	36	22 ABB00639	Viral DP178/107-11
38	193	100.0	36	22 ABB02116	Viral core polypep
39	193	100.0	36	22 AAU13187	DP178-1-like/DP107-1
40	193	100.0	36	22 AAB77634	Core polypeptide T
41	193	100.0	269	19 AAY22832	SEQ ID NO. 28 from
42	193	100.0	269	23 ABB68303	Envelope protein g
43	193	100.0	268	19 AAY22817	SEQ ID NO. 13 from
44	193	100.0	268	23 ABB68288	Envelope protein g
45	193	100.0	855	12 AAR14905	HIV-1 Ba-L clone-e

#### ALIGNMENTS

RESULT 1  
ID AAR98401 standard; peptide; 36 AA.  
XX  
AC AAR98401:  
XX  
DT 17-FEB-1997 (first entry)  
XX  
DE Peptide corresponding to residues 638-673 of HIV-1(MN) gp41.  
XX  
KW Antifusogenic activity; antiviral capability; coiled-coil peptide;  
KW ALMOTIS; 107x178x4; PLZIP search motif; viral transmission; HIV;  
KW Influenza virus; hepatitis B virus.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO9619495-A1.  
XX  
PD 27-JUN-1996.  
XX  
PF 20-DEC-1995; 95WO-US16733.  
XX  
PR 06-JUN-1995; 95US-0470896.  
XX  
PR 20-DEC-1994; 94US-0360107.  
XX  
PA (TRIM-) TRIMERIS INC.  
PA (UYDU-) UNIV DUKE.  
XX  
XX Barney SO, Bologna DP, Lambert DM, Langlois AJ;  
PI Matthews TJ, Petteway SR, Wild CT;  
XX WPT; 1996-309517/31.  
XX

PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP  
 PT sequence search motif  
 PS  
 XX Disclosure: Fig 1; 471pp; English.  
 CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALLMOT15.  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
 CC hepatitis B virus, to a cell.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 100.0%; Score 193; DB 17; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 36  
 1 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 36  
 RESULT 2  
 ID AAM17014 standard; peptide; 36 AA.  
 XX  
 AC AAM17014;  
 XX  
 DT 01-JUL-1997 (first entry)  
 XX  
 DE DP-178-like peptide useful for treatment of HIV infection.  
 XX  
 KW HIV: HIV: human; simian immunodeficiency virus; glycoprotein 41;  
 KW transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
 KW replication; transmission.  
 XX  
 OS Human immunodeficiency virus type 1 MN isolate.  
 XX  
 PN WO9640191-A1.  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US09499.  
 XX  
 PP 07-JUN-1995; 95US-0481957.  
 XX  
 (TRIM-) TRIMERIS INC.  
 XX  
 PI Johnson RM, Lambert DM;  
 XX  
 DR WPI: 1997-099886/09.  
 XX  
 PT Compns. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.  
 XX  
 PS Disclosure: Figure 1; 84pp; English.  
 CC AAM17012-WI7016 are DP-178 homologues that are useful in the  
 CC treatment of HIV infection. DP-178 is a peptide corresponding to  
 CC residues 638-673 of HIV type 1 glycoprotein 41 (gp41) transmembrane  
 CC protein. DP-178 and its derivatives/homologues are used in combination  
 CC with a therapeutic agent, e.g. a reverse transcriptase, viral protease,  
 CC cytochrome, glycosylation or viral mRNA processing inhibitor or a  
 CC nucleoside inhibitor. The peptides work by inhibiting viral replication  
 CC or inhibiting transmission. They may also be used in vaccines for  
 CC protecting against HIV infection.  
 XX  
 SQ Sequence 36 AA:

Query Match 100.0%; Score 193; DB 18; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 36  
 1 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 36  
 RESULT 3  
 ID AAG67042 standard; peptide; 36 AA.  
 XX  
 AC AAG67042;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE HIV-1 gp41 peptide DP178 homologue.  
 XX  
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection; DP178.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200164013-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 07-FEB-2001; 2001WO-US03988.  
 XX  
 PR 29-FEB-2000; 2000US-0515965.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX  
 DR WPI: 2001-514829/56.  
 XX  
 PT Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 XX  
 PS Disclosure: Fig 1; 587pp; English.  
 XX  
 CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1/IIA1 transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 100.0%; Score 193; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 36  
 1 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 36  
 RESULT 4  
 ID AAU14014 standard; peptide; 36 AA.  
 XX  
 AC AAU14014;



XX		21-NOV-2001	(first entry)	
DT				
XX		DPI78 homologue derived from HIV-1 isolate MN.		
DE				
XX		Anti-retroviral; DPI78-like; DP107-like; transmembrane protein gp41;		
KW		antifusogenic; antiviral; HIV transmission.		
XX				
OS		Human immunodeficiency virus 1 isolate MN.		
XX				
PN		MO200151673-A2.		
XX				
PD		19-JUL-2001.		
XX				
PE		05-JUL-2000; 2000WO-US35727.		
XX				
PR		09-JUL-1999; 99US-0350841.		
PA		(TRIM-) TRIMERIS INC.		
XX				
XC		Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;		
DR		WPI: 2001-442157/47.		
XX				
PT		Identifying a compound that inhibits the formation of or disrupts a		
PT		DP107/DPI78 complex, especially compounds with antifusogenic, antiviral		
PT		or intracellular modulatory activity, by detecting the formation of a		
XT		DP107/DPI78 complex -		
XX				
XX		Disclosure; Fig 1; 259pp; English.		
CC				
CC		The present invention relates to peptides which exhibit anti-retroviral		
CC		activity. The peptides of the invention (AAU12559-AAU14009) comprise		
CC		DP178-like and DP107-like peptides. The DP178 peptide corresponds		
CC		to amino acids 639-673 of the transmembrane protein gp41 from human		
CC		immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide		
CC		corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention		
CC		also relates to a method of identifying compounds that inhibit the		
CC		formation of or disrupts a DP107/DPI78 complex. The method comprises		
CC		detecting the formation of a DP107/DPI78 complex, both in the presence		
CC		or absence of a test compound, in a reaction mixture containing DP107		
CC		and DP178 peptides. The method is useful for identifying compounds,		
CC		including small molecule compounds, which may themselves exhibit,		
CC		antifusogenic, antiviral or intracellular modulatory activity. The		
CC		DP178-like/DP107-like peptides are useful to inhibit human and non-human		
CC		retroviral, particularly HIV, transmission to uninfected cells. The		
CC		present sequence represents a DP178 homologue derived from		
CC		HIV-1 isolate MN.		
●				
	Sequence	36 AA:		
	Query Match	100.0%; Score 193; DB 22; Length 36;		
	Best Local Similarity	100.0%; Pred. No. 2.9e-17;		
	Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 YTSLIYSLEKSQTQOEKNEDELLEDKWSAMNMF 36			
DB	1 YTSLIYSLEKSQTQOEKNEDELLEDKWSAMNMF 36			
RESULT 5				
ID	AAB92247			
AC	AAB92247 standard; Peptide: 36 AA.			
XX				
AC	AAB92247;			
XX				
DT	22-JUN-2001 (first entry)			
XX				
DE	Virus related peptide SEQ ID NO:1423.			
KW	Protection; endogenous therapeutic peptide; peptidase; conjugation;			
KW	blood component; modification; succinylamide; maleimido group; amino;			
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.			

XX	Homio sapiens.
OS	Synthetic.
PN	WO200069900-A2.
XX	
PD	23-NOV-2000.
XX	
PF	17-MAY-2000; 2000WO-US13576.
XX	
PR	17-MAY-1999; 99US-0134406.
PR	10-SEP-1999; 99US-0153406.
PR	15-OCT-1999; 99US-0159783.
XX	
PA	(CONJ-) CONJUCHEM INC.
XX	
PI	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX	
DR	WPI: 2001-112059/12.
XX	
PT	Modifying and attaching therapeutic peptides to albumin prevents
PT	peptidase degradation, useful for increasing length of in vivo activity
PT	-
PS	Disclosure; Page 663; 733pp; English.
XX	
CC	The present invention describes a modified therapeutic peptide (I)
CC	comprising a therapeutically active amino acid region (II) and a
CC	reactive group (II) (e.g. succinimide) and maleimido groups) attached to
CC	a less therapeutically active amino acid region (IV), which covalently
CC	bonds with amino/hydroxyl/thiol groups on blood components to form a
CC	peptide stable therapeutic peptide composed of 3-50 amino acids.
CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC	factors and neurotransmitters, to protect them from peptidase activity
CC	in vivo for the treatment of various disorders. Endogenous therapeutic
CC	peptides are not suitable as drug candidates as they require frequent
CC	administration due to rapid degradation by peptidases in the body.
CC	Modifying and attaching therapeutic peptides to albumin prevents or
CC	reduces the action of peptidases to increase length of activity (half
CC	life) and specifically as bonding to large molecules decreases
CC	intracellular uptake and interference with physiological processes.
CC	AAB90829 to AAB9441 represent peptides which can be used in the
CC	exemplification of the present invention.
XX	
SO	Sequence 36 AA;
Query Match	100.0%; Score 193; DB 22; Length 36;
Best Local Similarity	100.0%; Pred. No. 2,9e-17;
Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 YTSLSLEKSTOQEKNEDELLELDKASIMNF 36
DB	1 YTSLSLEKSTOQEKNEDELLELDKASIMNF 36
RESULT 6	
AAB54788	
ID	AAB54788 standard; Peptide; 36 AA.
XX	
AC	AAB54788;
XX	
DT	05-MAR-2001 (first entry)
XX	
DE	HIV antiviral activity exhibiting peptide SEQ ID NO:5.
XX	
KW	Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW	antifusogenic; mobile blood component; measles virus; MeV; SIV;
KW	simian immunodeficiency virus; human parainfluenza virus; HIV; RSV;
KW	human respiratory syncytial virus; human immunodeficiency virus; HIV.
OS	Human immunodeficiency virus type 1.
XX	
PN	WO200069902-A1.

XX 23-NOV-2000.  
PD  
XX  
XX 17-MAY-2000; 2000WO-US13651.  
PE  
XX  
XX 17-MAY-1999; 99US-0134406.  
PR 10-SEP-1999; 99US-0153406.  
XX  
XX (CONJ-) CONJUCHEM INC.  
PA  
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;  
XX  
XX WPI; 2001-007496/01.  
DR  
XX  
XX A modified peptide and a reactive group which is reactive with amino  
PT groups, hydroxyl groups, or thiol groups on blood components to form  
PT stable covalent bonds useful for treatment of viral infections, e.g.  
PT human immunodeficiency virus  
XX  
XX Claim 6; Page 174; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)  
CC comprising a peptide that exhibits anti-viral activity and a reactive  
CC group which is reactive with amino groups, hydroxyl groups, or thiol  
CC groups on blood components to form stable covalent bonds. (I) has  
CC anti-viral and anti-fusogenic activities. (I) inhibits viral infection  
CC of cells by inhibiting cell-cell fusion or free virus infection or to  
CC reduce the level of membrane fusion events between two or more entities,  
CC e.g., virus-cell or cell-cell, relative to the level of membrane fusion  
CC that occurs in the absence of the peptide. (I) is useful in the  
CC treatment of patients who are suffering from viral infection, e.g. HIV,  
CC RSV, HPIV, MCV, and SV. (I) may be administered prophylactically to  
CC previously uninfected individuals. This is useful in cases where an  
CC individual has been subjected to a high risk of exposure to a virus.  
CC By bonding of long-lived components of the blood, such as immunoglobulin,  
CC serum albumin, red blood cells and platelets the activity in vivo and a  
CC for days to weeks. This is due to improved stability in vivo and a  
CC reduced susceptibility to peptidase or protease degradation. This  
CC minimises the need for more frequent, or even continual, administration  
CC of the peptides. AAB54784 to AAB55431 represent peptides used in the  
CC exemplification of the present invention.  
XX  
XX

Sequence 36 AA:

Query Match 100.0%; Score 193; DB 22; Length 36;  
Best Local Similarity 100.0%; Pred. NO. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSYLSLEKSOQOQEKNEQELLELDKWSLMMNF 36  
1 YTSLSYLSLEKSOQOQEKNEQELLELDKWSLMMNF 36

RESULT 7

ID AAY22819 standard; Protein: 267 AA.

AC AAY22819;

DT 19-AUG-1999 (first entry)

DE SEQ ID NO. 15 from WO9820036.

XX HIV; gp41 protein; constrained helical peptide; HIV infection;

KW vaccine; antibody; viral membrane fusion; viral infectivity;

KW ligand affinity purification; protein A replacement;

XX immunoglobulin purification; epitope mimic.

OS Human immunodeficiency virus.

XX WO9820036-A1.  
XX  
XX  
XX  
XX 14-MAY-1998.  
PD

XX 05-NOV-1997; 97WO-US20069.  
PE  
XX  
XX 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
XX (GETH ) GENENTECH INC.  
PA  
PI Braisted A, Judice JK, McDowell RS, Pheelan JC, Starovasnik MA;  
XX  
XX Wells JA;  
XX  
XX WPI; 1998-286866/25.  
DR  
XX

XX Production of constrained helical peptide(s) by linking side chains  
PT on termini of octapeptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
XX Claim 11; Page 155; 279pp; English.

XX Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAY22871, AAY22880, AAY22888 and  
CC AAY22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification), as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
XX

Sequence 267 AA:

Query Match 100.0%; Score 193; DB 19; Length 267;  
Best Local Similarity 100.0%; Pred. NO. 2.7e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSYLSLEKSOQOQEKNEQELLELDKWSLMMNF 36  
Db 167 YTSLSYLSLEKSOQOQEKNEQELLELDKWSLMMNF 202

RESULT 8

ID ABG68290 standard; Protein: 267 AA.

AC ABG68290;

DT 07-OCT-2002 (first entry)

DE Envelope protein gp41 from HIV clade B strain #9.

XX HIV; glycoprotein; gp41; antigen; helical conformation;

KW virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;

KW viral envelope protein; vaccine; virucide; anti-HIV.

OS Human immunodeficiency virus type 1 clade B.

XX US6271198-B1.  
XX  
XX  
XX  
XX 07-AUG-2001.  
XX

PF 05-NOV-1997; 97US-0965056.  
 XX  
 PR 16-JUN-1997; 97US-049787P.  
 PR 06-NOV-1996; 96US-0743698.  
 PR 16-JUN-1997; 97US-0876698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovassnik MA;  
 PI Wells JA;  
 XX WPI: 2002-487624/52.  
 DR  
 XX  
 PR New cyclic peptides from human immune deficiency virus gp41, useful for  
 PR treatment or prevention of HIV infection, are constrained to have  
 PR alpha-helical conformation -  
 PS Disclosure: Column 151-152; 175pp; English.  
 XX  
 CC The invention relates to cyclic peptides (A) with a constrained helical  
 CC conformation, derived from gp41 (glycoprotein 41), a viral envelope  
 CC protein of human immunodeficiency virus (HIV). The cyclic  
 CC peptides have formulas given in the specification part of which are  
 CC derived from a consensus sequence of gp41 derived from HIV clades A, B,  
 CC C, D, E or O. The peptides are used to cause induction of a specific  
 CC immune response, resulting in antibodies that prevent virus-induced  
 CC membrane fusion. The peptides are used to treat subjects with, or at risk  
 CC of, HIV infection, either as antifusion/anti-infection agents or,  
 CC preferably where associated with a carrier, as an immunogen (including as  
 CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or  
 CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency  
 CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in  
 CC cases of health care accidents. The peptides can be based on specific HIV  
 CC strains, e.g. breakthrough isolates of HIV that have developed during  
 CC vaccine trials, so a combination of them should cover a wide range of  
 CC protection. The present sequence is gp41 protein from a particular  
 CC HIV clade used to derive a consensus sequence of gp41.  
 XX  
 SQ Sequence 267 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 23; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNMF 36  
 DB 167 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNMF 202  
 XX  
 ULT 9  
 AAW43068  
 ID AAW43068 standard; peptide; 854 AA.  
 XX  
 AC AAW43068;  
 XX  
 DT 11-SEP-1998 (first entry)  
 XX  
 DE HIV-1 gp120 protein fragment from isolate MN.  
 XX  
 KW gp120 protein: purification; fractionation; ion exchange; chromatography;  
 KW binding affinity; CD4; hydrophobic interaction; size exclusion; vaccine.  
 XX  
 OS Human immunodeficiency virus type 1.  
 OS  
 PN US5696238-A.  
 XX  
 PD 09-DEC-1997.  
 XX  
 PF 11-MAY-1995; 95US-0439286.  
 XX  
 PR 20-AUG-1991; 91US-0684963.  
 PR 16-AUG-1993; 93US-0109002.  
 PR 09-MAY-1994; 94US-0240073.

PR 11-MAY-1995; 95US-0439286.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Haigwood NL, Scandella C;  
 XX  
 DR WPI: 1998-041353/04.  
 XX  
 PT Purification of HIV gp120 - using chromatographic methods  
 XX  
 PS Disclosure: Fig 2A-W; 53pp; English.  
 XX  
 CC AAW43066-W43080 are fragments of the gp120 protein from different human  
 CC immunodeficiency virus type I (HIV-1) isolates. These proteins are used  
 CC in a novel method for purifying HIV gp120 so as to provide a purified  
 CC gp120 glycoprotein having protein/protein binding properties  
 CC substantially identical to natural viral HIV gp120. The method involves  
 CC fractionating a crude gp120 preparation containing full-length,  
 CC glycosylated gp120 using ion exchange chromatography so as to provide a  
 CC first collection of fractions. A fraction from the first collection is  
 CC selected that exhibits specific binding affinity for CD4 peptide.  
 CC thereby producing a first fractionated material. The first fractionated  
 CC material is fractionated by hydrophobic interaction chromatography so as  
 CC to provide a second collection of fractions from which a second  
 CC collection is selected that exhibits specific binding affinity for CD4  
 CC peptide. This second fraction is fractionated by size exclusion  
 CC chromatography so as to provide a third collection of fractions  
 CC exhibiting specific binding affinity for CD4 peptide, thereby providing  
 CC the purified gp120. The purified gp120 can be used for antibody  
 CC production and in vaccines.  
 XX  
 SQ Sequence 854 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 19; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNMF 36  
 DB 637 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNMF 672  
 XX  
 RESULT 10  
 AAR14903  
 ID AAR14903 standard; Protein; 856 AA.  
 XX  
 AC AAR14903;  
 XX  
 DT 17-DEC-2001 (updated)  
 DT 05-FEB-1992 (first entry)  
 XX  
 DE HIV-1(MN) env protein.  
 XX  
 KW human immunodeficiency virus; United States; MN isolate; AIDS;  
 KW envelope protein.  
 XX  
 OS Human immunodeficiency virus-1 (MN).  
 OS  
 PN USN7599491-N.  
 XX  
 PD 15-OCT-1991.  
 XX  
 PF 17-OCT-1990; 90US-0183830.  
 XX  
 PR 17-OCT-1990; 90US-0599491.  
 XX  
 PA (USSH ) NAT INST OF HEALTH.  
 XX  
 PI Reitz M;  
 PI  
 DR WPI: 1991-346752/47.  
 DR N-PSDB; AAO14751.  
 XX

PT US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are  
 XX useful in therapeutics, vaccines and diagnostic tests  
 PS Example 1; Fig 3; 61pp; English.  
 XX  
 CC The permuted circular unintegrated viral DNA representing the  
 CC complete HIV-1(MN) genome was cloned into the EcoRI site of lambda  
 CC gTWS.Lambda B DNA from total DNA of H9 cells producing HIV-1 (MN).  
 CC This clone was designated lambda MN-PH1; it was subcloned in M13mp18  
 CC and M13mp19 and the DNA sequence of the entire clone was obtained  
 CC the amino acid sequence of the env protein was deduced from it.  
 CC (Note: Revised entry submitted to correct the patent number format of  
 CC US Government-owned NTIS applications to prevent clashes with ongoing US  
 CC granted patent numbers. For further information please visit the Derwent  
 CC web site at [www.derwent.com/dwpi/updates/ntis\\_us.html](http://www.derwent.com/dwpi/updates/ntis_us.html).)  
 CC  
 SQ Sequence 856 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 12; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLYSLEKSOTOEKNQELLEDKWSLWMPF 36  
 DB 639 YTSLYSLEKSOTOEKNQELLEDKWSLWMPF 674  
 RESULT 11  
 AAR79173  
 ID AAR79173 standard; protein; 856 AA.  
 AC AAR79173;  
 XX  
 DT 09-MAR-1996 (first entry)  
 XX  
 DE HIV virus-1 isolate MN gp120 sequence.  
 XX  
 KW HIV virus-1; gp120; therapeutic; immunogen; diagnostic; peptomer.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT Protein 1..856  
 FT /note= "HIV-1 isolate MN gp120 sequence"  
 FT Misc-difference 301..400  
 FT /note= "V3 loop"  
 FT Region 401..800  
 FT /note= "CD4 binding region"  
 FT Region 419..436  
 FT /note= "CD4 binding region consensus sequence"  
 FT Region 801..856  
 FT /note= "MHC II homology region"  
 FT Region 824..830  
 FT /note= "MHC II homology region consensus sequence"  
 XX  
 PN WO9520162-A1.  
 XX  
 PD 27-JUL-1995.  
 XX  
 PF 19-JAN-1995; 95WO-US00760.  
 XX  
 PR 19-JAN-1994; 94US-0184330.  
 XX  
 PA (USSH ) US SEC DEPT HEALTH.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Harris-Kelson TA, Robert-Guioff M, Robey FA;  
 XX  
 DR WPI; 1995-269543/35.  
 XX  
 PT Peptide analogues useful as therapeutic agents, immunogens, or for  
 PT diagnosis of disease - maintain conformation of native protein,  
 PT e.g. HIV gp120 peptide.

XX  
 PS Disclosure; Fig 1; 55pp; English.  
 XX  
 CC Peptide analogues of HIV virus antigen contain a plurality of  
 CC peptide monomers, each comprising the gp120 CD4 binding region  
 CC consensus sequence (amino acids 419-436) (see AAR79172). The  
 CC synthetic peptomers are useful as therapeutic agents, immunogens  
 CC in vaccine compositions or for the diagnosis of disease.  
 CC Since the analogues maintain the conformation of the native proteins  
 CC from which they are derived (the consensus sequence), they are  
 CC useful against infection by various HIV-1 and HIV-2 isolates (see  
 CC AAR79174-84).  
 CC  
 SQ Sequence 856 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 16; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLYSLEKSOTOEKNQELLEDKWSLWMPF 36  
 DB 639 YTSLYSLEKSOTOEKNQELLEDKWSLWMPF 674  
 RESULT 12  
 AAW1579  
 ID AAW1579 standard; Protein; 856 AA.  
 AC AAW1579;  
 XX  
 DT 25-MAR-1997 (first entry)  
 XX  
 DE Human Immunodeficiency Virus-1 strain MN-PH1 envelope protein.  
 XX  
 KW Acquired immune deficiency syndrome; AIDS; envelope protein;  
 KW env gene; vaccine.  
 XX  
 OS Human immunodeficiency virus type 1 (strain MN-PH1).  
 XX  
 PN US5576000-A.  
 XX  
 PD 19-NOV-1996.  
 XX  
 PF 17-OCT-1990; 90US-0599491.  
 XX  
 PR 17-OCT-1990; 90US-0599491.  
 PR 25-FEB-1993; 93US-0022835.  
 PR 15-FEB-1995; 95US-0388809.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Franchini G, Gallo RC, Gartner S, Lori FC, Markham PD;  
 PI Popovic M, Reitz MS;  
 XX  
 DR WPI: 1997-011206/01.  
 DR N-PSDB: AAT58549.  
 XX  
 PD New isolated envelope protein of HIV-1 strain BA-L and recombinant  
 PT equivalents - useful as immunogens for vaccines and antibody prodn.,  
 PT typical of US clinical isolates  
 XX  
 PS Example; Fig 3; 86pp; English.  
 XX  
 CC The permuted circular unintegrated viral DNA representing the  
 CC complete HIV-1(MN) genome was cloned into the EcoRI site of lambda  
 CC gTWS.Lambda B DNA from total DNA of H9 cells producing HIV-1(MN)  
 CC isolate. The clone was designated lambda MN-PH1. The present sequence  
 CC was deduced from the env gene region of the MN-PH1 genome.  
 CC  
 SQ Sequence 856 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 18; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;

	Matches	36	Conservative	0	Mismatches	0	Indels	0	Gaps	0
OY	1	YTSLIYSLEKSTQTOEKNEDELLEIDKWSIWMNF	36							
Db	639	YTSLIYSLEKSTQTOEKNEDELLEIDKWSIWMNF	674							
RESULT 13										
AAW58805	1	AAW58805 standard; protein; 856 AA.								
AAW58805	1	AAW58805; 23-JUL-1998 (first entry)								
XX	DE	HIV-1 isolate MN envelope protein gp120.								
XX	XX	Envelope protein; gp120; peptomer; peptides oligomer; detection;								
XX	KW	CD4-binding region; anti-HIV antibody; therapeutic; infection;								
XX	FT	inhibition; T cell; immunogenic agent; antibody; vaccine; epitope.								
XX	FT	Human immunodeficiency virus type 1.								
XX	XX	Key	Location/Qualifiers							
XX	FT	Region	301..335							
XX	FT	Region	/label= V3 loop							
XX	FT	Region	401..800							
XX	FT	Region	/label= CD4_binding_region							
XX	FT	Region	801..855							
XX	FT	Region	/note= "region with MHC II homology"							
XX	PM	US5750332-A.								
XX	PD	12-MAY-1998.								
XX	PE	19-JAN-1995; 95US-0375100.								
XX	PR	19-JAN-1995; 95US-0375100.								
XX	PR	19-JAN-1994; 94US-0184330.								
XX	PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.								
XX	PI	Harris-Kelson TA, Robert-Guroff M, Robey FA;								
XX	DR	WPI; 1998-296756/26.								
XX	PT	HIV gp120 peptide oligomers - useful as diagnostic, immunogenic or								
XX	PT	therapeutic agents								
XX	XX	Disclosure: Fig 1; 25pp; English.								
XX	XX	This sequence represents the Human Immunodeficiency Virus Type I (HIV-1)								
XX	CC	isolate MN envelope protein gp120. This protein is used in a novel								
XX	CC	method to produce and analyse peptides oligomers, "peptomers", consisting								
XX	CC	of several peptide monomers arranged head to tail, each monomer								
XX	CC	comprising a sequence from a CD4-binding region of HIV gp120. Such								
XX	CC	peptides are useful as assay reagents for detecting anti-HIV antibodies								
XX	CC	in biological samples, e.g. blood samples, or as a therapeutic agent for								
XX	CC	inhibiting infection of T cells by HIV and as an immunogenic agent for								
XX	CC	antibody production e.g. in vaccines. They are preferably synthetically								
XX	CC	produced and thus are consistent in their sequence and structure. Most								
XX	CC	HIV vaccines and detection peptides used currently rely on fragments of								
XX	CC	inactivated live viruses and thus may not contain the correct epitopes								
XX	CC	to elicit an immune response.								
XX	SO	Sequence 856 AA;								
XX	XX	Query Match 100.0%; Score 193; DB 19; Length 856;								
XX	XX	Best Local Similarity 100.0%; Pred. No. 9.9e-16;								
XX	XX	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0								
XX	XX	1 YTSLIYSLEKSTQTOEKNEDELLEIDKWSIWMNF 36								
XX	XX									
XX	XX	YTSLIYSLEKSTQTOEKNEDELLEIDKWSIWMNF 674								

```

DB      639 YTSLIYSLEKSGTOOEKNEQELLELDKWSALMNMF 674
RESULT 14
ID      AAW88111 standard; Protein: 856 AA.
XX      AC
XX      AAW88111;
XX      DT 09-APR-1999 (first entry)
XX      DE Predicted amino acid sequence of the MN-PH1 envelope (env) protein.
XX      KW MN-PH1 clone; HIV-1; HIV-1 strain BA-L; envelope protein; vaccine;
XX      immunotherapy; HIV infection; immunogen; HIV-1 diagnosis; env; ds.
XX      OS Human immunodeficiency virus type 1.
XX      PN US5869313-A.
XX      PD 09-FEB-1999.
XX      PE 14-MAY-1996; 96US-0647714.
XX      PF 17-OCT-1990; 90US-0599491.
XX      PR 25-FEB-1993; 93US-0022835.
XX      PR 15-FEB-1993; 95US-0388809.
XX      PR 14-MAY-1996; 96US-0647714.
XX      PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX      PI Franchini G, Gallo RC, Gartner S, Lori FC, Markham PD,
PI      Popovic M, Reitz MS.
XX      DR WPI: 1999-152779/13.
XX      PT DNA encoding env protein of the human immune deficiency virus
PT      isolate BA-L - useful for producing protein for use in vaccines, as
PT      assay reagent and to generate antibodies
XX      PS Example 1; Fig 3A-C; 87pp; English.
XX      CC The present sequence represents the predicted amino acid sequence
CC      of the MN-PH1 clone envelope (env) protein. MN-PH1 is a Human
CC      immunodeficiency virus type 1 (HIV-1) clone. The specification
CC      also describes the env and rev coding sequences of the HIV-1
CC      strain BA-L (ATCC 40890). BA-L is more typical of United States
CC      isolates of HIV-1 than previously known strains. Recombinant,
CC      complete env protein of the BA-L strain is used as a vaccine
CC      component and for immunotherapy of existing HIV infections, to
CC      detect HIV-specific antibodies, e.g. in donated blood, and as
CC      an immunogen to raise specific antibodies, for HIV-1 diagnosis.
XX      SQ Sequence 856 AA;
XX
Query Match 100.0%; Score 193; DB 20; Length 856;
Best Local Similarity 100.0%; Pred. No. 9,9e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY      1 YTSLIYSLEKSGTOOEKNEQELLELDKWSALMNMF 36
        |||
Db      639 YTSLIYSLEKSGTOOEKNEQELLELDKWSALMNMF 674
        |||
RESULT 15
ID      AAR94622 standard; Protein: 1188 AA.
XX      AC
XX      AAR94622;
XX      DT 29-AUG-1996 (first entry)
XX      DE HIV-1 gp160-NV5 p55 protein fusion

```

XX	HIV-1; gp160; p55; immunogen; vaccine; AIDS; baculovirus; vector.
XX	Human immunodeficiency virus type 1.
OS	Key Location/Qualifiers
XX	Peptide 1..18
FH	/label= Sig-peptide
FT	/note= "61k signal peptide"
FT	22..504
FT	/label= gp120
FT	117..152
FT	/label= V1
FT	154..191
FT	/label= V2
FT	292..325
FT	/label= V3
FT	Region 380..408
FT	/label= V4
FT	505..743
●	Domain /label= gp41
FT	745..875
FT	/label= p17
FT	Domain 876..1120
FT	/label= p14
FT	1121..1180
FT	Domain /label= p15
PN	W09532000-A1.
XX	30-NOV-1995.
XX	19-MAY-1995; 95WO-US06346.
XX	20-MAY-1994; 94US-0247208.
PR	(MICR-) MICROGENESYS INC.
PA	Debartolomeis J, Hackett CS, Knell JD, Smith GE;
XX	Volvovitz F;
PI	MP1: 1996-020357/02.
XX	N-P5DB; AAT15143.
DR	Isolated nucleic acid encoding HIV gp120-gag fusion protein - useful
XX	as immunogen in vaccines, for detecting antibodies and treating HIV
PT	infections etc.
PT	Example 6; Fig 8A-8J; 74pp; English.
XX	Plasmid A9760 contains a gene fusion (AAT15143) coding for a fusion
CC	protein (AAR94622) between HIV-1 gp160 and p55 proteins. The gene
CC	fusion was obtd. by cloning the gp160 coding sequence into pUC19,
CC	cloning the qP55 coding sequence into Novablue TA PCR vector,
CC	ligating the p55 and gp160 sequences, and cloning the construct into
CC	the baculovirus expression vector MCS12, giving A9760, for
CC	expression in Spodoptera frugiperda cells. The fusion protein is
CC	useful as an immunogen in AIDS vaccines (e.g. to prevent mother to
CC	baby transmission of HIV) or for diagnostic detection of HIV antibodies.
CC	Sequence 1188 AA;
SO	Query Match 100.0%; Score 193; DB 17; Length 1188;
QY	Best Local Similarity 100.0%; Pred. No. 1,4e-15;
Db	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
	1 YTSLYISLEKSSOTOERKEOEELLETDKNASLWNMF 36
	630 YTSLYISLEKSSOTOERKEOEELLETDKNASLWNMF 665

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Search completed: May 16, 2003, 11:12:02
Job time : 32.4578 secs
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GenCore version 5.1.4\_p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-5

Perfect score: 193

Sequence: 1 YTSLLYSLEKSGTQOEKNEDELLELDKMASLMMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_L3:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	193	100.0	859	1 VCLJMN	env polypotein pr
2	179	92.7	358	2 S21998	envelope protein g
3	179	92.7	443	2 C41621	env polypotein p
4	179	92.7	856	1 VCLJ3W	env polypotein pr
5	179	92.7	861	1 VCLJ3C	env polypotein pr
6	178	92.2	853	2 S54384	envelope polypote
7	178	92.2	855	2 VCLJZR	env polypotein pr
8	177	91.7	851	2 S33985	env polypotein -
9	177	91.7	854	2 S13288	env protein - huma
10	177	91.7	856	1 VCLJH3	env polypotein pr
11	177	91.7	861	1 VCLJLV	env polypotein pr
12	176	91.2	357	2 S21994	envelope protein g
13	175	90.7	357	2 S21996	envelope protein g
14	173	89.6	846	1 VCLJMD	env polypotein pr
15	173	89.6	855	1 VCLJAZ	env polypotein pr
16	172	89.1	847	2 T09448	envelope glycoprot
17	172	89.1	847	2 S13289	env protein - huma
18	172	89.1	852	1 VCLJBR	env polypotein -
19	171	88.6	445	2 A41621	env polypotein M
20	170	88.1	357	2 S21992	envelope protein g
21	170	88.1	358	2 S22002	envelope protein g
22	170	88.1	358	2 S22000	envelope protein g
23	170	88.1	358	2 S70417	envelope protein g
24	170	88.1	352	2 T12016	envelope glycoprot
25	169	87.6	357	2 S22004	envelope protein g
26	169	87.6	843	1 H44001	env polypotein pr
27	168	87.0	856	1 T01672	env polypotein pr
28	168	87.0	859	1 VCLJVL	envelope polypote
29	166	86.0	357	2 S22006	envelope protein g

30	161	83.4	729	1 VCLJRX	env polypotein pr
31	161	83.4	861	1 VCLJKB	env polypotein pr
32	159	82.4	136	2 J00266	envelope polypote
33	159	82.4	136	2 J00954	envelope polypote
34	157	81.3	454	2 B41621	env polypotein D
35	156	80.8	868	1 VCLJH4	env polypotein -
36	153	79.3	854	1 VCLJST	env polypotein pr
37	153	79.3	856	1 A44963	env polypotein pr
38	143	74.1	357	2 S21990	envelope protein g
39	134	69.4	877	2 S49197	envelope protein p
40	129	66.8	863	2 A53034	gag polypotein -
41	86	44.6	366	2 B41365	env polypotein -
42	86	44.6	881	1 VCLJG3	env polypotein -
43	86	44.6	881	2 S03068	env protein - huma
44	86	44.6	889	1 VCLJG5	env polypotein -
45	85	44.0	151	2 S30448	env protein - huma

## ALIGNMENTS

RESULT 1  
VCLJMN  
env polypotein precursor - human immunodeficiency virus type 1 (isolate MN)  
N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: A28922  
R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Vitrology 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091  
A:Accession: A28922  
A:Molecule type: DNA  
A:Residues: 1-859 <GUR>  
A:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polypotein; transmembrane pr  
F:1-29/Domain: Signal sequence #status predicted <Sig>  
F:30-859/Product: env polypotein #status predicted <EPP>  
F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,  
F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,  
Query Match 100.0% Score 193; DB 1; Length 859;  
Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLLYSLEKSGTQOEKNEDELLELDKMASLMMNF 36  
DB 642 YTSLLYSLEKSGTQOEKNEDELLELDKMASLMMNF 677  
RESULT 2  
S21998  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 28  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21998; S70425  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL data library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
A:Reference number: S21990  
A:Accession: S21998  
A:Molecule type: DNA  
A:Residues: 1-358 <STE1>  
A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70425

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222,'X',224-358 <STE2>  
 A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:g60183  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 92.7%; Score 179; DB 2; Length 358;  
 Best Local Similarity 88.9%; Pred. No. 2,2e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWMMF 36  
 |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|  
 Db 140 YTSLLYTLIESQNOEQEKNEQELLELDKWSLWMMF 175

## RESULT 3

env polyprotein p - human immunodeficiency virus type 1 (fragment)  
 N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Accession: C41621  
 C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
 A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: C41621

A:Molecule type: DNA

A:Residues: 1-443 <BUR>  
 A:Cross-references: GB:M77230; NID:g328631; PIDN:AAE03792.1; PID:g555015

A:Note: this virus was isolated from the mother's sexual partner

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro  
 F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
 F:252-443/Product: coat protein gp41 (fragment) #status predicted <TMN>  
 F:424-443/Product: transmembrane #status predicted <TMN>  
 F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ce

Query Match 92.7%; Score 179; DB 2; Length 443;  
 Best Local Similarity 88.9%; Pred. No. 2.8e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWMMF 36  
 |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|  
 378 YTSLLYTLIESQNOEQEKNEQELLELDKWSLWMMF 413

## RESULT 4

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)

N:Contains: coat protein gp120; coat protein gp41  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997

C:Accession: A24774  
 R:Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986

A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; MUID:86218077; PMID:2423250

A:Accession: A24774

A:Molecule type: DNA

A:Residues: 1-856 <STA>

A:Cross-references: GB:K03455; GB:M38432; NID:g1906382

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>

F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,  
 Query Match 92.7%; Score 179; DB 1; Length 856;  
 Best Local Similarity 88.9%; Pred. No. 5.9e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWMMF 36  
 |||||:|:|:| |||||:|:~|| |||||:|:~|| |||||:|:~||  
 Db 638 YTSLLYTLIESQNOEQEKNEQELLELDKWSLWMMF 673

## RESULT 5

env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997

C:Accession: B28922  
 R:Gurgoo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-  
 Virolgy 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.

A:Reference number: A28922; MUID:88219542; PMID:3369091

A:Accession: B28922

A:Molecule type: DNA

A:Residues: 1-861 <GUR>

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane pr  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-861/Product: env polyprotein #status predicted <EPP>  
 F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,

Query Match 92.7%; Score 179; DB 1; Length 861;  
 Best Local Similarity 88.9%; Pred. No. 5.9e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWMMF 36  
 |||||:|:|:| |||||:|:~|| |||||:|:~|| |||||:|:~||  
 Db 643 YTSLLYTLIESQNOEQEKNEQELLELDKWSLWMMF 678

## RESULT 6

env polyprotein precursor - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999

C:Accession: S54384  
 R:Theodore, T.; Buckler-White, A.J.  
 submitted to the EMBL Data Library, July 1989

A:Reference number: S54377

A:Accession: S54384

A:Molecule type: genomic RNA

A:Residues: 1-853 <THE>

A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: polyprotein

Query Match 92.2%; Score 178; DB 2; Length 853;  
 Best Local Similarity 88.9%; Pred. No. 7.8e-14;  
 Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWMMF 36  
 |||||:|:~|| |||||:|:~|| |||||:|:~|| |||||:|:~||  
 Db 635 YTGLLYRLIESQNOEQEKNEQELLELDKWSLWMMF 670

## RESULT 7

env polyprotein precursor - human immunodeficiency virus Zr-6  
 N:Alternate names: coat polyprotein



C:Species: human immunodeficiency virus Zr-6  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
C:Accession: D26192  
R:Strinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
Gene 52, 71-82, 1987  
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti  
A:Reference number: A26192; MUID:87248097; PMID:3036660  
A:Accession: D26192  
A:Molecule type: DNA  
A:Residues: 1-855 <SRI>  
A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypot  
F:1-19/Domain: signal sequence #status predicted <STIG>  
F:20-855/Product: env polypotein #status predicted <MNT>  
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:501-855/Product: transmembrane glycoprotein #status predicted <TMM>  
F:87-129,140,145,154,158,186,189,199,226,243,264,278,291,297,333,340,355,386,392,398,404  
Query Match 92.2%; Score 178; DB 1; Length 855;  
Best Local Similarity 88.9%; Pred. No. 7.8e-14;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTSLYSLEKSOQOEKNEQELLELDKWSLMMNF 36  
DB 637 YTGILYRIEESQTOEKNQELLELDKWSLMMNF 672

RESULT 8  
env polypotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
Submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAN>  
A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.7%; Score 177; DB 2; Length 851;  
Best Local Similarity 88.9%; Pred. No. 1e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLYSLEKSOQOEKNEQELLELDKWSLMMNF 36  
DB 633 YTSLIHSLEESQNOEKNQELLELDKWSLMMNF 668

RESULT 9  
env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namezile, A.; Zhao, J.Q.; Dlagne, A.; Idler, K.; Zack, J.A  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.7%; Score 177; DB 2; Length 854;  
Best Local Similarity 88.9%; Pred. No. 1e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLYSLEKSOQOEKNEQELLELDKWSLMMNF 36  
DB 636 YTSLIHSLEESQNOEKNQELLELDKWSLMMNF 671

RESULT 10  
env polypotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH  
VCLJH3  
N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03973  
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; D  
nberger, J.A.; Pappas, T.S.; Chryabeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A03353; MUID:85111123; PMID:2578615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <STIG>  
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TMM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 91.7%; Score 177; DB 1; Length 856;  
Best Local Similarity 88.9%; Pred. No. 1e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLYSLEKSOQOEKNEQELLELDKWSLMMNF 36  
DB 638 YTSLIHSLEESQNOEKNQELLELDKWSLMMNF 673

RESULT 11  
VCLJH3  
env polypotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A0866; MUID:85099333; PMID:2981635  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <MAT>  
A:Cross-references: GB:K02013; NID:g326417; PIDN:AA59751.1; PID:g326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <STIG>  
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TMM>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 91.7%; Score 177; DB 1; Length 861;  
Best Local Similarity 88.9%; Pred. No. 1e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 36  
 Db 643 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 678

## RESULT 12

envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Vary: isolate 278  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined  
 A:Reference number: S21990  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE1>  
 A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:960180  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:960179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 91.2%; Score 176; DB 2; Length 357;  
 Best Local Similarity 86.1%; Pred. No. 5.1e-14;  
 Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 36  
 Db 139 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 174

## RESULT 13

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S70422; S21996  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE2>  
 A:Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:91067129  
 A:Experimental source: patient 27L  
 A:Note: submitted to the EMBL Data Library, July 1991  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 90.7%; Score 175; DB 2; Length 357;  
 Best Local Similarity 86.1%; Pred. No. 6.8e-14;  
 Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 36  
 Db 139 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 174

## RESULT 14

VCLJND  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)  
 N:Alternate names: coat polyprotein  
 N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
 C:Accession: J00066  
 R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, Gene 81, 275-284, 1989  
 A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunodeficiency virus  
 A:Reference number: J00065; MUID:90034200; PMID:2806917  
 A:Accession: J00066  
 A:Molecule type: DNA  
 A:Residues: 1-846 <SPI>  
 A:Cross-references: GB:M27323; NID:9328154; PIDN:AAA44873.1; PID:9328162  
 A:Note: the authors translated the codon GCG for residue 523 as Arg  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-501/Product: coat protein gp120 #status predicted <CP1>  
 F:502-846/Product: coat protein gp41 #status predicted <CP2>  
 F:502-520/Domain: transmembrane #status predicted <TM1>  
 F:674-692/Domain: transmembrane #status predicted <TM2>  
 F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,

Query Match 89.6%; Score 173; DB 1; Length 846;  
 Best Local Similarity 86.1%; Pred. No. 3.2e-13;  
 Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 36  
 Db 628 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 663

## RESULT 15

env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
 C:Accession: A03976  
 R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown Science 227, 484-492, 1985  
 A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
 A:Reference number: A04003; MUID:85090453; PMID:2578227  
 A:Accession: A03976  
 A:Molecule type: DNA  
 A:Residues: 1-855 <SAN>  
 A:Cross-references: GB:K02007; NID:9328658; PIDN:AB59882.1; PID:9328666  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
 F:510-855/Product: transmembrane glycoprotein #status predicted <TM>  
 F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445, F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.6%; Score 173; DB 1; Length 855;  
 Best Local Similarity 86.1%; Pred. No. 3.2e-13;  
 Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 36  
 Db 637 YTSLSYLSLEKSOQOEKNEOELLELDKWSLWNNF 672

Search completed: May 16, 2003, 11:25:07  
 Job time : 13.1446 secs



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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97140 MW; D197D809940BE732 CnC64;

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Query Match 100.0%; Score 193; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 YTSLYSLEKSQTOEQNEQLLELDKWSLMMNF 36
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DB 639 YTSLYSLEKSQTOEQNEQLLELDKWSLMMNF 674

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RESULT 2
ENV_HV1S3 STANDARD; PRT: 852 AA.
ID ENV_HV1S3 STANDARD; PRT: 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE ENV.
GN Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).

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OX NCBI_TaxID=11690;
RN SEQUENCE FROM N.A.
RP MEDLINE=90317906; PubMed=2370688;
RX YORK-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome."
RL J. Virol. 64:4016-4020(1990).

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CC
CC EMBL; M38427; AAA45067.1; -
CC HIV; M38427; ENV5SE33.
CC InterPro: IPR000328; ENV.GP41.
CC InterPro: IPR000777; GP120.
CC Pfam; PF00516; GP120; 1.

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DR DR EMBL; M38427; AAA45067.1; -
DR DR HIV; M38427; ENV5SE33.
DR DR InterPro: IPR000328; ENV.GP41.
DR DR InterPro: IPR000777; GP120.
DR DR Pfam; PF00516; GP120; 1.

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DR Pfam; PF00517; GP41; 1.
KV AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KV Signal.
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FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
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FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 331 BY SIMILARITY.
FT DISULFID 297 431 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
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SQ SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C9910D CnC64;

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Query Match 93.8%; Score 181; DB 1; Length 852;
Best Local Similarity 91.7%; Pred. No. 7e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 YTSLYSLEKSQTOEQNEQLLELDKWSLMMNF 36
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DB 634 YTSLYSLEKSQTOEQNEQLLELDKWSLMMNF 669

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RESULT 3
ENV_HV1EL STANDARD; PRT: 853 AA.
ID ENV_HV1EL STANDARD; PRT: 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
DE ENV.
GN Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).

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OX NCBI_TaxID=11689;
RN SEQUENCE FROM N.A.
RP MEDLINE=86245056; PubMed=2424612;
RX Allison M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis

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RA RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RA RT "Genetic variability of the AIDS virus: nucleotide sequence analysis

```

RT of two isolates from African patients.";  
 CC Cell 46:63-74(1986).  
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 CC -----  
 CC EMBL: K03454; AAA44329.1; -  
 CC EMBL: A07108; CAA00616.1; -  
 CC DR HIV; K03454; ENVSEL1.  
 CC DR Interpro: IPR000328; Env\_GP41.  
 CC DR Interpro: IPR000777; GP120.  
 CC DR Pfam: PF00516; GP120.1.  
 CC DR Pfam: PF00517; GP41.1.  
 CC DR AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 CC Signal.  
 CC -----  
 CC SIGNAL 1 31 BY SIMILARITY.  
 CC CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 CC FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.  
 CC FT DISULFID 53 73 BY SIMILARITY.  
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 CC FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SO SEQUENCE 853 AA; 96721 MW; F9CD864DAAD07A5 CRC64;  
 CC -----  
 CC Query Match 92.7%; Score 179; DB 1; Length 853;  
 CC Best Local Similarity 88.9%; Pred. No. 1.2e-14;  
 CC Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 4  
 ENV\_HV1SC STANDARD; PRT; 856 AA.  
 AC P05878;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88219542; PubMed=3369091;  
 RA Guirgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;  
 RT "Envelope sequences of two new United States HIV-1 isolates.";  
 RT Virology 164:531-536(1988).  
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.  
 CC -----  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M17450; -; NOT\_ANNOTATED\_CDS.  
 CC DR HIV; B28922; VCLJSC.  
 CC DR HIV; M17450; ENVSSC.  
 CC DR Interpro: IPR000328; Env\_GP41.  
 CC DR Interpro: IPR000777; GP120.  
 CC DR Pfam: PF00516; GP120.1.  
 CC DR Pfam: PF00517; GP41.1.  
 CC KW AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 CC Signal.  
 CC -----  
 CC SIGNAL 1 29  
 CC CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 CC FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.  
 CC FT SITE 760 760 IN-FRAME TERMINATION CODON.  
 CC FT DISULFID 53 73 BY SIMILARITY.  
 CC FT DISULFID 118 206 BY SIMILARITY.  
 CC FT DISULFID 125 197 BY SIMILARITY.  
 CC FT DISULFID 130 160 BY SIMILARITY.  
 CC FT DISULFID 219 247 BY SIMILARITY.  
 CC FT DISULFID 228 239 BY SIMILARITY.  
 CC FT DISULFID 296 330 BY SIMILARITY.  
 CC FT DISULFID 376 439 BY SIMILARITY.  
 CC FT DISULFID 383 412 BY SIMILARITY.  
 CC FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).



FT	DISUFID	219	248	BY SIMILARITY.		(POTENTIAL)
FT	DISULFID	229	240	BY SIMILARITY.		(POTENTIAL)
FT	DISULFID	297	330	BY SIMILARITY.		(POTENTIAL)
FT	DISULFID	376	442	BY SIMILARITY.		(POTENTIAL)
FT	DISULFID	383	415	BY SIMILARITY.		(POTENTIAL)
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	137	137	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	144	144	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	153	153	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	185	185	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	188	188	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	235	235	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	277	277	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	338	338	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	353	353	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	384	384	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	390	390	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	402	402	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	441	441	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	445	445	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	459	459	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	462	462	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	608	608	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	613	613	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	622	622	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	634	634	N-LINKED (GLCNAC. .)		(POTENTIAL)
FT	CARBOHYD	671	671	N-LINKED (GLCNAC. .)		(POTENTIAL)
SEQ	SEQUENCE	853 AA;	97043 MW;	849E0B8CBCEFF008 CRC64;		

Query Match	92.2%	Score 178;	DB 1;	Length 853;
Best Local Similarity	88.9%	Pred. No. 1.6e-14;		
Matches 32;	Conservative	2;	Mismatches 2;	Indels 0;
			Gaps	0

Qy 1 YTSLIYSLEKSQFOQEKNEQELLELDKASLWNWF 36  
||| : : : : :  
Db 635 YTGILYRLIEESQFOQEKNEQELLELDKASLWNWF 670

## RESULT 7

	ENV_HV1Z6	PRT;	855 AA.
ENV_HV1Z6	STANDARD;		
D0750			

DT\_13-AUG-1987 (Rel. 05, Created)  
DT\_13-AUG-1987 (Rel. 05, Last sequence update)  
DT\_15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
DE EN.  
CN Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).  
OS Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OC NCBI\_TaxID=11708;

RP SEQUENCE FROM N.A.  
RX MEDLINE=87248097; Pubmed=3036660;  
RA Srinivasan A., Anand R., York D., Ranganathan P., Peorino P.,  
RA Schochman G., Curran J., Kalyanaraman V.S., Luciw P.A.,  
RA Sanchez-Pescador R.;  
RT "Molecular characterization of human immunodeficiency virus from  
RT zaire: nucleotide sequence analysis identifies conserved and variable  
RT domains in the envelope gene.";  
RL Gene 52:71-82(1987).

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CC  
DR EMBL; K03458; AAA45380.1; -.  
DR PIR; D26192; VCLJ26.  
DR HIV; K03458; ENV526.  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane  
KW signal. 1 30  
com

F1	SIGNAL	1	30
FT	CHAIN	31	510
FT	CHAIN	511	855
FT	CHAIN	512	856
FT	CHAIN	513	857
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FT	CHAIN	629	973
FT	CHAIN	630	974
FT	CHAIN	631	975
FT	CHAIN	632	976

FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	207	BY SIMILARITY.
FT	DISULFID	125	198	BY SIMILARITY.

FT	DISULFID	130	155	BY SIMILARITY.
FT	DISULFID	220	249	BY SIMILARITY.
FT	DISULFID	230	241	BY SIMILARITY.

FT	DISULFID	298	332	BY SIMILARITY.
FT	DISULFID	378	444	BY SIMILARITY.
FT	DISULFID	385	417	BY SIMILARITY.

FT	CARBOHYD	87	N-LINKED (GLCNAC, . .)	(POTENT
FT	CARBOHYD	129	N-LINKED (GLCNAC, . .)	(POTENT
FT	CARBOHYD	140	N-LINKED (GLCNAC, . .)	(POTENT

FT	140	140	N-LINKED (GLCNAC. . .)	(POTENT
CARBOHYD	145	145	N-LINKED (GLCNAC. . .)	(POTENT
FT	154	154	N-LINKED (GLCNAC. . .)	(POTENT
CARBOHYD	154	154	N-LINKED (GLCNAC. . .)	(POTENT

FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	189	189	N-LINKED (GLCNAC. . .)	(POTENT

FT	CARBOHYD	199	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	236	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	243	N-LINKED (GLCNAC. . .)	(POTENT

FT	CARBOHYD	264	264	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	278	278	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	291	291	N-LINKED (GLCNAC. . .)	(POTENT

FT	CARBOHYD	297	N-LINKED (GLCNAC. .)	(POTENT
FT	CARBOHYD	333	N-LINKED (GLCNAC. .)	(POTENT
FT	CARBOHYD	340	N-LINKED (GLCNAC. .)	(POTENT

Compound	Yield (%)	Structure
FT CARBOHYD	340	N-LINKED (GLCNAC. . .)
FT CARBOHYD	355	N-LINKED (GLCNAC. . .)
FT CARBOHYD	386	N-LINKED (GLCNAC. . .)
FT CARBOHYD	386	N-LINKED (GLCNAC. . .)
FT CARBOHYD	386	N-LINKED (GLCNAC. . .)

FI	CARBOHYD	392	392	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	398	398	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	404	404	N-LINKED (GLCNAC. . .)	(POTENT

FT	CARBOHYD	443	443	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	447	447	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	460	460	N-LINKED (GLCNAC. . .)	(POTENT

FT	CARBOHYD	461	461	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	464	464	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	610	610	N-LINKED (GLCNAC. . .)	(POTENT

FT	CARBOHYD	615	615	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .)	(POTENT
FT	CARBOHYD	636	636	N-LINKED (GLCNAC. . .)	(POTENT

FT	SEQUENCE	855 AA;	96971 MW;	3B4D3D6E239C3457	CRC64;
CARBOHYD	673	673	N-LINKED (GLCNAC. . .)	(POTENT	

Query Match	92.2%;	Score 178;	DB 1;	Length 855;
Best Local Similarity	88.9%;	Pred. No. 1.7e-14;		

Matches	32; Conservative	2; Mismatches	2; Indels
QY	1	YTSLIYSLLEKSQTQOEKNEQELLELDKWSLWNWF	36

Db 637 YTGILYRLIEESQTQEKNEQELLELDKWSLWNWF 672

RESULT 8  
ENTV HV1D8

ENV_HV1B0	STANDARD;	PRT;	851 AA.
ID ENV_HV1B8			
AC P04582;			

Very Match	92.2%;	Score 178;	DB 1;	Length 855;
1st Local Similarity	88.9%;	Pred. NO. 1.7e-14;		
Matches 32; Conservative	2;	Mismatches 2;	Indels 0;	Gaps 0

QY 1 YTSLIYSLIEKSQTQOEKNEQELLELDKMWASLWNWF 36  
|||:::||||||||||||||||||  
Db 637 YTGILYRLIEESQTQOEKNEQELLELDKMWASLWNWF 672

## RESULT 8

ENV_HV1B8		
ID	ENV_HV1B8	STANDARD;
AC	P04582;	PRT; 851 AA.



DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DE GP120; Transmembrane glycoprotein (GP41).  
 ENV.  
 OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11684;  
 [1]  
 RN NCBI\_TaxID=11684;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8511123; PubMed=2578615;  
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,  
 Josephs S.F., Doran E.R., Ratafski J.A., Whitehorn E.A.,  
 Baumanster K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,  
 Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,  
 Wong-Staal F.;  
 "Complete nucleotide sequence of the AIDS virus, HTLV-III.";  
 Nature 313:277-284(1985).  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 CC EMBL: K02011; AAA4661.1;  
 CC HIV: K02011; ENVS88.  
 DR GlycoSuiteDB: P04582;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 KM  
 FT CHAIN 1 30  
 FT CHAIN 507 851  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 440  
 FT DISULFID 385 413  
 FT CARBOHYD 88  
 FT CARBOHYD 136  
 FT CARBOHYD 141  
 FT CARBOHYD 156  
 FT CARBOHYD 160  
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 FT CARBOHYD 332  
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 FT CARBOHYD 356  
 FT CARBOHYD 386  
 FT CARBOHYD 392  
 FT CARBOHYD 401  
 FT CARBOHYD 443  
 FT CARBOHYD 458  
 FT CARBOHYD 606  
 FT CARBOHYD 611

FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;  
 Query Match 91.7%; Score 177; DB 1; Length 851;  
 Best Local Similarity 88.9%; Pred. No. 2.2e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 YTSILYSLEKSPQEQEKNQEDLELDKMASIMNMF 36  
 Db 633 YTSILHSLEESQNOQEKNEDELELDKMASIMNMF 668  
 -----  
 RESULT 9  
 ENV\_HVIB1  
 ID ENV\_HVIB1 STANDARD: PRT: 856 AA.  
 AC P03375;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41).  
 ENV.  
 OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11678;  
 [1]  
 RN NCBI\_TaxID=11678;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8511123; PubMed=2578615;  
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,  
 Josephs S.F., Doran E.R., Ratafski J.A., Whitehorn E.A.,  
 Baumanster K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,  
 Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,  
 Wong-Staal F.;  
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 Nature 313:277-284(1985).  
 RT Nature 313:277-284(1985).  
 RL Nature 313:277-284(1985).  
 RM Nature 313:277-284(1985).  
 RN Nature 313:277-284(1985).  
 RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=90285159; PubMed=2355006;  
 RA Leonard C.K., Spelham M.W., Riddle L., Harris R.J., Thomas J.N.,  
 Gregory T.J.;  
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 potential glycosylation sites of the type 1 recombinant human  
 immunodeficiency virus envelope glycoprotein (gp120) expressed in  
 Chinese hamster ovary cells.";  
 J. Biol. Chem. 265:10373-10382(1990).  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 CC HIV: A03973; VCLJH3.  
 DR PIR: M15654; ENVS88102.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
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Oy 1 YTSLSYLSLEKSQTOQEKNEDELELDKWSLWNF 36
Db 638 YTSLSHSLIESONOQEKNEDELELDKWSLWNF 673

HIV10
ENV_HV1H2 STANDARD; PRT; 856 AA.
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DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
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RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
virus."
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RA REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
Gallo R.C., Wong-Staal F.;

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RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
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CC or send an email to license@isb-sib.ch).
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DR EMBL; K03455; AAB50262.1; -
DR EMBL; AF038399; AAB99976.1; -
DR EMBL; AF033819; AAC82596.1; -
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DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120.1.
DR Pfam; PF00517; GP41.1.
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KW Signal.
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Oy 1 YTSLSYLSLEKSQTOQEKNEDELELDKWSLWNF 36
Db 638 YTSLSHSLIESONOQEKNEDELELDKWSLWNF 673

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OY 1 YTSLIYSLEKSQTOQEKNEDELLELDKWSLWNMF 36
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
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GN ENV.
NM Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
NN Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Allison M.;
  "Nucleotide sequence of the AIDS virus, LAV.";
  Cell 40:9-17(1985).
RL
CC
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  or send an email to license@sib-sib.ch).
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CC EMBL: K02013; AAB59751.1; -
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CC HIV: K02013; ENVSBRD.
CC InterPro: IPR000328; Env_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120. 1.

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Query Match 91.7%; Score 177; DB 1; Length 861;  
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OY 1 YTSLIYSLEKSQTOQEKNEDELLELDKWSLWNMF 36
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DB 643 YTSLIHSLEESQNOQEKNEDELLELDKWSLWNMF 678

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DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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GN ENV.
NM Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
NN Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
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DR HIV: M38428; ENVSF162.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
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Best Local Similarity 86.1%; Pred. No. 2.9e-14;
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AC P19551.
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DR 01-FEB-1991 (Rel. 17, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Wasiaik A.;
RA Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis.";
RL J. Virol. 64:3792-3803(1990).
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DR HIV: M3943; ENVSF162.
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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
Signal.
AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL. 1 30
FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN..
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
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Title: US-09-623-533a-5  
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Gapop 10.0 , Gapext 0.5

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Number of hits satisfying chosen parameters: 671580

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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- 2: sp-bacteria:\*
- 3: sp-fungi:\*
- 4: sp-human:\*
- 5: sp-invertebrate:\*
- 6: sp-mammal:\*
- 7: sp-mhc:\*
- 8: sp-organelle:\*
- 9: sp-phage:\*
- 10: sp-plant:\*
- 11: sp-rodent:\*
- 12: sp-virus:\*
- 13: sp-vertebrate:\*
- 14: sp-unclassified:\*
- 15: sp-virus:\*
- 16: sp-bacteriap:\*
- 17: sp-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	100.0	857	15	Q9YUL5 human immun
2	193	100.0	861	15	O90294 human immun
3	193	100.0	861	15	O90295 human immun
4	184	95.3	117	15	O9YIM3 human immun
5	184	95.3	122	15	O9EAB1 human immun
6	183	94.8	127	15	O9YX0 human immun
7	183	94.8	129	15	O9YX25 human immun
8	183	94.8	852	15	O69992 human immun
9	182	94.3	848	15	O69990 human immun
10	181	93.8	49	15	O69909 human immun
11	181	93.8	122	15	O9IJN3 human immun
12	181	93.8	851	15	O56562 human immun
13	181	93.8	851	15	O73304 human immun
14	181	93.8	855	15	O9E1R7 human immun
15	181	93.8	857	15	O90296 human immun
16	181	93.8	858	15	O80867 human immun

17	181	93.8	858	15	O80865 human immun
18	181	93.8	864	15	O9E610 human immun
19	180	93.3	49	15	O69906 human immun
20	180	93.3	117	15	O9YIM3 human immun
21	180	93.3	122	15	O9YX0 human immun
22	180	93.3	122	15	O9YX1 human immun
23	180	93.3	122	15	O9QIW7 human immun
24	180	93.3	122	15	O9QIU8 human immun
25	180	93.3	122	15	O9IJM8 human immun
26	180	93.3	127	15	O9YX20 human immun
27	180	93.3	127	15	O9YX12 human immun
28	180	93.3	128	15	O9YX11 human immun
29	180	93.3	838	15	O03806 human immun
30	180	93.3	848	15	O03806 human immun
31	180	93.3	854	15	O994A7 human immun
32	180	93.3	855	15	O78225 human immun
33	180	93.3	855	15	O03805 human immun
34	180	93.3	857	15	O9DQ26 human immun
35	180	93.3	860	15	O72494 human immun
36	179	92.7	42	15	O41532 human immun
37	179	92.7	122	15	O69910 human immun
38	179	92.7	122	15	O9EAB9 human immun
39	179	92.7	122	15	O9EAB2 human immun
40	179	92.7	122	15	O9EAB0 human immun
41	179	92.7	132	15	O9IWO5 human immun
42	179	92.7	358	15	O78120 human immun
43	179	92.7	443	15	O80023 human immun
44	179	92.7	807	15	O8Q2X2 human immun
45	179	92.7	841	15	O41536 human immun

## ALIGNMENTS

## RESULT 1

Q9YUL5 PRELIMINARY: PRT; 857 AA.

AC Q9YUL5;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NN;  
 RA MEDLINE-98362112; PubMed-9696803;  
 RX Park E.J., Vujoic L.K., Anand R., Theodore T.S., Quinn G.V. Jr.;  
 RT "Mutations in both gp120 and gp41 are responsible for the broad  
 RT neutralization resistance of variant human immunodeficiency virus type  
 RT 1 MN to antibodies directed at V3 and non-V3 epitopes.";  
 RL J. Virol. 72:7099-7107(1998).  
 DR EMBL; AF075722; AAC31819.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 857 AA; 97095 MW; 922D362E10C60DA8 CRC64;

Query Match 100.0%; Score 193; DB 15; Length 857;

Best Local Similarity 100.0%; Pred. NO. 3e-15; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYSLEKSQTQOEKNEQELLELDKWSLWNF 36  
 Db 639 YTSLIYSLEKSQTQOEKNEQELLELDKWSLWNF 674

RESULT 2

090294  
ID 090294 PRELIMINARY; PRT; 861 AA.  
AC 090294;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
EN Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=NM;  
RX MEDLINE=98362112; PubMed=9696803;  
RA Park E.J., Vujcic L.K., Anand R., Theodore T.S., Quinnan G.V. Jr.,  
RT "Mutations in both gp120 and gp41 are responsible for the broad  
neutralization resistance of variant human immunodeficiency virus type  
1 MN to antibodies directed at V3 and non-V3 epitopes."  
J. Virol. 72:7099-7107(1998).  
[2]  
SEQUENCE FROM N.A.  
RC STRAIN=NM;  
RA Park E.J., Quinnan G.V. Jr., Theodore T.S.;  
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF075719; AAC33788.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 861 AA; 97671 MW; 8136732E4445E56 CRC64;  
  
Query Match 100.0%; Score 193; DB 15; Length 861;  
Best Local Similarity 100.0%; Pred. No. 3e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YTSLIYSLEKSOTQOEKNEQELLELDKNASLWNMF 36  
DB 639 YTSLIYSLEKSOTQOEKNEQELLELDKNASLWNMF 674  
  
RESULT 3  
090295  
ID 090295 PRELIMINARY; PRT; 861 AA.  
AC 090295;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
EN Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=NM;  
RX MEDLINE=98362112; PubMed=9696803;  
RA Park E.J., Vujcic L.K., Anand R., Theodore T.S., Quinnan G.V. Jr.,  
RT "Mutations in both gp120 and gp41 are responsible for the broad  
neutralization resistance of variant human immunodeficiency virus type  
1 MN to antibodies directed at V3 and non-V3 epitopes."  
J. Virol. 72:7099-7107(1998).  
DR EMBL: AF075720; AAC31817.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 861 AA; 97617 MW; 36593D08429DC700 CRC64;  
  
Query Match 100.0%; Score 193; DB 15; Length 861;  
Best Local Similarity 100.0%; Pred. No. 3e-15;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YTSLIYSLEKSOTQOEKNEQELLELDKNASLWNMF 36  
DB 639 YTSLIYSLEKSOTQOEKNEQELLELDKNASLWNMF 674  
  
RESULT 4  
09YWM3  
ID 09YWM3 PRELIMINARY; PRT; 117 AA.  
AC 09YWM3;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
EN Gp41 (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=501.045;  
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,  
RT Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.,  
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in  
Uganda."  
J. Virol. 72:7099-7107(1998).  
DR EMBL: AF069447; AAD01391.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR Pfam: PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
SQ SEQUENCE 117 AA; 14014 MW; 507434356041176E CRC64;  
  
Query Match 95.3%; Score 184; DB 15; Length 117;  
Best Local Similarity 91.7%; Pred. No. 5.1e-15;  
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YTSLIYSLEKSOTQOEKNEQELLELDKNASLWNMF 36  
DB 82 YTSLIYSLEKSOTQOEKNEQELLELDKNASLWNMF 117  
  
RESULT 5  
09EA81  
ID 09EA81 PRELIMINARY; PRT; 122 AA.  
AC 09EA81;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
EN Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=BX923;  
RX MEDLINE=20134570; PubMed=10669328;  
RA Weidle P.J., Ganea C.E., Irwin K.L., Plenzl D., McGowan J.P.,  
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B  
subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic  
diversity in the United States."  
J. Infect. Dis. 181:470-475(2000).  
DR EMBL: AF190971; AAG02333.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR Pfam: PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1 1  
SQ SEQUENCE 122 AA; 14753 MW; C3FE4DB1E8B5ECBD CRC64;







Query Match 93.8%; Score 181; DB 15; Length 851;  
 Best Local Similarity 88.9%; Pred. No. 8.6e-14;  
 Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYISLLEKSOTOOEKNEQELLEDKWSLWMP 36  
 |||:||||:|||||  
 DB 633 YTNLTITLLEKSOTOOEKNEQELLEDKWSLWMP 668

## RESULT 13

073304 PRELIMINARY; PRT; 851 AA.  
 AC 073304;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 ENV Envelope glycoprotein.  
 GN Human immunodeficiency virus type 1.  
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96263682; PubMed=8924250;  
 RA Douglas N.W., Knight A.I., Hayhurst A., Barrett W.Y., Keyany M.J.,  
 RA Daniels R.S.;  
 RT "An efficient method for the rescue and analysis of functional HIV-1  
 RT env genes: evidence for recombination in the vicinity of the tat/rev  
 RT splice site."  
 RL AIDS 10:39-46(1996).  
 DR EMBL: U36879; AAC5538.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 851 AA; 96525 MW; F985DB4E881F718 CRC64;

Query Match 93.8%; Score 181; DB 15; Length 851;  
 Best Local Similarity 91.7%; Pred. No. 8.6e-14;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLYISLLEKSOTOOEKNEQELLEDKWSLWMP 36  
 |||:||||:|||||  
 DB 633 YTSLYITLLEKSOTOOEKNEQELLEDKWSLWMP 668

## RESULT 14

09E1R7 PRELIMINARY; PRT; 855 AA.  
 AC 09E1R7;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 ENV Envelope protein.  
 GN Human immunodeficiency virus type 1.  
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20442410; PubMed=10984542;  
 RA Cleghorn F.R., Jack N., Carr J.K., Edwards J., Mahabir B., Sill A.,  
 RA McDaniel C.B., Connolly S.M., Goodman D., Bennetts R.O., O'Brien T.R.,  
 RA Weidhold K.J., Bartholomew C., Blatner W.A., Greenberg M.L.;  
 RT "A distinctive clade B HIV type 1 is heterosexually transmitted in  
 RT Trinidad and Tobago."  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:10532-10537(2000).  
 DR EMBL: AF277071; AAG22514.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.

DR Pfam: PF00517; GP41.1.  
 KW Transmembrane.  
 SQ SEQUENCE 855 AA; 97102 MW; 26271D6CCCCCFAC CRC64;

Query Match 93.8%; Score 181; DB 15; Length 855;  
 Best Local Similarity 91.7%; Pred. No. 8.6e-14;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLYISLLEKSOTOOEKNEQELLEDKWSLWMP 36  
 |||:||||:|||||  
 DB 637 YTSLYITLLEKSOTOOEKNEQELLEDKWSLWMP 672

## RESULT 15

090296 PRELIMINARY; PRT; 857 AA.  
 ID 090296;  
 AC 090296;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 ENV Envelope glycoprotein.  
 GN Human immunodeficiency virus type 1.  
 OS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MN;  
 RX MEDLINE=98362112; PubMed=9696803;  
 RA Park E.J., Vujcic L.R., Anand R., Theodore T.S., Quinnan G.V. Jr.;  
 RT "Mutations in both gp120 and gp41 are responsible for the broad  
 RT neutralization resistance of variant human immunodeficiency virus type  
 RT 1 MN to antibodies directed at V3 and non-V3 epitopes."  
 RL J. Virol. 72:7099-7107(1998).  
 DR EMBL: AF075721; AAC31818.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 857 AA; 97064 MW; E0D8599CC50C2F47 CRC64;

Query Match 93.8%; Score 181; DB 15; Length 857;  
 Best Local Similarity 94.4%; Pred. No. 8.6e-14;  
 Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLYISLLEKSOTOOEKNEQELLEDKWSLWMP 36  
 |||:||||:|||||  
 DB 639 YTSLYISLLEKSOTOOEKNEQELLEDKWSLWMP 674

Search completed: May 16, 2003, 11:19:44  
 Job time : 26.3124 secs

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GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-5

Perfect score: 193

Sequence: 1 YTSLSYSLLEKSTQOEKNEQELLELDKWSLMMWF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued\_Patents\_AA.\*

- 1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2.6/ptodata/1/1aa/PCITUS.COMB.pep.\*
- 6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	100.0	36	1 US-08-073-028-5	Sequence 5, Appli
2	193	100.0	36	3 US-08-486-099-5	Sequence 5, Appli
3	193	100.0	36	3 US-08-360-107A-5	Sequence 5, Appli
4	193	100.0	36	3 US-08-484-223B-5	Sequence 5, Appli
5	193	100.0	36	3 US-08-919-597-5	Sequence 5, Appli
6	193	100.0	36	3 US-08-475-668A-5	Sequence 5, Appli
7	193	100.0	36	3 US-08-485-551A-5	Sequence 5, Appli
8	193	100.0	36	3 US-08-471-913A-5	Sequence 5, Appli
9	193	100.0	36	4 US-08-554-616-5	Sequence 5, Appli
10	193	100.0	36	4 US-08-485-264A-5	Sequence 5, Appli
11	193	100.0	36	4 US-08-474-349A-5	Sequence 5, Appli
12	193	100.0	36	4 US-08-255-208A-5	Sequence 5, Appli
13	193	100.0	138	4 US-09-570-921-15	Sequence 15, Appli
14	193	100.0	267	4 US-08-965-056-15	Sequence 15, Appli
15	193	100.0	856	1 US-08-022-835-2	Sequence 15, Appli
16	193	100.0	856	1 US-08-388-809-2	Sequence 2, Appli
17	193	100.0	856	1 US-08-375-100-1	Sequence 2, Appli
18	193	100.0	856	2 US-08-647-714-2	Sequence 2, Appli
19	193	100.0	856	2 US-07-956-483-11	Sequence 11, Appli
20	193	100.0	887	4 US-08-472-240A-2	Sequence 2, Appli
21	187	96.9	36	3 US-08-484-223B-240	Sequence 240, App
22	187	96.9	36	4 US-09-082-279B-1360	Sequence 1360, Ap
23	187	96.9	160	4 US-09-315-304B-1360	Sequence 1360, Ap
24	187	96.9	857	1 US-08-022-835-4	Sequence 4, Appli
25	187	96.9	857	1 US-08-388-809-4	Sequence 4, Appli
26	187	96.9	857	1 US-08-647-714-4	Sequence 4, Appli
27	187	96.9	857	2 US-08-647-714-4	Sequence 4, Appli

28	184	95.3	36	4 US-09-082-279B-1361	Sequence 1361, Ap
29	184	95.3	36	4 US-09-315-304B-1361	Sequence 1361, Ap
30	182	94.3	36	4 US-09-082-279B-642	Sequence 642, App
31	182	94.3	36	4 US-09-315-304B-642	Sequence 642, App
32	182	94.3	850	2 US-08-448-603A-28	Sequence 28, Appli
33	182	94.3	850	3 US-09-134-075-28	Sequence 28, Appli
34	182	94.3	850	4 US-09-492-739-28	Sequence 28, Appli
35	181	93.8	36	4 US-09-082-279B-643	Sequence 643, App
36	181	93.8	36	4 US-09-315-304B-643	Sequence 643, App
37	181	93.8	138	4 US-09-570-921-19	Sequence 19, Appli
38	181	93.8	269	4 US-08-965-056-28	Sequence 28, Appli
39	180	93.3	268	4 US-08-965-056-13	Sequence 13, Appli
40	180	93.3	855	1 US-08-022-835-6	Sequence 6, Appli
41	180	93.3	855	1 US-08-388-809-6	Sequence 6, Appli
42	180	93.3	855	2 US-08-647-714-6	Sequence 6, Appli
43	179	92.7	138	4 US-09-570-921-3	Sequence 3, Appli
44	179	92.7	138	4 US-09-570-921-12	Sequence 12, Appli
45	179	92.7	138	4 US-09-570-921-27	Sequence 27, Appli

## ALIGNMENTS

```
RESULT 1
US-08-073-028-5
; Sequence 5, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-073-028-5

Query Match      100.0%; Score 193; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTSLSYSLLEKSTQOEKNEQELLELDKWSLMMWF 36
|||||
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DB 1 YTSLSYLSLEKSQTQOEKNEQELLELDKWSLWMNF 36

RESULT 2

US-08-486-099-5

Sequence 5, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNTE

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-5

Query Match 100.0%; Score 193; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSYLSLEKSQTQOEKNEQELLELDKWSLWMNF 36

DB 1 YTSLSYLSLEKSQTQOEKNEQELLELDKWSLWMNF 36

RESULT 3

US-08-360-107A-5

Sequence 5, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNTE

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-5

Query Match 100.0%; Score 193; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSYLSLEKSQTQOEKNEQELLELDKWSLWMNF 36

DB 1 YTSLSYLSLEKSQTQOEKNEQELLELDKWSLWMNF 36

RESULT 4

US-08-484-223B-5

Sequence 5, Application US/08484223B

Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
8-484-223B-5

Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLSLEKSQTQOEKNEDELLDLKWSLWNNF 36  
DB 1 YTSLSLSLEKSQTQOEKNEDELLDLKWSLWNNF 36

RESULT 5  
US-08-919-597-5  
Sequence 5, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-5

Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLSLEKSQTQOEKNEDELLDLKWSLWNNF 36  
DB 1 YTSLSLSLEKSQTQOEKNEDELLDLKWSLWNNF 36

RESULT 6  
US-08-475-668A-5  
Sequence 5, Application US/08475668A  
Patent No. 606065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-5

Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLSLEKSQTQOEKNEDELLDLKWSLWNNF 36  
DB 1 YTSLSLSLEKSQTQOEKNEDELLDLKWSLWNNF 36

RESULT 7  
US-08-485-551A-5  
Sequence 5, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Danl P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-5  
Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity: 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYISLSEKSTOEKNEQELLEDKWASLWNMF 36  
DB 1 YTSLYISLSEKSTOEKNEQELLEDKWASLWNMF 36  
RESULT 8  
US-08-471-913A-5  
Sequence 5, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Danl P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 869-9741/8864  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-5  
Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity: 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYISLSEKSTOEKNEQELLEDKWASLWNMF 36  
DB 1 YTSLYISLSEKSTOEKNEQELLEDKWASLWNMF 36  
RESULT 9  
US-08-554-616-5  
Sequence 5, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Danl P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993



ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8664/9741  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-5

Query Match 100.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36  
1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36

RESULT 10  
US-08-485-264A-5  
Sequence 5, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-485-264A-5

Query Match 100.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36  
1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36

RESULT 11  
US-08-474-349A-5  
Sequence 5, Application US/08474349A  
Patent No. 6333395  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
TITLE OF INVENTION: VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 517  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,349A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-474-349A-5

Query Match 100.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36  
1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36

RESULT 12  
US-08-255-208A-5  
Sequence 5, Application US/08255208A  
Patent No. 6440656

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Jr., Stephen R.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/255,208A  
FILING DATE: 07-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-010  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-255-208A-5

Query Match 100.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNNF 36  
1 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNNF 36

RESULT 13  
US-09-570-921-15  
Sequence 15, Application US/09570921  
Patent No. 6453265  
GENERAL INFORMATION:  
APPLICANT: SERRES, PIERRE-FRANCOIS  
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE  
TITLE OF INVENTION: PATHOGENIC EFFECTS RELATED TO A RETROVIRAL INFECTION  
FILE REFERENCE: 106213  
CURRENT APPLICATION NUMBER: US/09/570,921  
CURRENT FILING DATE: 2000-05-15  
PRIOR APPLICATION NUMBER: PCT/FR98/02447  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: FR/97/14387  
PRIOR FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 144  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 15  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Human  
US-09-570-921-15

Query Match 100.0%; Score 193; DB 4; Length 138;  
Best Local Similarity 100.0%; Pred. No. 1,2e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNNF 36  
1 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNNF 134

RESULT 14  
US-08-965-056-15  
Sequence 15, Application US/08965056  
Patent No. 6271198  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
APPLICANT: J. Kevin Judice  
APPLICANT: Robert S. McDowell  
APPLICANT: J. Christopher Phelan  
APPLICANT: Melissa A. Staravastnik  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/965,056  
FILING DATE: 05-No. 6271198-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-965-056-15

Query Match 100.0%; Score 193; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 2,5e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNNF 36  
167 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNNF 202

RESULT 15  
US-08-022-835-2  
Sequence 2, Application US/08022835  
Patent No. 5420030  
GENERAL INFORMATION:  
APPLICANT: Reitz Jr., Marvin S.  
APPLICANT: Franchini, Genoveffa  
APPLICANT: Markham, Phillip D.  
APPLICANT: Gallo, Robert C.  
APPLICANT: Lori, Franco C.

APPLICANT: Popovic, Mikulas  
APPLICANT: Gartner, Suzanne  
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: Eleventh Floor, 1615 L. Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/022,835  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/599,491  
FILING DATE: 17-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Scott, Watson T.  
REGISTRATION NUMBER: 26,581  
REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 856 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-022-835-2

Query Match 100.0%; Score 193; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. NO. 8.7e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYSLEKSTQEQEKNEQELLEDKWASLWNP 36  
|||  
DB 639 YTSLIYSLEKSTQEQEKNEQELLEDKWASLWNP 674

Job time : 11.1928 secs  
Job completed: May 16, 2003, 11:22:11

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GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-5  
Perfect score: 193  
Sequence: 1 YTSLYSLERKQTOEKNEQELLDKRWASIMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 segs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA.\*  
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4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	100.0	267	10	US-09-854-816-15 Sequence 15, Appl
2	181	93.8	269	10	US-09-854-816-28 Sequence 28, Appl
3	180	93.3	268	10	US-09-854-816-13 Sequence 13, Appl
4	179	92.7	233	10	US-09-854-816-50 Sequence 50, Appl
5	179	92.7	268	10	US-09-854-816-9 Sequence 9, Appl
6	179	92.7	269	10	US-09-854-816-12 Sequence 12, Appl
7	178	92.2	269	10	US-09-854-816-46 Sequence 46, Appl
8	177	91.7	36	9	US-09-874-475-16 Sequence 16, Appl
9	177	91.7	36	9	US-10-116-797-1 Sequence 1, Appl
10	177	91.7	36	9	US-09-493-346-1 Sequence 1, Appl
11	177	91.7	36	10	US-09-796-202-10 Sequence 10, Appl
12	177	91.7	36	10	US-09-779-451-5 Sequence 5, Appl
13	177	91.7	36	10	US-09-834-628-1 Sequence 1, Appl
14	177	91.7	36	10	US-09-854-816-1 Sequence 1, Appl
15	177	91.7	36	10	US-09-854-816-108 Sequence 108, App
16	177	91.7	37	9	US-09-848-616-176 Sequence 176, App
17	177	91.7	46	10	US-09-779-451-41 Sequence 41, Appl
18	177	91.7	56	10	US-09-779-451-4 Sequence 4, Appl
19	177	91.7	177	9	US-10-040-349B-2 Sequence 2, Appl

20	177	91.7	221	9	US-10-059-271-84 Sequence 84, Appl
21	177	91.7	232	9	US-10-059-271-81 Sequence 81, Appl
22	177	91.7	254	9	US-10-059-271-82 Sequence 82, Appl
23	177	91.7	256	9	US-10-059-271-97 Sequence 97, Appl
24	177	91.7	268	10	US-09-854-816-16 Sequence 16, Appl
25	177	91.7	268	10	US-09-854-816-17 Sequence 17, Appl
26	177	91.7	268	10	US-09-854-816-18 Sequence 18, Appl
27	177	91.7	344	9	US-10-040-349B-1 Sequence 1, Appl
28	177	91.7	345	9	US-10-026-741-49 Sequence 49, Appl
29	177	91.7	345	10	US-09-779-451-8 Sequence 8, Appl
30	177	91.7	391	9	US-10-059-271-93 Sequence 93, Appl
31	177	91.7	519	10	US-09-756-551A-8 Sequence 8, Appl
32	177	91.7	853	9	US-10-003-035-33 Sequence 33, Appl
33	177	91.7	856	10	US-09-476-242-1 Sequence 1, Appl
34	177	91.7	861	9	US-10-026-741-103 Sequence 103, App
35	177	91.7	1101	9	US-10-003-035-53 Sequence 53, Appl
36	177	91.7	1186	9	US-10-003-035-55 Sequence 55, Appl
37	176	91.2	36	10	US-09-779-451-50 Sequence 50, Appl
38	176	91.2	46	10	US-09-779-451-48 Sequence 48, Appl
39	176	91.2	268	10	US-09-854-816-26 Sequence 26, Appl
40	176	91.2	268	10	US-09-854-816-40 Sequence 40, Appl
41	176	91.2	269	10	US-09-854-816-45 Sequence 45, Appl
42	176	91.2	619	10	US-09-891-609-4 Sequence 4, Appl
43	176	91.2	646	10	US-09-891-609-2 Sequence 2, Appl
44	176	91.2	847	10	US-09-476-242-2 Sequence 2, Appl
45	175	90.7	46	10	US-09-854-816-109 Sequence 109, App

## ALIGNMENTS

RESULT 1  
US-09-854-816-15  
Sequence 15, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasknik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: I DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854, 816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-854-816-15

Query Match 100.0%; Score 193; DB 10; Length 267;  
Best Local Similarity 100.0%; Pred. No. 6.8e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYSLEKSOTQOEKNEDELLELDKWSLWNWF 36  
DB 167 YTSLIYSLEKSOTQOEKNEDELLELDKWSLWNWF 202

## RESULT 2

US-09-854-816-28  
Sequence 28, Application US/09854816  
Patent No. US20020151473A1

## GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854, 816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965, 056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-854-816-28

Query Match 93.8%; Score 181; DB 10; Length 269;

Best Local Similarity 91.7%; Pred. No. 1.9e-14;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIYSLEKSOTQOEKNEDELLELDKWSLWNWF 36  
DB 169 YTSLIYSLEKSOTQOEKNEDELLELDKWSLWNWF 204

RESULT 3

## US-09-854-816-13

Sequence 13, Application US/09854816  
Patent No. US20020151473A1

## GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854, 816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965, 056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-854-816-13

Query Match 93.3%; Score 180; DB 10; Length 268;

Best Local Similarity 88.9%; Pred. No. 2.5e-14;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIYSLEKSOTQOEKNEDELLELDKWSLWNWF 36

DB 168 YTSLIYSLEKSOTQOEKNEDELLELDKWSLWNWF 203

## RESULT 4

US-09-854-816-50

Sequence 50, Application US/09854816

Patent No. US20020151473A1

## GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way









TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: DP178  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-854-816-1

Query Match 91.7%, Score 177; DB 10; Length 36;  
 Best Local Similarity 88.9%, Pred. No. 6.7e-15;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSLSEKSOEQEKNQELLEDKWSLWNF 36  
 Db 1 YTSLSLSEKSOEQEKNQELLEDKWSLWNF 36

LT 15

US-854-816-108  
 Sequence 108, Application US/09854816  
 Patent No. US20020151473A1

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovansnk

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
 Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: P1005R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 108:

US-09-854-816-108

Query Match 91.7%, Score 177; DB 10; Length 36;  
 Best Local Similarity 88.9%, Pred. No. 6.7e-15;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSLSEKSOEQEKNQELLEDKWSLWNF 36

Db 1 YTSLSLSEKSOEQEKNQELLEDKWSLWNF 36  
 Search completed: May 16, 2003, 12:10:23  
 Job time : 16.759 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 31.5562 seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533a-117  
Perfect score: 188  
Sequence: 1 TSLHSLIEESQNOEKNEDELRLDKWASLWMP 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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- 9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.\*
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- 11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.\*
- 12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.\*
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- 22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*
- 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	35	16	AA64397
2	188	100.0	35	21	AA62687
3	188	100.0	35	21	AA814670
4	188	100.0	35	21	AA89388
5	188	100.0	35	22	AB80634
6	188	100.0	35	22	AB800796
7	188	100.0	35	22	AB802111
8	188	100.0	35	22	AB802272
9	188	100.0	35	22	AAU13182
10	188	100.0	35	22	AAU13342

11	188	100.0	35	22	AA877629	Core polypeptide T
12	188	100.0	35	22	AA877789	Core polypeptide T
13	188	100.0	35	22	AA854934	Anti-HIV peptide D
14	188	100.0	36	16	AA64364	DP-178 derived firo
15	188	100.0	36	17	AA89398	DP178 corresponds
16	188	100.0	36	18	AAW17011	HIV-1 derived pept
17	188	100.0	36	19	AA822912	SEQ ID NO. 108 firo
18	188	100.0	36	19	AA822805	from
19	188	100.0	36	20	AA831955	Synthetic peptide
20	188	100.0	36	20	AA831974	HIV-1 IAI gp41 T-2
21	188	100.0	36	21	AA852655	T20/DP178 peptide
22	188	100.0	36	21	AA852688	T20/DP178 peptide
23	188	100.0	36	21	AA852818	HIV-1 isolate IAI
24	188	100.0	36	21	AA814533	HIV-1 isolate IAI
25	188	100.0	36	21	AA886655	Core polypeptide f
26	188	100.0	36	21	AA888729	Core polypeptide f
27	188	100.0	36	21	AA888729	Core polypeptide f
28	188	100.0	36	21	AA89135	Core polypeptide f
29	188	100.0	36	21	AA89136	Core polypeptide f
30	188	100.0	36	21	AA89201	Core polypeptide f
31	188	100.0	36	21	AA89242	Core polypeptide f
32	188	100.0	36	21	AA89424	Core polypeptide f
33	188	100.0	36	21	AA89592	Core polypeptide f
34	188	100.0	36	21	AA89735	Core polypeptide f
35	188	100.0	36	21	AA89777	Core polypeptide f
36	188	100.0	36	21	AA89982	Core polypeptide f
37	188	100.0	36	21	AA89983	Core polypeptide f
38	188	100.0	36	21	AA89999	Core polypeptide f
39	188	100.0	36	21	AA90031	Core polypeptide f
40	188	100.0	36	22	AAU70179	HIV viral envelope
41	188	100.0	36	22	AAU70741	HXB2 transmembrane
42	188	100.0	36	22	AA862961	Anti-HIV peptide T
43	188	100.0	36	22	AA867039	HIV-1 gp41 peptide
44	188	100.0	36	22	AB800024	HIV-1 gp41 peptide
45	188	100.0	36	22	AB800087	Biotin-labeled HT
						Viral DP178/107-11

## ALIGNMENTS

RESULT 1  
ID AAR64397 standard; Peptide: 35 AA.  
XX AAR64397;  
AC  
XX  
DT 25-AUG-1995 (first entry)  
XX  
XX DP-178 homologue 66 derived from HIV-1 has antiviral activity.  
DE  
XX  
KW antiviral activity: DP-178; DP-107; diagnostic: HIV-1IAI;  
KW human immunodeficiency virus; transmembrane protein; gp41;  
KW alpha helix; leucine zipper; DP-185.  
XX  
XX Synthetic.  
OS  
XX  
XX  
FT Key Location/Qualifiers  
FT Modified-site 1 /note= "optionally has an amino, acetyl,  
FT Modified-site 35 9-fluorenylmethoxy-carbonyl, hydrophobic or  
FT Modified-site 35 macromolecular carrier gp. attached"  
FT Modified-site 35 /note= "optionally has a carboxyl, amido, hydrophobic  
FT Modified-site 35 or macromolecular carrier gp. attached"

W09428920-A.  
22-DEC-1994.  
07-JUN-1994; 94WO-US05739.  
07-JUN-1993; 93US-0073028.

PA (UYDU-) UNIV DUKE.  
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Peteway SR, Wild CT;  
 XX WPI: 1995-036105/05.  
 DR  
 XX Computer search generated synthetic peptides - are inhibitors of  
 PT HIV transmission  
 XX  
 PS Claim 11, Page 133; 182pp; English.  
 XX  
 CC AAR64365-97 are peptide derivs. of DP-178 (AAR64364) which have been  
 CC truncated at the amino terminus. DP-178 corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. The peptide derivs. were identified by a computer assisted  
 CC peptide sequence search. The peptides inhibit transmission to  
 CC uninfected cells, and can also be used as type and/or subtype  
 CC specific diagnostic tools.  
 XX  
 SQ Sequence 35 AA;  
 XX  
 Query Match 100.0%; Score 188; DB 16; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TSLHSLIEESONQOEKNEQELLELDKWSIWNMF 35  
 Db 1 TSLHSLIEESONQOEKNEQELLELDKWSIWNMF 35  
 XX  
 RESULT 2  
 AAB52687  
 ID AAB52687 standard; Peptide: 35 AA.  
 XX  
 AC AAB52687;  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DE T20/DP178 peptide fragment #65.  
 XX  
 KW Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemoattractant.  
 KW  
 XX Human immunodeficiency virus type 1.  
 XX  
 PN WO200066622-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 05-MAY-2000; 2000WO-US12371.  
 XX  
 PR 05-MAY-1999; 99US-0132686.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 DR WPI: 2000-656493/63.  
 XX  
 PT Administration of peptide agents with a sequence corresponding to a  
 PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
 PT antagonist is used to modulate inflammation.  
 XX  
 PS Claim 12; Page 25; 148pp; English.  
 XX  
 CC The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
 CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is a

CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
 CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
 CC interacts with members of the formyl peptide receptor (FPR) family and  
 CC thereby up-regulates an inflammatory response, and acts as a potent  
 CC chemoattractant and activator of human peripheral blood phagocytes  
 CC (but not T cells). The present peptide can be used to modulate an  
 CC inflammatory response in a subject.  
 XX  
 SQ Sequence 35 AA;  
 XX  
 Query Match 100.0%; Score 188; DB 21; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TSLHSLIEESONQOEKNEQELLELDKWSIWNMF 35  
 Db 1 TSLHSLIEESONQOEKNEQELLELDKWSIWNMF 35  
 XX  
 RESULT 3  
 AAB14670  
 ID AAB14670 standard; peptide: 35 AA.  
 XX  
 AC AAB14670;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE HIV-1 isolate LAI gp41 C-helical domain peptide P-18, fragment #64.  
 XX  
 KW HIV-1; gp41 C-helical domain;  
 KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KW core 6-helix bundle; viral entry inhibition; immunogenic;  
 KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;  
 KW isolate LAI.  
 KW  
 XX Human immunodeficiency virus type 1.  
 XX  
 OS  
 XX  
 PN WO200040616-A1.  
 XX  
 PD 13-JUL-2000.  
 XX  
 PF 10-JAN-2000; 2000WO-US00456.  
 XX  
 PR 08-JAN-1999; 99US-0115404.  
 PR 07-JAN-2000; 2000US-0460336.  
 XX  
 PA (WILD/) WILD C T.  
 PA (WEISS/) WEISS C D.  
 XX  
 PI Wild CT, Weiss CD;  
 XX  
 DR WPI: 2000-465959/40.  
 XX  
 PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure.  
 XX  
 PS Disclosure; Page 34; 97pp; English.  
 XX  
 CC Sequences AAB14604-B14606 and AAB14607-B14670 represent peptides derived  
 CC from the C-helical domain of the gp41 envelope glycoprotein from  
 CC HIV-1 group M, subtype B, isolate LAI. The invention relates to raising  
 CC a neutralizing antibody response to a broad spectrum of HIV (human  
 CC immunodeficiency virus) strains and isolates, comprising the  
 CC administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of a gp41 which are important in mediating the  
 CC process of viral entry into host cells. Such peptides can correspond  
 CC to or mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides

CC can be administered either singly or as a combination (particularly  
 CC a combination of N-helical and C-helical peptides), and can be  
 CC multimerized. For example, N- and C-helical domain peptides can be  
 CC alternately linked together to form a peptide which mimics the core  
 CC 6-helix bundle. Administration of the peptide(s) generates a humoral  
 CC response, with the production of antibodies against gp41 structures  
 CC involved in viral entry. As these portions of gp41 are well conserved,  
 CC such antibodies may be effective against a broad range of HIV strains  
 CC and isolates. The peptide compositions may be administered as a  
 CC prophylactic or therapeutic vaccine to generate antibodies which reduce  
 CC or inhibit the ability of HIV to infect uninfected cells. A composition  
 CC comprising polyclonal or monoclonal antibodies can be administered to  
 CC reduce HIV infection of uninfected cells. Antibodies raised against  
 CC entry-relevant gp41 structures may also be used therapeutically and as  
 CC tools to further elucidate the mechanism of HIV cell entry.

SO Sequence 35 AA:

Query Match 100.0%; Score 188; DB 21; Length 35;

Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35  
 ||||||||||||||||||||||||||||||||  
 DB 1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35

#### RESULT 4

AA89388 standard; peptide: 35 AA.

AA89388;

23-MAY-2000 (first entry)

Core polypeptide fragment T No. 923.

Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.

Unidentified.

MO9959615-A1.

25-NOV-1999.

20-MAY-1999; 99WO-US11219.

20-MAY-1998; 98US-0082279.

(TRIM-) TRIMERIS INC.

Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

WPI: 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties  
 comprises enhancer sequence -

Disclosure: Page 35; 14pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide  
 sequence linked to core polypeptides. The enhancer polypeptides are  
 derived from various retroviral envelope (gp41) protein sequences,  
 especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 pharmacokinetic properties such as increasing the half-life of any core  
 polypeptide that they are linked to. The core polypeptides are any  
 polypeptide that may be introduced into a living system and that can  
 function as a pharmacologically useful peptide for the treatment or  
 prevention of a disease. The core polypeptides are bioactive peptides  
 selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AA88651-99005 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 and form hybrid polypeptides.

SO Sequence 35 AA:

Query Match 100.0%; Score 188; DB 21; Length 35;

Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35  
 ||||||||||||||||||||||||||||||||  
 DB 1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35

#### RESULT 5

ABB00634 standard; Peptide: 35 AA.

ABB00634;

03-JAN-2002 (first entry)

Viral DP178/107-like region peptide T715.

Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 infection.

Viridiae.

Key Location/Qualifiers

Modified-site 1 /note= "N-terminal is substituted by Ac"

Modified-site 35 /note= "C-terminal amide"

WO200164013-A2.

07-SEP-2001.

07-FEB-2001; 2001WO-US03988.

29-FEB-2000; 2000US-0515965.

(TRIM-) TRIMERIS INC.

Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

WPI: 2001-514829/56.

Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 fusion, useful for treating HIV and Respiratory Syncytial Virus  
 infection -

Disclosure: Page 45; 587pp; English.

The invention relates to isolated analogues of the heptad repeat region  
 peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 and HR2 regions of proteins interact non-covalently with each other,  
 and/or with peptides derived from them. This interaction is required for  
 normal infectivity of viruses such as RSV and HIV. The heptad  
 repeat region peptide analogs may be used to inhibit respiratory  
 syncytial virus (RSV) infection in a cell. They may also be used to  
 inhibit HIV infection. The present sequence is a peptide provided in  
 the specification.

SQ Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;

Best Local Similarity 100.0%; Pred. No. 2.5e-16; Mismatches 0; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
 |||||||  
 DB 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35

RESULT 6

ABB00796  
 ID ABB00796 standard; Peptide: 35 AA.

AC ABB00796;

DT 03-JAN-2002 (first entry)

DE Viral DP178/107-like region peptide T923.

KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 infection; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
 infection.

XX Viridae.

XX OS

XX FH

XX FT

XX PN

XX PD

XX PF

XX PR

XX PA

XX PI

XX DR

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

Disclosure: Page 49; 587pp; English.

The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HRI and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification.

SQ Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;

Best Local Similarity 100.0%; Pred. No. 2.5e-16; Mismatches 0; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
 |||||||  
 DB 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35

RESULT 7

ABB02111  
 ID ABB02111 standard; Peptide: 35 AA.

AC ABB02111;

DT 03-JAN-2002 (first entry)

DE Viral core polypeptide, SEQ ID NO: 638.

KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
 infection.

XX Viridae.

XX OS

XX PN

XX PD

XX PF

XX PR

XX PA

XX PI

XX DR

XX WPI: 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells

XX fusion, useful for treating HIV and Respiratory Syncytial Virus

XX infection -

XX Disclosure: Page 336; 587pp; English.

The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HRI and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification.

SQ Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;

Best Local Similarity 100.0%; Pred. No. 2.5e-16; Mismatches 0; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
 |||||||  
 DB 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35

RESULT 8

ABB02272  
 ID ABB02272 standard; Peptide: 35 AA.

AC ABB02272;

DT 03-JAN-2002 (first entry)

DE Viral core polypeptide, SEQ ID NO: 799.

KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
 infection.

XX Viridiae.  
OS  
XX  
PN WO200164013-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 07-FEB-2001; 2001WO-US03988.  
XX  
PR 29-FEB-2000; 2000US-0515965.  
XX  
PA (TRIM-) TRIMERIS INC.  
PI Autczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
XX WPI; 2001-514829/56.  
DR  
XX  
PT Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection -  
XX  
XX Disclosure; Page 379; 587pp; English.  
XX  
CC The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
CC and HR2 regions of proteins interact non-covalently with each other  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.  
XX  
XX  
SQ Sequence 35 AA:  
Query Match 100.0%; Score 188; DB 22; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
DB 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
RESULT 9  
AAU13182  
AC AAU13182; standard; Peptide: 35 AA.  
XX  
XX 21-NOV-2001 (first entry)  
XX  
XX DP178-like/DP107-like peptide T-715.  
DE  
XX  
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
KW antitumorigenic; antiviral; HIV transmission; mutant; mutein.  
XX  
XX Human immunodeficiency virus 1 isolate LAI.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT Modified-site /note= "N-terminal is substituted by Ac"  
FT Modified-site 35  
FT Modified-site /note= "C-terminal amide"  
XX  
XX WO200151673-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JUL-2000; 2000WO-US35727.  
PF

XX  
PR 09-JUL-1999; 99US-0350841.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
XX WPI; 2001-442157/47.  
DR  
XX  
XX Identifying a compound that inhibits the formation of or disrupts a  
PT DP107/DP178 complex, especially compounds with antitumorigenic, antiviral  
PT or intracellular modulatory activity, by detecting the formation of a  
PT DP107/DP178 complex -  
XX  
XX Disclosure; Page 65; 259pp; English.  
XX  
XX The present invention relates to peptides which exhibit anti-retroviral  
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds  
CC to amino acids 639-673 of the transmembrane protein gp41 from human  
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
CC also relates to a method of identifying compounds that inhibit the  
CC formation of or disrupts a DP107/DP178 complex. The method comprises  
CC detecting the formation of a DP107/DP178 complex, both in the presence  
CC or absence of a test compound, in a reaction mixture containing DP107  
CC and DP178 peptides. The method is useful for identifying compounds,  
CC including small molecule compounds, which may themselves exhibit  
CC antitumorigenic, antiviral or intracellular modulatory activity. The  
CC DP178-like/DP107-like peptides are useful to inhibit human and non-human  
CC retroviral, particularly HIV, transmission to uninfected cells. The  
CC present sequence represents one of the DP178-like/DP107-like peptides  
CC of the invention.  
XX  
XX  
SQ Sequence 35 AA:  
Query Match 100.0%; Score 188; DB 22; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
DB 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
RESULT 10  
AAU13342  
ID AAU13342 standard; Peptide: 35 AA.  
XX  
XX AAU13342;  
AC  
XX  
XX 21-NOV-2001 (first entry)  
XX  
XX DP178-like/DP107-like peptide T-923.  
DE  
XX  
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
KW antitumorigenic; antiviral; HIV transmission; mutant; mutein.  
XX  
XX Human immunodeficiency virus 1 isolate LAI.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 35  
FT Modified-site /note= "C-terminal amide"  
FT Modified-site 35  
FT Modified-site /note= "C-terminal amide"  
XX  
XX WO200151673-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JUL-2000; 2000WO-US35727.  
XX  
XX 09-JUL-1999; 99US-0350841.  
PR

PA (TRIM-) TRIMERIS INC.  
 XX  
 PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
 XX  
 DR WPI: 2001-442157/47.  
 XX  
 PT Identifying a compound that inhibits the formation of or disrupts a  
 CC DP107/DP178 complex, especially compounds with antitumor, antiviral  
 CC or intracellular modulatory activity, by detecting the formation of a  
 PT DP107/DP178 complex -  
 XX  
 PS Disclosure: Page 68; 259pp; English.  
 XX  
 CC The present invention relates to peptides which exhibit anti-retroviral  
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds  
 CC to amino acids 639-673 of the transmembrane protein gp41 from human  
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
 CC also relates to a method of identifying compounds that inhibit the  
 CC formation of or disrupts a DP107/DP178 complex. The method comprises  
 CC detecting the formation of a DP107/DP178 complex, both in the presence  
 CC or absence of a test compound, in a reaction mixture containing DP107  
 CC and DP178 peptides. The method is useful for identifying compounds,  
 CC including small molecule compounds, which may themselves exhibit  
 CC antitumor, antiviral or intracellular modulatory activity. The  
 CC DP178-like/DP107-like peptides are useful to inhibit human and non-human  
 CC retroviral, particularly HIV, transmission to uninfected cells. The  
 CC present sequence represents one of the DP178-like/DP107-like peptides  
 CC of the invention.  
 CC  
 XX  
 SQ Sequence 35 AA:  
 Query Match 100.0%; Score 188; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TSLHSLIEESQNOEKNEQELLELDKWSLWNMF 35  
 DB 1 TSLHSLIEESQNOEKNEQELLELDKWSLWNMF 35  
 RESULT 11  
 AAB77629  
 ID AAB77629 standard; Peptide: 35 AA.  
 XX  
 AC AAB77629;  
 XX  
 XX 19-APR-2001 (first entry)  
 DE Core polypeptide T715.  
 KW Core polypeptide; enhancer; antiviral; anti-HIV;  
 KW virucide; hepatotropic; antiinflammatory; hybrid polypeptide;  
 KW coiled-coil peptide interaction; fusion-related disorder;  
 KW bacterial infection; viral infection.  
 OS Unidentified.  
 XX  
 PN WO200103723-A1.  
 PD 18-JAN-2001.  
 PF 10-JUL-2000; 2000WO-US18772.  
 PR 09-JUL-1999; 99US-0350641.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 DR WPI: 2001-147136/15.  
 XX

PT New hybrid polypeptide, useful for preventing, treating and diagnosing  
 CC e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide -  
 XX  
 PS Disclosure: Page 44; 151pp; English.  
 XX  
 CC The present sequence is a core polypeptide which may be linked to  
 CC an enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of  
 CC the core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving  
 CC coiled-coil peptide interactions. Other uses include preventing,  
 CC treating and/or diagnosing disorders involving fusion events (e.g.  
 CC modulation of neurotransmitter exchange and sperm-egg fusion),  
 CC intracellular processes involving coiled-coil peptides (e.g. bacterial  
 CC infections) and viral infections that involve cell-cell and/or  
 CC virus-cell fusion (e.g. viral infections caused by human  
 CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr  
 CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
 CC The enhancer peptide sequence increases the half-life and reduces the  
 CC clearance rate of therapeutic peptides, which increases their efficacy  
 CC and minimises the incidence and severity of adverse side effects.  
 CC In addition, this increases the sensitivity of the diagnostic procedure  
 CC in which they are used.  
 CC  
 XX  
 SQ Sequence 35 AA:  
 Query Match 100.0%; Score 188; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TSLHSLIEESQNOEKNEQELLELDKWSLWNMF 35  
 DB 1 TSLHSLIEESQNOEKNEQELLELDKWSLWNMF 35  
 RESULT 12  
 AAB77789  
 ID AAB77789 standard; Peptide: 35 AA.  
 XX  
 AC AAB77789;  
 XX  
 XX 19-APR-2001 (first entry)  
 DE Core polypeptide T923.  
 KW Core polypeptide; enhancer; antiviral; anti-HIV;  
 KW virucide; hepatotropic; antiinflammatory; hybrid polypeptide;  
 KW coiled-coil peptide interaction; fusion-related disorder;  
 KW bacterial infection; viral infection.  
 OS Unidentified.  
 XX  
 PN WO200103723-A1.  
 PD 18-JAN-2001.  
 PF 10-JUL-2000; 2000WO-US18772.  
 PR 09-JUL-1999; 99US-0350641.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 DR WPI: 2001-147136/15.  
 XX  
 PT New hybrid polypeptide, useful for preventing, treating and diagnosing  
 CC e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide -  
 XX



PS Disclosure: Page 48; 151pp; English.  
 XX  
 CC The present sequence is a core polypeptide which may be linked to  
 CC an enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of  
 CC the core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving  
 CC cell-cell peptide interactions. Other uses include preventing,  
 CC treating and/or diagnosing disorders involving fusion events (e.g.  
 CC modulation of neurotransmitter exchange and sperm-egg fusion),  
 CC intracellular processes involving coiled-coil peptides (e.g. bacterial  
 CC infections) and viral infections that involve cell-cell and/or  
 CC virus-cell fusion (e.g. viral infections caused by human  
 CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr  
 CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
 CC The enhancer peptide sequence increases the half-life and reduces the  
 CC clearance rate of therapeutic peptides, which increases their efficacy  
 CC and minimises the incidence and severity of adverse side effects.  
 CC In addition, this increases the sensitivity of the diagnostic procedure  
 CC in which they are used.

XX Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEELLELDKNASLWNMF 35  
 ||||||||||||||||||||||||||||||||  
 DB 1 TSLHSLIEESONQOEKNEELLELDKNASLWNMF 35

RESULT 13

ID AAB54934 standard; Peptide; 35 AA.

XX AAB54934;

DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP178 amino truncation peptide #32.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;

KW antifusogenic; mobile blood component; measles virus; MeV; SIV;

KM simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;

KH human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX Human immunodeficiency virus type 1.

PN WO200069902-A1.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13651.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

DR WPI, 2001-007496/01.

XX A modified peptide and a reactive group which is reactive with amino  
 PT groups, hydroxyl groups, or thiol groups on blood components to form  
 PT stable covalent bonds useful for treatment of viral infections, e.g.  
 XX human immunodeficiency virus  
 PS Disclosure: Page 135; 211pp; English.

CC The present invention describes a modified anti-viral peptide (I)  
 CC comprising a peptide that exhibits anti-viral activity and a reactive  
 CC group which is reactive with amino groups, hydroxyl groups, or thiol  
 CC groups on blood components to form stable covalent bonds. (I) has  
 CC anti-viral and anti-fusogenic activities. (I) inhibits viral infection  
 CC of cells by inhibiting cell-cell fusion or free virus infection or to  
 CC reduce the level of membrane fusion events between two or more entities,  
 CC e.g., virus-cell or cell-cell, relative to the level of membrane fusion  
 CC that occurs in the absence of the peptide. (I) is useful in the  
 CC treatment of patients who are suffering from viral infection, e.g. HIV,  
 CC RSV, HPIV, MeV, and SIV. (I) may be administered prophylactically to  
 CC previously uninfected individuals. This is useful in cases where an  
 CC individual has been subjected to a high risk of exposure to a virus.  
 CC By bonding of long-lived components of the blood, such as immunoglobulin,  
 CC serum albumin, red blood cells and platelets the activity is extended  
 CC for days to weeks. This is due to improved stability in vivo and a  
 CC reduced susceptibility to peptidase or protease degradation. This  
 CC minimises the need for more frequent, or even continual, administration  
 CC of the peptides. AAB54784 to AAB54784 to AAB54784 represent peptides used in the  
 CC exemplification of the present invention.

XX Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEELLELDKNASLWNMF 35  
 ||||||||||||||||||||||||||||||||  
 DB 1 TSLHSLIEESONQOEKNEELLELDKNASLWNMF 35

RESULT 14

ID AAR64364 standard; Peptide; 36 AA.

XX AAR64364;

DT 24-AUG-1995 (first entry)

DE DP-178 derived from HIV-1 isolate LAI has antiviral activity.

XX antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;

KW human immunodeficiency virus; transmembrane protein; gp41;

KM alpha helix; leucine zipper; DP-185.

OS Synthetic.

XX Key

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

FT Modified-site

Location/Qualifiers  
 1  
 /note= "optionally has an amino, acetyl,  
 9-fluorenylmethoxy-carbonyl, hydrophobic or  
 macromolecular carrier gp. attached"  
 38  
 /note= "optionally has a carboxyl, amido, hydrophobic  
 or macromolecular carrier gp. attached"

WO9428920-A.

PD 22-DEC-1994.

PF 07-JUN-1994; 94WO-US05739.

PR 07-JUN-1993; 93US-0073028.

XX (UYDU-) UNIV DUKE.

PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;

PI Peteway SR, Wild CT;

DR WPI, 1995-036105/05.

XX Computer search generated synthetic peptides - are inhibitors of

PT HIV transmission  
XX  
PS Claim 11, page 132, 182pp; English.  
CC AAR64364 is designated DP-178, and corresponds to amino acids  
CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
CC forms a putative alpha helix at the C-terminal end of the gp41  
CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
CC 558-595) which contains a leucine zipper motif. The peptides complex  
CC via non-covalent protein-protein interactions, and possess anti-viral  
CC activity. Homologues of these peptides were identified by a computer  
CC assisted peptide sequence search. The peptides inhibit transmission to  
CC uninfected cells, and can also be used as type and/or subtype specific  
CC diagnostic tools.  
XX  
SO Sequence 36 AA:  
  
Query Match 100.0%; Score 188; DB 16; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 TSLHSLIEESONOEKNEQELLELDKWSLWNP 35  
|||||  
2 TSLHSLIEESONOEKNEQELLELDKWSLWNP 36  
Db  
  
RESULT 15  
AAR98398  
ID AAR98398 standard; peptide: 36 AA.  
XX  
AC AAR98398;  
XX  
DT 17-FEB-1997 (first entry)  
XX  
DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.  
XX  
KW Antifusogenic activity; antiviral capability; coiled-coil peptide;  
ALMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;  
KW Influenza virus; hepatitis B virus.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN W09619495-A1.  
XX  
PD 27-JUN-1996.  
XX  
PF 20-DEC-1995; 95WO-US16733.  
XX  
06-JUN-1995; 95US-0470896.  
20-DEC-1994; 94US-0360107.  
XX  
PA (TRIM-) TRIMERIS INC.  
PA (UYDU-) UNIV DUKE.  
XX  
PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
PI Matthews TJ, Petteway SR, Wild CT;  
XX  
DR WPI; 1996-309517/31.  
XX  
PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
PT isolated peptide recognised by an ALMOT15, 107x178x4 or PLZIP  
PT sequence search motif  
XX  
PS Disclosure; Fig 1; 471pp; English.  
XX  
CC The sequences given in AAR98398-408 represent peptides which exhibit  
CC antifusogenic activity, antiviral capability and/or the ability to  
CC modulate intracellular processes involving coiled-coil peptide  
CC structures. These peptides are recognised by the ALMOT15,  
CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
CC hepatitis B virus, to a cell.  
XX

SO Sequence 36 AA:  
  
Query Match 100.0%; Score 188; DB 17; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 TSLHSLIEESONOEKNEQELLELDKWSLWNP 35  
|||||  
DB 2 TSLHSLIEESONOEKNEQELLELDKWSLWNP 36  
  
Search completed: May 16, 2003, 11:12:03  
Job time : 32.5562 secs

GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 11.8072 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-117

Perfect score: 188  
Sequence: 1 TSLIHSLEESONQOEKNEOELLELDKWSLWMP 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	100.0	851	2 S33985	env polyprotein -
2	188	100.0	854	2 S13288	env polyprotein - huma
3	188	100.0	856	1 VCLJH3	env polyprotein pr
4	188	100.0	861	1 VCLJLV	env polyprotein pr
5	179	95.2	443	2 C41621	env polyprotein p
6	179	95.2	856	1 VCLJVL	env polyprotein pr
7	179	95.2	856	1 VCLJWC	env polyprotein pr
8	179	95.2	861	1 VCLJSC	env polyprotein pr
9	176	93.6	357	2 S21994	env polyprotein pr
10	176	93.6	358	2 S21998	env polyprotein g
11	175	93.1	357	2 S21996	env polyprotein g
12	172	91.5	847	2 T09448	env polyprotein g
13	172	91.5	847	2 S13289	env polyprotein - huma
14	171	91.0	445	2 A41621	env polyprotein M
15	170	90.4	358	2 S22002	env polyprotein g
16	170	90.4	358	2 S22000	env polyprotein g
17	170	90.4	358	2 S70417	env polyprotein g
18	170	90.4	859	2 T12016	env polyprotein g
19	170	90.4	859	1 VCLJMN	env polyprotein pr
20	169	89.9	357	2 S22004	env polyprotein g
21	169	89.9	855	1 VCLJAJ	env polyprotein pr
22	167	88.8	853	2 S54384	env polyprotein pr
23	167	88.8	855	1 VCLJZR	env polyprotein pr
24	166	88.3	357	2 S22006	env polyprotein pr
25	166	88.3	843	1 H44001	env polyprotein pr
26	165	87.8	846	1 VCLJND	env polyprotein pr
27	163	86.7	357	2 S21992	env polyprotein g
28	163	86.7	852	1 VCLJBR	env polyprotein -
29	161	85.6	729	1 VCLJRX	env polyprotein pr

30	161	85.6	861	1 VCLJKB	env polyprotein pr
31	160	85.1	859	2 T01672	env polyprotein pr
32	157	83.5	454	2 B41621	env polyprotein D
33	156	83.0	868	1 VCLJH4	env polyprotein -
34	153	81.4	136	2 JU0266	env polyprotein pr
35	153	81.4	136	2 JU0954	env polyprotein pr
36	144	76.6	854	1 VCLJST	env polyprotein pr
37	142	75.5	357	2 S21990	env polyprotein pr
38	140	74.5	357	2 S21997	env polyprotein pr
39	136	72.3	877	2 S49197	env polyprotein p
40	119	63.3	863	2 A53034	env polyprotein -
41	86	45.7	881	1 VCLJG3	env polyprotein -
42	86	45.7	881	1 S03068	env polyprotein -
43	86	45.7	889	1 VCLJG5	env polyprotein -
44	85	45.2	151	2 S30448	env polyprotein -
45	85	45.2	151	2 S30452	env polyprotein -

## ALIGNMENTS

## RESULT 1

S33985  
env polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1.  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
Submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-references: EMBL:211530; NID:960192; PIDN:CAA7628.1; PID:960199  
C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 188; DB 2; Length 851;

Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSLEESONQOEKNEOELLELDKWSLWMP 35  
DB 634 TSLIHSLEESONQOEKNEOELLELDKWSLWMP 668

RESULT 2  
env polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
R:O'Brien, W.A.; Koyanagi, Y.; Nemaize, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 188; DB 2; Length 854;

Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSLEESONQOEKNEOELLELDKWSLWMP 35  
DB 637 TSLIHSLEESONQOEKNEOELLELDKWSLWMP 671

RESULT 3  
VCLJH3

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03973  
R:Butler, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran, B.; Rabenold, P.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A93353; M01D:85111123; PMID:2578615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAAA442  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:12-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:18,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status predic  
Query Match 100.0%; Score 188; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TSLIHSIESQNOQEKNEDELLELDKWSLWMMF 35  
DB 639 TSLIHSIESQNOQEKNEDELLELDKWSLWMMF 673  
RESULT 4  
VCLJLV  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; M01D:85099333; PMID:2981635  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <MAT>  
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (asn) (covalent) #status predic  
Query Match 100.0%; Score 188; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TSLIHSIESQNOQEKNEDELLELDKWSLWMMF 35  
DB 644 TSLIHSIESQNOQEKNEDELLELDKWSLWMMF 678  
RESULT 5  
VCLJLV  
env polyprotein precursor - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polyprotein

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; M01D:92107924; PMID:1763038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015  
A:Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:1-522-443/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:424-443/Domain: transmembrane #status predicted <TM>  
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:  
Query Match 95.2%; Score 179; DB 2; Length 443;  
Best Local Similarity 94.3%; Pred. No. 7e-14;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TSLIHSIESQNOQEKNEDELLELDKWSLWMMF 35  
DB 379 TSLIHSIESQNOQEKNEDELLELDKWSLWMMF 413  
RESULT 6  
VCLJLV  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03974  
R:Wensing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr  
A:Reference number: A93355; M01D:85111157; PMID:2982104  
A:Accession: A03974  
A:Molecule type: DNA  
A:Residues: 1-856 <MUE>  
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status pre  
Query Match 95.2%; Score 179; DB 1; Length 856;  
Best Local Similarity 97.1%; Pred. No. 1.5e-13;  
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TSLIHSIESQNOQEKNEDELLELDKWSLWMMF 34  
DB 639 TSLIHSIESQNOQEKNEDELLELDKWSLWMMF 672  
RESULT 7  
VCLJLV  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997

C:Accession: A24774  
 R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; M0ID:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STA>  
 A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 95.2%; Score 179; DB 1; Length 856;  
 Best Local Similarity 94.3%; Pred. No. 1.5e-13;  
 Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSIESONQOEKNEDELLELDKWSLWMP 35  
 DB 639 TSLIYNLIESONQOEKNEDELLELDKWSLWMP 673

RESULT 8  
 VCLJSC  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Gargio, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sue  
 Virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; M0ID:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-861/Product: env polyprotein #status predicted <EPP>  
 F:7,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 95.2%; Score 179; DB 1; Length 861;  
 Best Local Similarity 94.3%; Pred. No. 1.5e-13;  
 Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSIESONQOEKNEDELLELDKWSLWMP 35  
 DB 644 TSLIYTLIESONQOEKNEDELLELDKWSLWMP 678

RESULT 9  
 S21994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 278  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ  
 A:Reference number: S21994  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE1>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; M0ID:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140; 'X', 142-312; 'X', 314-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:g60179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 93.6%; Score 176; DB 2; Length 357;  
 Best Local Similarity 91.4%; Pred. No. 1.3e-13;  
 Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSIESONQOEKNEDELLELDKWSLWMP 35  
 DB 140 TSLIYTLIESONQOEKNEDELLELDKWSLWMP 174

RESULT 10  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 28  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21998; S70425  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21998  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STE1>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; M0ID:92144209; PMID:1736940  
 A:Accession: S70425  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222; 'X', 224-358 <STE2>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 93.6%; Score 176; DB 2; Length 358;  
 Best Local Similarity 91.4%; Pred. No. 1.3e-13;  
 Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSIESONQOEKNEDELLELDKWSLWMP 35  
 DB 141 TSLIYTLIESONQOEKNEDELLELDKWSLWMP 175

RESULT 11  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S70422; S21996  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; M0ID:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <ST2>  
 A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129  
 A:Experimental source: patient 27L  
 A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polyprotein

Query Match 93.1%; Score 175; DB 2; Length 357;

Best Local Similarity 91.4%; Pred. No. 1.7e-13;

Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLIHSLSIESQNOQEKNEOELLELDKWSLWMMF 35

DB 140 TGLIYTLIESQNOQEKNEOELLELDKWSLWMMF 174

#### RESULT 12

T09448 envelope glycoprotein - human immunodeficiency virus type 1 (strain JRF1)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

C:Accession: T09448

R:Bang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09448

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-references: EMBL:U03632; NID:q1465777; PID:q1465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

Query Match 91.5%; Score 172; DB 2; Length 847;

Best Local Similarity 91.4%; Pred. No. 9.9e-13;

Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLIHSLSIESQNOQEKNEOELLELDKWSLWMMF 35

DB 630 TSEIYTLIESQNOQEKNEOELLELDKWSLWMMF 664

#### RESULT 13

S13289 env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13289

A:Molecule type: DNA

A:Residues: 1-847 <OBR>

C:Superfamily: type E retrovirus env polyprotein

Query Match 91.5%; Score 172; DB 2; Length 847;

Best Local Similarity 91.4%; Pred. No. 9.9e-13;

Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLIHSLSIESQNOQEKNEOELLELDKWSLWMMF 35

DB 630 TSEIYTLIESQNOQEKNEOELLELDKWSLWMMF 664

#### RESULT 14

A41621 env polyprotein M - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polyprotein

M:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

C:Accession: A41621

R:Burger, H.; Weisner, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: A41621

A:Molecule type: DNA

A:Residues: 1445 <BUR>

A:Cross-references: GB:W77228; MUID:9328627; PIDN:AAB03790.1; PID:9555013

A:Note: this virus was isolated from the mother

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:426-445/Domain: transmembrane #status predicted <TMN>

F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding si

Query Match 91.0%; Score 171; DB 2; Length 445;

Best Local Similarity 88.6%; Pred. No. 6.4e-13;

Matches 31; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSLSIESQNOQEKNEOELLELDKWSLWMMF 35

DB 381 TSLIYTLIESQNOQEKNEOELLELDKWSLWMMF 415

#### RESULT 15

S22002 envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: Isolate 3L

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22002; S70418

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22002

A:Molecule type: DNA

A:Residues: 1-358 <STEL>

A:Cross-references: EMBL:X61352; NID:G60186; PIDN:CAA43616.1; PID:G60187

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333, 'X', 335-358 <STEL>

A:Cross-references: EMBL:X61352; NID:G60186

C:Superfamily: type E retrovirus env polyprotein

Query Match 90.4%; Score 170; DB 2; Length 358;

Best Local Similarity 88.6%; Pred. No. 6.6e-13;

Matches 31; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLIHSLSIESQNOQEKNEOELLELDKWSLWMMF 35

DB 141 TSLIYTLIESQNOQEKNEOELLELDKWSLWMMF 175

Search completed: May 16, 2003, 11:25:07  
Job time: 11.8072 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 5.90361 seconds

(without alignments)  
245.895 Million cell updates/sec

Title: US-09-623-533A-117

Perfect score: 168

Sequence: 1 TSLIHSLEBSQNOEKNEQELTLDKWSLWNF 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	100.0	851	1 ENV_HV1B8	P04582 human immun
2	188	100.0	856	1 ENV_HV1B1	P03375 human immun
3	188	100.0	856	1 ENV_HV1B2	P04578 human immun
4	188	100.0	856	1 ENV_HV1B3	P04624 human immun
5	188	100.0	856	1 ENV_HV1B4	P07026 human immun
6	188	100.0	856	1 ENV_HV1B5	P03377 human immun
7	185	98.4	853	1 ENV_HV1B6	P03551 human immun
8	179	95.2	856	1 ENV_HV1B7	P03876 human immun
9	179	95.2	856	1 ENV_HV1B8	P03876 human immun
10	179	95.2	856	1 ENV_HV1B9	P03876 human immun
11	177	94.1	852	1 ENV_HV1B1	P31872 human immun
12	176	93.6	847	1 ENV_HV1S1	P19549 human immun
13	173	92.0	847	1 ENV_HV1S2	P05880 human immun
14	172	91.5	867	1 ENV_HV1J3	P12489 human immun
15	170	90.4	856	1 ENV_HV1A1	P05877 human immun
16	169	89.9	855	1 ENV_HV1A2	P05877 human immun
17	168	89.4	853	1 ENV_HV1E1	P04581 human immun
18	168	89.4	865	1 ENV_HV1R1	P04579 human immun
19	167	88.8	853	1 ENV_HV1Z2	P12488 human immun
20	167	88.8	855	1 ENV_HV1Z6	P04580 human immun
21	166	88.3	843	1 ENV_HV1Y2	P35961 human immun
22	165	87.8	846	1 ENV_HV1D1	P18799 human immun
23	165	87.8	855	1 ENV_HV1O1	P18799 human immun
24	163	86.7	852	1 ENV_HV1B1	P12488 human immun
25	162	86.2	848	1 ENV_HV1J1	P20888 human immun
26	161	85.6	861	1 ENV_HV1K1	P31819 human immun
27	160	85.1	859	1 ENV_HV1A1	P04583 human immun
28	156	83.0	868	1 ENV_HV1C4	P05879 human immun
29	155	82.4	863	1 ENV_HV1Z8	P05881 human immun
30	144	76.6	854	1 ENV_HV1C2	P17281 chimpanzee
31	142	75.5	856	1 ENV_HV1Z1	P05881 human immun
32	90	47.9	854	1 ENV_HV1Z1	O02837 simian immun
33	86	45.7	881	1 ENV_HV1A1	P05884 simian immun

34	86	45.7	882	1 ENV_HV1M1	P05885 simian immun
35	85	45.2	885	1 ENV_HV1S4	P12492 simian immun
36	84	44.7	859	1 ENV_HV2D2	P15831 human immun
37	84	44.7	860	1 ENV_HV2B1	P18094 human immun
38	82	43.6	880	1 ENV_HV1M1	P12677 simian immun
39	80	42.6	859	1 ENV_HV2C1	P24105 human immun
40	80	42.6	889	1 ENV_HV2S1	P19503 simian immun
41	77	41.0	846	1 ENV_HV2S1	P12449 human immun
42	77	41.0	851	1 ENV_HV2D1	P17755 human immun
43	77	41.0	851	1 ENV_HV2G1	P18040 human immun
44	77	41.0	858	1 ENV_HV2R1	P04577 human immun
45	77	41.0	859	1 ENV_HV2S1	P20872 human immun

## ALIGNMENTS

RESULT 1	ID	ENV_HV1B8	STANDARD:	PRT:	851 AA.
AC	P04582:				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	13-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein gp160 precursor [Contans: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]				
GN	ENV.				
OC	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).				
OS	Viruses; Retroviral viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11684;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8511123; PubMed=2578615;				
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumanster K., Ivanoff L., Petteney S.R., Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C., Wong-Staal F.;				
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III."				
RL	Nature 313:277-284(1985).				
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CC	-----				
CC	EMBL: K02011; AAA4461.1; -				
DR	HIV: K02011; ENV5B8.				
DR	Glycosylated: P04582; -				
DR	InterPro: IPR000328; ENV_GP41.				
DR	InterPro: IPR000777; GP120.				
DR	Pfam: PF00516; GP120; 1.				
DR	Pfam: PF00517; GP41; 1.				
KW	AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.				
FT	SIGNAL	1	30		
FT	CHAIN	31	506		
FT	CHAIN	507	851		
FT	DISULFID	54	74		
FT	DISULFID	119	205		
FT	DISULFID	126	196		
FT	DISULFID	131	157		
FT	DISULFID	218	247		
FT	DISULFID	228	239		
FT	DISULFID	296	331		
FT	DISULFID	378	440		
FT	DISULFID	385	413		
FT	CARBOHYD	88	88		
FT	CARBOHYD	136	136		
FT	CARBOHYD	141	141		

EXTERIOR MEMBRANE GLYCOPROTEIN.

TRANSMEMBRANE GLYCOPROTEIN.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

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Query Match 100.0%; Score 188; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 1,9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TSLHSLIEESQOEKNEOELELDKNASLWNMF 35
    |||||
DB 634 TSLHSLIEESQOEKNEOELELDKNASLWNMF 668

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RESULT 2
ENV_HV1B1 STANDARD: PRT: 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=6511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.,
RA Josephs S.F., Doran E.R., Ratafski J.A., Whitehorn E.A.,
RA Baumanster K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,
RA Lantenderger J.A., Pappas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RA Nature 313:277-284(1985).
RL [2]
RN DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RA "Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
Chinese hamster ovary cells."
RA J. Biol. Chem. 265:10373-10382(1990).
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CC -----
CC EMBL: M15654; AAA4205.1;
CC PIR: A03973; VCLJH3.
CC HIV: M15654; ENVSBI02.
CC InterPro: IPR000328; ENV GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC AIDS: Coat protein; Glycoprotein; Transmembrane;
CC Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
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FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931BB27 CRC64;

```

```

Query Match 100.0%; Score 188; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1,9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 TSLHSLIEESQOEKNEOELELDKNASLWNMF 35
    |||||
DB 639 TSLHSLIEESQOEKNEOELELDKNASLWNMF 673

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RESULT 3
ENV_HV1B2 STANDARD: PRT: 856 AA.
AC P04578; O09779;

```



FT	CARBOHYD	397	397	N-LINKED (GLCNAC...)	(POTENTIAL).				
FT	CARBOHYD	406	406	N-LINKED (GLCNAC...)	(POTENTIAL).				
FT	CARBOHYD	448	448	N-LINKED (GLCNAC...)	(POTENTIAL).				
FT	CARBOHYD	463	463	N-LINKED (GLCNAC...)	(POTENTIAL).				
FT	CARBOHYD	611	611	N-LINKED (GLCNAC...)	(POTENTIAL).				
FT	CARBOHYD	616	616	N-LINKED (GLCNAC...)	(POTENTIAL).				
FT	CARBOHYD	624	624	N-LINKED (GLCNAC...)	(POTENTIAL).				
FT	CARBOHYD	637	637	N-LINKED (GLCNAC...)	(POTENTIAL).				
FT	CARBOHYD	674	674	N-LINKED (GLCNAC...)	(POTENTIAL).				
FT	CARBOHYD	750	750	N-LINKED (GLCNAC...)	(POTENTIAL).				
SO	SEQUENCE	856 AA;	97212 MW;	66AB16AFB85107FED CRC64;	(POTENTIAL).				
<hr/>									
Query Match		100.0%;	Score 188;	DB 1;	Length 856;				
Best Local Similarity		100.0%;	Pred. No. 1,9e-15;						
Matches 35;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
<hr/>									
Db	1 TSLHLSLIEESONOEKNEQDELLEIDKKASLWNMF 35   639 TSLHLSLIEESONOEKNEQDELLEIDKKASLWNMF 673								
<hr/>									
RESULT 4									
ENV_HV1H3	STANDARD:	PRT:	856 AA.						
ID ENV_HV1H3									
AC P04624;									
DT 13-AUG-1987 (Rel. 05, Created)									
DR 01-FEB-1996 (Rel. 33, Last sequence update)									
DF 15-JUL-1999 (Rel. 38, Last annotation update)									
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]1.									
GN ENV.									
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).									
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.									
OX NCBI_TaxID=11707;									
[1]									
RX MEDLINE=8528248; PubMed=2988795;									
RA Ciowal R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;									
RL "HIV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";									
Cell 41:979-986(1985).									
CC -----									
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CC -----									
DR EMBL: M14100; AAA44679.1; -. HIV: M14100; ENVSHXBS.									
DR InterPro: IPR000328; Env.GP41.									
DR InterPro: IPR000777; GP120.									
DR Pfam: PF00516; GP120; 1.									
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.									
KW SIGNAL.									
FT CHAIN 1 30									
FT CHAIN 31 511									
FT DISULEID 512 856									
FT DISULEID 119 205									
FT DISULEID 126 196									
FT DISULEID 131 157									
FT DISULEID 218 247									
FT DISULEID 228 239									
FT DISULEID 296 331									
FT DISULEID 378 445									
FT DISULEID 385 418									
FT CARBOHYD 136 136									
FT CARBOHYD 88 88									
FT CARBOHYD 136 136									
FT CARBOHYD 88 88									

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;

```

```

Query Match 100.0%; Score 188; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 TSLHSLIEESONQOEKNEDELLELDKWSLWNMF 35
    |||||
Db 639 TSLHSLIEESONQOEKNEDELLELDKWSLWNMF 673

```

```

RESULT 5
ENV_HV1LW STANDARD; PRT; 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RU AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC
CC EMBL: U12055; AAA76690.1; -
CC GlycosultedB: Q70626; -
CC InterPro: IPR000328; Env_Gp41.
DR

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT SIGNAL 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

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```

Query Match 100.0%; Score 188; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 1 TSLHSLIEESONQOEKNEDELLELDKWSLWNMF 35
    |||||
Db 639 TSLHSLIEESONQOEKNEDELLELDKWSLWNMF 673

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```

RESULT 6
ENV_HV1BR STANDARD; PRT; 861 AA.
ID ENV_HV1BR
AC P03377;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA: 96912 MW: 3377B93B6F22ABA CRC64:

Query Match
Best Local Similarity 97.1%; Score 185; DB 1; Length 853;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TSLHSLIESONQOEKNEQELLELDKMASLNMWF 35
|||||:|||||:|||||:|||||:|||||:
637 TSLHSLIDESONQOEKNEQELLELDKMASLNMWF 671

RESULT 8
ENV_HV1PV STANDARD: PRT: 856 AA.
ID ENV_HV1PV
AC P03376:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OC Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OS Viruses: Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11700;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Mueing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/Lymphadenopathy retrovirus.";
RC Nature 313:450-458(1985).
CC -----
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CC -----
CC EMBL: K02083; AAB59873.1;
CC EMBL: X01762; CA225903.1; ALT_SEQ.
CC PIR: A03974; VCLJVL.
CC HIV: K02083; ENVSPV22.
CC InterPro: IPR000328; Env_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120.1.
DR DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT CHAIN 512 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 54 74 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.

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FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 366 366
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA: 97339 MW: 5FCDB1DC3C1209B3 CRC64:

Query Match
Best Local Similarity 95.2%; Score 179; DB 1; Length 856;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TSLHSLIESONQOEKNEQELLELDKMASLNMW 34
|||||:|||||:|||||:|||||:|||||:
639 TSLHSLIESONQOEKNEQELLELDKMASLNMW 672

RESULT 9
ENV_HV1SC STANDARD: PRT: 856 AA.
ID ENV_HV1SC
AC P05878:
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OC Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OS Viruses: Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11702;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reltz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RT Virology 164:531-536(1988).
CC -----
CC MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC -----

DR EMBL: M17450: -; NOT\_ANNOTATED\_CDS.

DR PIR: B28922; VCLJSC.

DR HIV: M17450; ENVSSC.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT CHAIN 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT SITE 760 760

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 160

FT DISULFID 219 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 439

FT DISULFID 383 412

FT CARBOHYD 87 87

FT CARBOHYD 129 129

FT CARBOHYD 135 135

FT CARBOHYD 140 140

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 295 295

FT CARBOHYD 301 301

FT CARBOHYD 302 302

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 384 384

FT CARBOHYD 394 394

FT CARBOHYD 400 400

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

FT CARBOHYD 674 674

FT CARBOHYD 816 816

SO SEQUENCE 856 AA: 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match

Best Local Similarity 94.3%; Score 179; DB 1; Length 856;

Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLISLIEESONQOEKNEQLELLDKNASLWNMF 35

DB 639 TSLIYTLIEESONQOEKNEQLELLDKNASLWNMF 673

RESULT 10

ENV\_HV1M1

AC P31872;

DR 01-JUL-1993 (Rel. 26, Created)

STANDARD: PRT: 856 AA.

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].

DE ENV.

GN Human immunodeficiency virus type 1 (WM1 isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=31678;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86218077; PubMed=2423250;

RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS."

RL Cell 45:637-648(1986).

CC -i- MISCELLANEOUS: ISOLATES WMU1, WMU2, AND WMU3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

CC PIR: A24774; VCLJ3W.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT CHAIN 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT DISULFID 53 73

FT DISULFID 118 205

FT DISULFID 125 196

FT DISULFID 130 152

FT DISULFID 218 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 444

FT DISULFID 383 417

FT CARBOHYD 87 87

FT CARBOHYD 134 134

FT CARBOHYD 140 140

FT CARBOHYD 151 151

FT CARBOHYD 155 155

FT CARBOHYD 183 183

FT CARBOHYD 197 197

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 289 289

FT CARBOHYD 295 295

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 390 390

FT CARBOHYD 394 394

FT CARBOHYD 404 404

FT CARBOHYD 447 447

FT CARBOHYD 459 459

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

SO SEQUENCE 856 AA: 97526 MW; DB68D1E49C404DE3 CRC64;

Query Match

Best Local Similarity 94.3%; Score 179; DB 1; Length 856;

Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLISLIEESONQOEKNEQLELLDKNASLWNMF 35

Db 635 TSLIYNLIESONQOEKNEOELLELDKMSLWNMF 673

RESULT 11

ENV\_HV153 STANDARD: PRT: 852 AA.

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11690;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90317906; PubMed=2370688;

RT J. Virol. 64:4016-4020(1990).

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CC EMBL: M38427; AAA45067.1; -

CC HIV: M38427; EVNSF33.

DR InterPro: IPR000328; Env-GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW Aids; Coat protein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 31 BY SIMILARITY.

FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT DISULFID 507 852 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 156 BY SIMILARITY.

FT DISULFID 219 248 BY SIMILARITY.

FT DISULFID 229 240 BY SIMILARITY.

FT DISULFID 257 331 BY SIMILARITY.

FT DISULFID 377 439 BY SIMILARITY.

FT DISULFID 384 412 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 852 852 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 852 AA: 96663 MW: EE7BF8D23C9910D CRC64;

Query Match 94.1% Score 177; DB 1; Length 852;

Best Local Similarity 91.4% Pred No. 4.3e-14;

Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIYNLIESONQOEKNEOELLELDKMSLWNMF 35

Db 635 TSLIYNLIESONQOEKNEOELLELDKMSLWNMF 669

RESULT 12

ENV\_HV151 STANDARD: PRT: 847 AA.

AC PI9550:

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-VUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11691;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90347635; PubMed=2384920;

RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.

RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation."

RT J. Virol. 64:4390-4398(1990).

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CC EMBL: M65024; AAA5072.1; -

CC HIV: M38428; EVNSF162.

DR InterPro: IPR000328; Env-GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 29

FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 118 203 BY SIMILARITY.

FT DISULFID 125 194 BY SIMILARITY.

FT DISULFID 130 155 BY SIMILARITY.

FT DISULFID 216 245 BY SIMILARITY.

FT DISULFID 226 237 BY SIMILARITY.

FT DISULFID 294 328 BY SIMILARITY.

FT DISULFID 374 435 BY SIMILARITY.

FT DISULFID 381 408 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 166 186 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 847 AA; 96135 MW; 0A901317FD7FE2AB CRC64;

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Query Match 93.6%; Score 176; DB 1; Length 847;
Best Local Similarity 91.4%; Pred. No. 5.6e-14;
Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TSLHSLIEESONOEKNEOELLELDKWSLWNMF 35
DB 630 TNLITLIEESONOEKNEOELLELDKWSLWNMF 664

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RESULT 13
ENV_HV1W2 STANDARD; PRT; 847 AA.
AC POS880;
DT 01-NOV-1988 (Rel. 09, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
R1 Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
R1 Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
R1 "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
R1 at risk for AIDS."
R1 Science 232:1548-1553(1986).
RL -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SPONTANEOUSLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC -----
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CC -----
CC EMBL: M12507; AAB12990.1; -
CC HIV: M12507; ENV:WMJ2.
CC InterPro: IPR000328; ENV_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
CC AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC Signal.

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```

FT SIGNAL 1 29
FT CHAIN 30 501
FT CHAIN 502 847
FT DISULFID 53 73
FT DISULFID 118 202
FT DISULFID 125 193
FT DISULFID 130 152
FT DISULFID 135 244
FT DISULFID 225 236
FT DISULFID 293 326
FT DISULFID 372 435
FT DISULFID 379 408
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 140 140
FT CARBOHYD 151 151
FT CARBOHYD 155 155
FT CARBOHYD 183 183
FT CARBOHYD 184 184
FT CARBOHYD 194 194
FT CARBOHYD 231 231
FT CARBOHYD 238 238
FT CARBOHYD 259 259
FT CARBOHYD 273 273
FT CARBOHYD 286 286
FT CARBOHYD 292 292
FT CARBOHYD 327 327
FT CARBOHYD 334 334
FT CARBOHYD 350 350
FT CARBOHYD 356 356
FT CARBOHYD 380 380
FT CARBOHYD 386 386
FT CARBOHYD 390 390
FT CARBOHYD 400 400
FT CARBOHYD 438 438
FT CARBOHYD 450 450
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SEQUENCE 847 AA; 96466 MW; C01E33D73AAB3CAE CRC64;

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Query Match 92.0%; Score 173; DB 1; Length 847;
Best Local Similarity 91.4%; Pred. No. 1.3e-13;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 1 TSLHSLIEESONOEKNEOELLELDKWSLWNMF 35
DB 630 TSLHSLIEESONOEKNEOELLELDKWSLWNMF 664

```

```

RESULT 14
ENV_HV1J3 STANDARD; PRT; 867 AA.
AC P12489;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUL-1999 (Rel. 12, Last sequence update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352108; PubMed=2669897;
R1 Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
R1 "Nucleotide sequences of gag and env genes of a Japanese isolate of
R1 HIV-1 and their expression in bacteria."
R1 AIDS Res. Hum. Retroviruses 5:411-419(1989).
CC -----
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 CC -----  
 DR EMBL; M21138; AAB03526.1; -  
 DR HIV; M21138; ENV5JH3.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 516  
 FT CHAIN 517 867  
 FT DISULFID 53 73  
 FT DISULFID 118 217  
 FT DISULFID 125 208  
 FT DISULFID 130 160  
 FT DISULFID 230 259  
 FT DISULFID 240 251  
 FT DISULFID 308 342  
 FT DISULFID 388 457  
 FT DISULFID 395 430  
 FT CARBOHYD 87 87  
 FT CARBOHYD 135 135  
 FT CARBOHYD 140 140  
 FT CARBOHYD 143 143  
 FT CARBOHYD 159 159  
 FT CARBOHYD 163 163  
 FT CARBOHYD 188 188  
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 FT CARBOHYD 199 199  
 FT CARBOHYD 209 209  
 FT CARBOHYD 246 246  
 FT CARBOHYD 253 253  
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 FT CARBOHYD 423 423  
 FT CARBOHYD 460 460  
 FT CARBOHYD 475 475  
 FT CARBOHYD 622 622  
 FT CARBOHYD 627 627  
 FT CARBOHYD 636 636  
 FT CARBOHYD 648 648  
 FT SEQUENCE 867 AA: 98399 MW: 5F2310146B8B8680 CRC64;  
 Query Match 91.5%; Score 172; DB 1; Length 867;  
 Best Local Similarity 91.4%; Pred. No. 1.8e-13;  
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).  
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11696;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88219542; PubMed=3369091;  
 RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;  
 RL "Envelope sequences of two new United States HIV-1 isolates.";  
 RT Virology 164:531-536(1988).  
 CC -I- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS  
 CC PATIENT IN 1984.  
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 CC -----  
 DR EMBL; M17449; AAA44857.1; -  
 DR PIR; A28922; VCLJMN.  
 DR HIV; M17449; ENV5MN.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 513  
 FT CHAIN 514 856  
 FT DISULFID 53 73  
 FT DISULFID 118 210  
 FT DISULFID 125 201  
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 FT DISULFID 223 252  
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 FT DISULFID 301 335  
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 FT CARBOHYD 406 406  
 FT CARBOHYD 413 413  
 FT CARBOHYD 448 448  
 FT CARBOHYD 465 465  
 FT SEQUENCE 513 AA: 98399 MW: 5F2310146B8B8680 CRC64;  
 Query Match 91.5%; Score 172; DB 1; Length 867;  
 Best Local Similarity 91.4%; Pred. No. 1.8e-13;  
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;



FT	CARBOHYD	612	612	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	617	617	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	626	626	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	638	638	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	816	816	N-LINKED (GLCNAC. . .)	(POTENTIAL)
SO	SEQUENCE	856 AA;	97140 MW;	D197D80940BE3732	CR664;

Query Match	90.48%	Score 170:	DB 1:	Length 856:
Best Local Similarity	88.68%	Pred. No. 3, 1e-13:		
Matches 31, Conservative		3;	Mismatches 1;	Indels 0; Gaps 0;

```

QY      1 TSLIHSLEESQNOQEKNEQELLEDKWLWNNF  35
        |||::|::|::|::|::|::|::|::|::|::|
Db      640 TSLIYSLEKSQTQOEKNEQELLELDKWLWNNF  674

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Search completed: May 16, 2003, 11:13:33  
Job time : 6.90361 secs

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F:424-443/Domain: transmembrane #status predicted <TMN>  
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 92.5%; Score 185; DB 2; Length 443;  
Best Local Similarity 88.9%; Pred. No. 1,9e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 36  
DB 378 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 413

RESULT 3  
VCLJ3M  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)

N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
F:45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the en  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382

C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <ST>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 92.5%; Score 185; DB 1; Length 856;  
Best Local Similarity 88.9%; Pred. No. 3.9e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 36  
DB 638 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 673

RESULT 4  
T01672  
envelope polyprotein precursor - human immunodeficiency virus type 1

Species: human immunodeficiency virus type 1, HIV-1  
C:Accession: T01672  
R:Alison, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
Cell 46, 63-74, 1986  
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol  
A:Reference number: Z14389; MUID:86245056; PMID:2424612  
A:Accession: T01672  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-859 <ALI>  
A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234  
C:Superfamily: type E retrovirus env polyprotein

Query Match 90.0%; Score 180; DB 2; Length 859;  
Best Local Similarity 88.9%; Pred. No. 1.6e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 36  
DB 640 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 675

RESULT 5  
S54384

envelope polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
C:Accession: S54384  
R:Rhodes, T.; Buckler-White, A.J.  
submitted to the EMBL Data Library, July 1989

A:Reference number: S54377  
A:Accession: S54384  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-853 <THE>  
A:Cross-references: EMBL:M26039; NID:g329377; PIDN:AAA5370.1; PID:g329385  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: polyprotein

Query Match 89.5%; Score 179; DB 2; Length 853;  
Best Local Similarity 86.1%; Pred. No. 2e-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 36  
DB 635 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 670

RESULT 6  
VCLJ2R  
env polyprotein precursor - human immunodeficiency virus ZR-6

N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus ZR-6  
C>Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
C:Accession: D26192  
R:Srivatsan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorlino, P.; Schochetman, G.;  
Gene 52, 71-82, 1987  
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucle  
A:Reference number: A26192; MUID:87248097; PMID:3036660  
A:Accession: D26192  
A:Molecule type: DNA  
A:Residues: 1-855 <SRD>  
A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA5380.1; PID:g329403

C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-15/Domain: signal sequence #status predicted <ST>  
F:16-855/Product: env polyprotein #status predicted <MA>  
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:501-855/Product: transmembrane glycoprotein #status predicted <TM>  
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,

Query Match 89.5%; Score 179; DB 1; Length 855;  
Best Local Similarity 86.1%; Pred. No. 2e-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 36  
DB 637 YTGIIYNLEESONOEKNEDELLELDKMANLNMWF 672

RESULT 7  
VCLJ3C  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922  
R:Gargio, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-  
Virollogy 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091  
A:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-4

Perfect score: 200  
Sequence: 1 YTGIIYNLEESONQOEKNEDELLEDKWANLWNP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: p11:\*  
2: p12:\*  
3: p13:\*  
4: p14:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	92.5	357	2 S21996	envelope protein g
2	185	92.5	443	2 C41621	env polypeptide p
3	185	92.5	856	1 VCLJ3W	env polypeptide pr
4	180	90.0	859	2 T01672	envelope glycoprote
5	179	89.5	853	2 S54384	envelope polypeptide
6	179	89.5	855	1 VCLJ2R	env polypeptide pr
7	179	89.5	861	1 VCLJ3C	env polypeptide pr
8	178	89.0	357	2 S22004	envelope protein g
9	178	89.0	855	1 VCLJ2A	env polypeptide pr
10	177	88.5	357	2 S22006	envelope protein g
11	177	88.5	357	2 S21994	envelope protein g
12	177	88.5	445	2 A41621	env polypeptide M
13	176	88.0	358	2 S21998	envelope protein g
14	175	87.5	851	2 S33985	envelope protein g
15	175	87.5	854	2 S13288	env polypeptide -
16	175	87.5	856	1 VCLJH3	env protein - huma
17	175	87.5	861	1 VCLJH3	env polypeptide pr
18	174	87.0	357	2 S21992	envelope protein g
19	174	87.0	847	2 T09448	envelope glycoprote
20	174	87.0	856	1 S13289	env protein - huma
21	174	87.0	856	1 VCLJ2V	env polypeptide pr
22	173	86.5	846	1 VCLJND	env polypeptide pr
23	172	86.0	859	1 VCLJMN	env polypeptide pr
24	171	85.5	843	1 H44001	env polypeptide pr
25	170	85.0	358	2 S22002	envelope protein g
26	170	85.0	358	2 S22000	envelope protein g
27	170	85.0	358	2 S70417	envelope protein g
28	170	85.0	729	1 VCLJXK	env polypeptide pr
29	170	85.0	861	1 VCLJKB	env polypeptide pr

30	168	84.0	852	2 T12016	envelope glycoprote
31	164	82.0	852	1 VCLJBR	env polypeptide -
32	163	81.5	454	2 B41621	env polypeptide D
33	162	81.0	136	2 JU0266	envelope polypeptide
34	162	81.0	136	2 JU0266	envelope polypeptide
35	162	81.0	856	1 A44963	env polypeptide pr
36	159	79.5	854	1 VCLJST	env polypeptide pr
37	159	79.5	868	1 VCLJH4	env polypeptide pr
38	143	71.5	357	2 S21990	envelope protein g
39	132	66.0	877	2 S49197	envelope protein g
40	115	57.5	863	2 A53034	gag polypeptide -
41	86	43.0	151	2 S30448	env protein - huma
42	86	43.0	151	2 S30452	env protein - huma
43	86	43.0	151	2 S30451	env protein - huma
44	86	43.0	366	2 B41565	env polypeptide -
45	86	43.0	885	2 S04322	env polypeptide -

## ALIGNMENTS

RESULT 1  
S21996  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S70422; S21996  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70422  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: EMBL:61356; NID:960181; PIDN:CA443624.1; PID:g1067129  
A:Experimental source: Patient 27L  
A>Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type E retrovirus env polypeptide

Query Match 92.5% Score 185; DB 2; Length 357;  
Best Local Similarity 88.9%; Pred. No. 1.5e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONQOEKNEDELLEDKWANLWNP 36  
DB 139 YTGIIYNLEESONQOEKNEDELLEDKWANLWNP 174

RESULT 2  
C41621  
env polypeptide p - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polypeptide  
N:Contents: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C>Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; MUID:92107924; PMID:1763038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:9328631; PIDN:AA03792.1; PID:g555015  
A>Note: This virus was isolated from the mother's sexual partner  
C:Genetics: A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX  
 DR WPI: 2001-147136/15.  
 XX

PT New hybrid polypeptide, useful for preventing, treating and diagnosing  
 PT e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide -  
 XX  
 PS

Disclosure: Page 58; 151pp: English.

XX The present sequence is a core polypeptide which may be linked to  
 CC an enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of  
 CC the core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving  
 CC coiled-coil peptide interactions. Other uses include preventing,  
 CC treating and/or diagnosing disorders involving fusion events (e.g.  
 CC modulation of neurotransmitter exchange and sperm-egg fusion),  
 CC intracellular processes involving coiled-coil peptides (e.g. bacterial  
 CC infections) and viral infections that involve cell-cell and/or  
 CC virus-cell fusion (e.g. viral infections caused by human  
 CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr  
 CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
 CC The enhancer peptide sequence increases the half-life and reduces the  
 CC clearance rate of therapeutic peptides, which increases their efficacy  
 CC and minimises the incidence and severity of adverse side effects.  
 CC In addition, this increases the sensitivity of the diagnostic procedure  
 CC in which they are used.  
 XX

SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLEESONQOEKNEQELLELDKWNANLMMNF 36  
 II  
 DB 1 YTGIIYNLEESONQOEKNEQELLELDKWNANLMMNF 36

Search completed: May 16, 2003, 11:12:02  
 Job time : 33.4578 secs



XX AAU13793;  
 AC Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
 XX antifusogenic; antiviral; HIV transmission; mutant; mutein.  
 DT 21-NOV-2001 (first entry)  
 XX DP178-like/DP107-like peptide T-1408.  
 DE  
 XX  
 XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
 KM antifusogenic; antiviral; HIV transmission; mutant; mutein.  
 KM  
 XX Human immunodeficiency virus 1 isolate LAI.  
 OS Synthetic.  
 OS  
 XX WO200151673-A2.  
 XX  
 XX 19-JUL-2001.  
 PD  
 XX 05-JUL-2000; 2000WO-US35727.  
 PF  
 XX 09-JUL-1999; 99US-0350841.  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 XX  
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
 PI WPI: 2001-442157/47.  
 DR  
 XX Identifying a compound that inhibits the formation of or disrupts a  
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
 PT or intracellular modulatory activity, by detecting the formation of a  
 PT DP107/DP178 complex -  
 PS Disclosure; Page 77; 259pp; English.  
 XX  
 XX The present invention relates to peptides which exhibit anti-retroviral  
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds  
 CC to amino acids 639-673 of the transmembrane protein gp41 from human  
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
 CC also relates to a method of identifying compounds that inhibit the  
 CC formation of or disrupts a DP107/DP178 complex. The method comprises  
 CC detecting the formation of a DP107/DP178 complex, both in the presence  
 CC or absence of a test compound, in a reaction mixture containing DP107  
 CC and DP178 peptides. The method is useful for identifying compounds,  
 CC including small molecule compounds, which may themselves exhibit  
 CC antifusogenic, antiviral or intracellular modulatory activity. The  
 CC DP178-like/DP107-like peptides are useful to inhibit human and non-human  
 CC retroviral, particularly HIV, transmission to uninfected cells. The  
 CC present sequence represents one of the DP178-like/DP107-like peptides  
 CC of the invention.  
 CC  
 SQ Sequence 36 AA;  
 XX  
 XX

Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLEESONQOEKNEELLELDKMANLNMWF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YTGIIYNLEESONQOEKNEELLELDKMANLNMWF 36

RESULT 12  
 AAU14013  
 ID AAU14013 standard; peptide; 36 AA.  
 XX  
 AC AAU14013;  
 XX  
 DT 21-NOV-2001 (first entry)  
 XX  
 DE DP178 homologue derived from HIV-1 isolate RF.  
 XX

KM Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
 KM antifusogenic; antiviral; HIV transmission.  
 OS  
 XX Human immunodeficiency virus 1 isolate RF.  
 OS  
 XX WO200151673-A2.  
 XX  
 XX 19-JUL-2001.  
 PD  
 XX 05-JUL-2000; 2000WO-US35727.  
 PF  
 XX 09-JUL-1999; 99US-0350841.  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 XX  
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
 PI WPI: 2001-442157/47.  
 DR  
 XX Identifying a compound that inhibits the formation of or disrupts a  
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
 PT or intracellular modulatory activity, by detecting the formation of a  
 PT DP107/DP178 complex -  
 PS Disclosure; Fig 1; 259pp; English.  
 XX  
 XX The present invention relates to peptides which exhibit anti-retroviral  
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds  
 CC to amino acids 639-673 of the transmembrane protein gp41 from human  
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
 CC also relates to a method of identifying compounds that inhibit the  
 CC formation of or disrupts a DP107/DP178 complex. The method comprises  
 CC detecting the formation of a DP107/DP178 complex, both in the presence  
 CC or absence of a test compound, in a reaction mixture containing DP107  
 CC and DP178 peptides. The method is useful for identifying compounds,  
 CC including small molecule compounds, which may themselves exhibit  
 CC antifusogenic, antiviral or intracellular modulatory activity. The  
 CC DP178-like/DP107-like peptides are useful to inhibit human and non-human  
 CC retroviral, particularly HIV, transmission to uninfected cells. The  
 CC present sequence represents a DP178 homologue derived from  
 CC HIV-1 isolate RF.  
 CC  
 SQ Sequence 36 AA;  
 XX  
 XX

Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLEESONQOEKNEELLELDKMANLNMWF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YTGIIYNLEESONQOEKNEELLELDKMANLNMWF 36

RESULT 13  
 AAB92246  
 ID AAB92246 standard; Peptide; 36 AA.  
 XX  
 AC AAB92246;  
 XX  
 DT 22-JUN-2001 (first entry)  
 XX  
 DE Virus related peptide SEQ ID NO:1422.  
 XX  
 XX Protection: endogenous therapeutic peptide; peptidase; conjugation;  
 KM blood component; modification; succinimidylyl; maleimido group; amino;  
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200069900-A2.

XX Sequence 36 AA:

Query Match 100.0%; Score 200; DB 22; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOQEKNEDELLELDKWNLMNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOQEKNEDELLELDKWNLMNMF 36

RESULT 9  
AB802832  
ID AB802832 standard; Peptide: 36 AA.

AC AB802832;  
XX  
DT 03-JAN-2002 (first entry)

Viral core polypeptide, SEQ ID NO: 1359.

KM Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
KM virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
infection.

XX Virididae.

PN WO200164013-A2.

PD 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US03988.

PR 29-FEB-2000; 2000US-0515965.

PA (TRIM-) TRIMERIS INC.

PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

DR WPI: 2001-514829/56.

PT Heptad repeat region peptide analogs useful for inhibiting virus/cell  
fusion, useful for treating HIV and Respiratory Syncytial Virus  
infection.

PS Disclosure: Page 525; 587pp; English.

CC The invention relates to isolated analogues of the heptad repeat region  
peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
HRI) respectively, of HIV-1LAI transmembrane protein gp41. The HRI  
CC and HR2 regions of proteins interact non-covalently with each other  
and/or with peptides derived from them. This interaction is required for  
normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.

XX Sequence 36 AA:

Query Match 100.0%; Score 200; DB 22; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOQEKNEDELLELDKWNLMNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOQEKNEDELLELDKWNLMNMF 36

RESULT 10  
AAU13792

ID AAU13792 standard; Peptide: 36 AA.

XX AAU13792;

AC AAU13792;

XX 21-NOV-2001 (first entry)

XX DP178-like/DP107-like peptide T-1407.

XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
KM antitumorigenic; antiviral; HIV transmission; mutant; mutein.

XX Human immunodeficiency virus 1 isolate LAI.

OS Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note="N-terminal is substituted by Ac"

XX Modified-site 36 /note="C-terminal amide"

XX WO200151673-A2.

XX 19-JUL-2001.

XX 05-JUL-2000; 2000WO-US35727.

XX 09-JUL-1999; 99US-0350841.

XX (TRIM-) TRIMERIS INC.

XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Nerutka G;

XX WPI: 2001-442157/47.

XX Identifying a compound that inhibits the formation of or disrupts a  
PT DP107/DP178 complex, especially compounds with antitumorigenic, antiviral  
PT or intracellular modulatory activity, by detecting the formation of a  
PT DP107/DP178 complex.

PS Disclosure: Page 77; 259pp; English.

CC The present invention relates to peptides which exhibit anti-retroviral  
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds  
CC to amino acids 639-673 of the transmembrane protein gp41 from human  
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
CC also relates to a method of identifying compounds that inhibit the  
CC formation of or disrupts a DP107/DP178 complex. The method comprises  
CC detecting the formation of a DP107/DP178 complex, both in the presence  
CC or absence of a test compound, in a reaction mixture containing DP107  
CC and DP178 peptides. The method is useful for identifying compounds,  
CC including small molecule compounds, which may themselves exhibit  
CC antitumorigenic, antiviral or intracellular modulatory activity. The  
CC DP178-like/DP107-like peptides are useful to inhibit human and non-human  
CC retroviral, particularly HIV, transmission to uninfected cells. The  
CC present sequence represents one of the DP178-like/DP107-like peptides  
CC of the invention.

XX Sequence 36 AA:

Query Match 100.0%; Score 200; DB 22; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOQEKNEDELLELDKWNLMNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOQEKNEDELLELDKWNLMNMF 36

RESULT 11  
AAU13793  
ID AAU13793 standard; Peptide: 36 AA.



XX 07-FEB-2001; 2001WO-US03988.  
 PF  
 XX 29-FEB-2000; 2000US-0515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI: 2001-514829/56.  
 DR  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 XX  
 PS Disclosure: Page 58; 587pp; English.  
 CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESQNOQEKNEDELLELDKMANIMNMF 36  
 DB 1 YTGIIYNLLEESQNOQEKNEDELLELDKMANIMNMF 36  
 RESULT 7  
 ABB01247  
 ID ABB01247 standard; Peptide; 36 AA.  
 AC ABB01247;  
 XX  
 AC ABB01247;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 XX Viral DP178/107-like region peptide T1408.  
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1, HR2;  
 KW infection.  
 XX  
 XX Viridiae.  
 OS  
 XX  
 XX WO200164013-A2.  
 PN  
 XX 07-SEP-2001.  
 PD  
 XX 07-FEB-2001; 2001WO-US03988.  
 PF  
 XX 29-FEB-2000; 2000US-0515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI: 2001-514829/56.  
 DR  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 PT

XX Disclosure: Page 58; 587pp; English.  
 PS  
 XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESQNOQEKNEDELLELDKMANIMNMF 36  
 DB 1 YTGIIYNLLEESQNOQEKNEDELLELDKMANIMNMF 36  
 RESULT 8  
 ABB02831  
 ID ABB02831 standard; Peptide; 36 AA.  
 AC ABB02831;  
 XX  
 AC ABB02831;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 XX Viral core polypeptide, SEQ ID NO: 1358.  
 DE  
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1, HR2;  
 KW infection.  
 XX  
 XX Viridiae.  
 OS  
 XX  
 XX WO200164013-A2.  
 PN  
 XX 07-SEP-2001.  
 PD  
 XX 07-FEB-2001; 2001WO-US03988.  
 PF  
 XX 29-FEB-2000; 2000US-0515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI: 2001-514829/56.  
 DR  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 PT  
 PS Disclosure: Page 524-525; 587pp; English.  
 CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 CC

DE	XX	HIV viral envelope protein stabilising peptide #3.
DE	XX	
XX	XX	Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
KW	KW	anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
KW	KW	alpha-helical region; ectodomain.
OS	OS	Homo sapiens.
XX	XX	
PN	PN	WO200170262-A2.
PD	PD	
XX	XX	27-SEP-2001.
XX	XX	
PF	PF	15-MAR-2001; 2001WO-US08108.
XX	XX	
PR	PR	17-MAR-2000; 2000US-189981P.
XX	XX	
PA	PA	(PANA-) PANACOS PHARM INC.
XX	XX	
XX	XX	Wild CT, Allaway GP.
XX	XX	WPI: 2001-626098/72.
PT	PT	Immunogenic composition for inhibiting HIV infection, comprises viral
PT	PT	envelope protein or its fragment exterior to viral membrane, a
PT	PT	stabilising peptide, and optionally, viral cell surface receptor or
PT	PT	its fragment
PS	PS	
XX	XX	Claim 6; Page 45; 84pp; English.
CC	CC	The invention relates to methods of generating immunogens that elicit
CC	CC	neutralising antibodies which target regions of viral envelope proteins
CC	CC	such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of
CC	CC	HIV-1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and
CC	CC	AAU70677-AAU70743 represent stabilising peptides modelling the
CC	CC	alpha-helical regions of the ectodomain of the HIV-1 transmembrane
CC	CC	protein to stabilise fusion-active intermediate structures, which can be
CC	CC	used as vaccine immunogens. Immunogenic compositions comprise a viral
CC	CC	envelope protein or its fragment exterior to the viral membrane, a
CC	CC	stabilising peptide to disrupt formation of structural intermediates
CC	CC	necessary for viral fusion and entry, and optionally, a viral cell
CC	CC	surface receptor or its fragment. The stabilising peptide is capable of
CC	CC	associating with the envelope protein or its fragment to form a
CC	CC	stabilised, fusion active structure. Antibody binding assays are used to
CC	CC	determine the ability of immunogen vaccines to generate an immune
CC	CC	response to various forms of envelope. Virus neutralisation assays can be
CC	CC	used to characterise the antibody response raised against HIV-1 gp41
CC	CC	domains. The sequences and methods are useful for inhibiting HIV
CC	CC	infection, for inducing an immune response in an animal and for raising
CC	CC	antibodies.
XX	XX	
SO	SO	Sequence 36 AA.
XX	XX	
XX	XX	Query Match 100.0%; Score 200; DB 22; Length 36;
XX	XX	Best Local Similarity 100.0%; Pred. No. 5.5e-18;
XX	XX	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	QY	1 YTGIIYNLEESQNOOEKNEDELLDKRANLMNMF 36
DB	DB	1 YTGIIYNLEESQNOOEKNEDELLDKRANLMNMF 36
XX	XX	
XX	XX	RESULT 5
XX	XX	AAAG67041
XX	XX	ID AAG67041 standard; Peptide: 36 AA.
XX	XX	AAAG67041;
XX	XX	03-JAN-2002 (first entry)
XX	XX	HIV-1 gp41 peptide DP178 homologue DP-185.
XX	XX	Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX	XX	

KW	virucide heptad repeat region; transmembrane protein; gp41; HRI; HR2;
KX	infection; DP185
XX	
OS	Human immunodeficiency virus type 1.
XX	
PN	MO200164013-A2.
XX	
PD	07-SEP-2001.
XX	
PF	07-FEB-2001; 2001WO-US03988.
XX	
PR	29-FEB-2000; 2000US-0515965.
XX	
PA	(TRIM-) TRIMERIS INC.
XX	
PI	Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX	
DR	WPI; 2001-514829/56.
XX	
PT	Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX	
PT	fusion, useful for treating HIV and Respiratory Syncytial Virus
XX	
PT	infection -
XX	
PS	Example; Fig 1; 587pp; English.
XX	
CC	The invention relates to isolated analogues of the heptad repeat region
CC	peptides DP178 and DP107. DP178 and DP107 correspond to amino acids
CC	638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region
CC	HRI) respectively, of HIV-1/IIAI transmembrane protein gp41. The HRI
CC	and HR2 regions of proteins interact non-covalently with each other
CC	and/or with peptides derived from them. This interaction is required for
CC	normal infectivity of viruses such as RSV and HIV. The heptad
CC	repeat region peptide analogues may be used to inhibit respiratory
CC	syncytial virus (RSV) infection in a cell. They may also be used to
CC	inhibit HIV infection. The present sequence is a peptide provided in
CC	the specification.
XX	
SQ	Sequence 36 AA:
XX	
XX	Query Match 100.0%; Score 200; DB 22; Length 36;
XX	Best Local Similarity 100.0%; Pred. No. 5.5e-18;
XX	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 YTGIIYNLLEESQNOEKNEQFLFLDKKMANLMMNF 36
XX	
DB	1 YTGIIYNLLEESQNOEKNEQFLFLDKKMANLMMNF 36
XX	
XX	RESULT 6
ID	ABB01246
XX	ABB01246 standard; Peptide; 36 AA.
AC	ABB01246;
XX	
DT	03-JAN-2002 (first entry)
XX	
DE	Viral DP178/107-like region peptide T1407.
XX	
XX	Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW	virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;
RW	infection.
XX	
OS	Virididae.
XX	
XX	
FH	Key
FT	1 Location/Qualifiers
FT	Modified-site
FT	/note= "N-terminal is substituted by Ac"
FT	36
FT	Modified-site
FT	/note= "C-terminal amide"
XX	
XX	MO200164013-A2.
XX	
XX	07-SEP-2001.

XX Example; Fig 1; 182pp; English.  
 PS  
 CC This peptide is isolated from HIV-1 isolate RF, and is a homologue of  
 CC the peptide DP-178. DP-178 corresponds to amino acids 638 to 673 of the  
 CC HIV-1 isolate LAI transmembrane protein gp41. It forms a putative alpha  
 CC helix at the C-terminal end of the gp41 ectodomain, and complexes with  
 CC DP-107 (corresponds to amino acids 558-595) which contains a leucine  
 CC zipper motif. The peptides complex via non-covalent protein-protein  
 CC interactions, and possess anti-viral activity. The peptide inhibits  
 CC transmission to uninfected cells, and can also be used as type and/or  
 CC subtype specific diagnostic tools.  
 SQ Sequence 36 AA:

Query Match 100.0%; Score 200; DB 16; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTGIIYNLLEESQNOEKNEQELLELDKKNANLMMNF 36  
 1 YTGIIYNLLEESQNOEKNEQELLELDKKNANLMMNF 36

RESULT 2  
 AAR98400  
 ID AAR98400 standard; peptide; 36 AA.  
 AC AAR98400;  
 DT 17-FEB-1997 (first entry)  
 DE Peptide corresponding to residues 638-673 of HIV-1(RF) gp41.  
 KM Antifusogenic activity; antiviral capability; coiled-coil peptide;  
 KM ALMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;  
 KM Influenza virus; hepatitis B virus.  
 OS Human immunodeficiency virus type 1.  
 XX WO9619495-A1.  
 PN 27-JUN-1996.  
 PD 20-DEC-1995; 95WO-US16733.  
 PF 06-JUN-1995; 95US-0470896.  
 PR 20-DEC-1994; 94US-0360107.  
 PA (TRIM-) TRIMERIS INC.  
 PA (UIDU-) UNIT DUKE.  
 PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
 PI Matthews TJ, Petteway SR, Wild CT;  
 DR WPI: 1996-309517/31.  
 DT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALMOT15, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX  
 PS Disclosure; Fig 1; 471pp; English.  
 CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALMOT15,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
 CC hepatitis B virus, to a cell.  
 XX  
 SQ Sequence 36 AA:

Query Match 100.0%; Score 200; DB 17; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOEKNEQELLELDKKNANLMMNF 36  
 DB 1 YTGIIYNLLEESQNOEKNEQELLELDKKNANLMMNF 36

RESULT 3  
 AAW17013  
 ID AAW17013 standard; peptide; 36 AA.  
 AC AAW17013;  
 DT 01-JUL-1997 (first entry)  
 DE DP-178-like peptide useful for treatment of HIV infection.  
 KM HIV; SIV; human; simian immunodeficiency virus; glycoprotein 41;  
 KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
 KM replication; transmission.  
 OS Human immunodeficiency virus type 1 RF isolate.  
 XX WO9640191-A1.  
 PN 19-DEC-1996.  
 PD 06-JUN-1996; 96WO-US09499.  
 PF 07-JUN-1995; 95US-0481957.  
 PR (TRIM-) TRIMERIS INC.  
 PA Johnson RM, Lambert DM;  
 PI WPI: 1997-099886/09.  
 DR  
 DT Compens. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.  
 XX  
 PS Disclosure; Figure 1; 84pp; English.

CC AAW17012-W17016 are DP-178 homologues that are useful in the  
 CC treatment of HIV infection. DP-178 is a peptide corresponding to  
 CC residues 638-673 of HIV type 1 glycoprotein 41 (gp41) transmembrane  
 CC protein. DP-178 and its derivatives/homologues are used in combination  
 CC with a therapeutic agent, e.g. a reverse transcriptase, viral protease,  
 CC cytokine, glycosylation or viral mRNA processing inhibitor or a  
 CC nucleoside inhibitor. The peptides work by inhibiting viral replication  
 CC or inhibiting transmission. They may also be used in vaccines for  
 CC protecting against HIV infection.  
 XX  
 SQ Sequence 36 AA:

Query Match 100.0%; Score 200; DB 18; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOEKNEQELLELDKKNANLMMNF 36  
 DB 1 YTGIIYNLLEESQNOEKNEQELLELDKKNANLMMNF 36

RESULT 4  
 AAU70181  
 ID AAU70181 standard; Peptide; 36 AA.  
 AC AAU70181;  
 DT 14-FEB-2002 (first entry)

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533a-4  
Perfect score: 200  
Sequence: 1 YTGIIYMLESONQOEKNEQELLEDKWMLMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues  
1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_101002:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200	100.0	36	16	AA67699
2	200	100.0	36	17	AA898400
3	200	100.0	36	18	AAW17013
4	200	100.0	36	22	AAU70181
5	200	100.0	36	22	AA67041
6	200	100.0	36	22	ABBO1246
7	200	100.0	36	22	ABBO1247
8	200	100.0	36	22	ABBO2831
9	200	100.0	36	22	ABBO2832
10	200	100.0	36	22	AAU13792

11	200	100.0	36	22	AAU13793
12	200	100.0	36	22	AAU14013
13	200	100.0	36	22	AA892246
14	200	100.0	36	22	AA878239
15	200	100.0	36	22	AA878240
16	200	100.0	36	22	AA854787
17	200	100.0	269	19	AAV22837
18	200	100.0	269	23	ABG68308
19	200	100.0	861	19	AAW43074
20	200	100.0	865	8	AAU70175
21	200	100.0	866	9	AA80966
22	185	92.5	233	19	AAV22854
23	185	92.5	233	23	ABG68325
24	185	92.5	267	19	AAV22842
25	185	92.5	267	23	ABG68313
26	185	92.5	268	15	AAV22845
27	185	92.5	268	23	ABG68315
28	185	92.5	284	10	AA894507
29	185	92.5	883	22	AA882761
30	184	92.0	36	16	AA867698
31	184	92.0	36	17	AA898399
32	184	92.0	36	18	AAW17012
33	184	92.0	36	22	AA67040
34	184	92.0	36	22	AAU14012
35	183	91.5	269	19	AAV22847
36	183	91.5	269	23	ABG68318
37	182	91.0	46	19	AAV22914
38	182	91.0	46	23	ABG68385
39	182	91.0	268	19	AAV22817
40	182	91.0	268	23	ABG68288
41	182	91.0	269	19	AAV22852
42	182	91.0	269	23	ABG68323
43	182	91.0	270	19	AAV22871
44	182	91.0	270	23	ABG68342
45	182	91.0	855	12	AA814905

## ALIGNMENTS

RESULT 1  
AA867699  
ID AA867699 standard; peptide: 36 AA.  
XX  
AC AA867699;  
XX  
24-AUG-1995 (first entry)  
DT  
XX  
DE DP-178 homologue derived from HIV-1 RF has antiviral activity.  
XX  
KW antiviral activity: DP-178; DP-107; diagnostic; HIV-11A1;  
KW human immunodeficiency virus; transmembrane protein; gp141;  
KW alpha helix; leucine zipper; DP-185.  
XX  
OS Human immunodeficiency virus (RF isolate).  
XX  
PN W09428920-A.  
XX  
PD 22-DEC-1994.  
XX  
PE 07-JUN-1994; 94W0-US05739.  
XX  
PR 07-JUN-1993; 93US-0073028.  
PA (UYDU-) UNIV DUKE.  
PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
PI Peteway SR, Wild CT;  
XX WPI: 1995-036105/05.  
XX Computer search generated synthetic peptides - are inhibitors of  
PT HIV transmission

Job time : 16.759 secs

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STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-854-816-12

Query Match          93.4%; Score 185; DB 10; Length 269;
Best Local Similarity 91.7%; Pred. No. 9.6e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNFTYTLLESQNOQEKNEQELLEDKWSLWNMF 36
Db 169 YTSLYTLLESQNOQEKNEQELLEDKWSLWNMF 204

RESULT 15
US-10-032-162-15
Sequence 15, Application US/10032162
Publication No. US20030052839A1
GENERAL INFORMATION:
APPLICANT: BINLEY, JAMES M
APPLICANT: SCHUELTE, NORBERT
APPLICANT: OLSON, WILLIAM C
APPLICANT: PAUL, MADDOX J
APPLICANT: JOHN, MOORE P
TITLE OF INVENTION: STABILIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF
FILE REFERENCE: 2048/59331a2
CURRENT APPLICATION NUMBER: US/10/032,162
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/602,864
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 579
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-10-032-162-15

Query Match          93.4%; Score 185; DB 9; Length 579;
Best Local Similarity 91.7%; Pred. No. 2.2e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNFTYTLLESQNOQEKNEQELLEDKWSLWNMF 36
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LENGTH: 46  
TYPE: PRF  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-45

Query Match 93.4%; Score 185; DB 10; Length 46;  
Best Local Similarity 91.7%; Pred. No. 9.6e-15;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNNTYTLLESQNOEKNEQELLEDKWSLWNMF 36  
DB 11 YTSEIYTLLESQNOEKNEQELLEDKWSLWNMF 46

RESULT 12  
US-09-854-816-8  
Sequence 8, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Phd., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-854-816-8

Query Match 93.4%; Score 185; DB 10; Length 268;

Best Local Similarity 91.7%; Pred. No. 9.6e-15;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNNTYTLLESQNOEKNEQELLEDKWSLWNMF 36

DB 168 YTSEIYTLLESQNOEKNEQELLEDKWSLWNMF 203

RESULT 13  
US-09-854-816-9

Sequence 9, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Phd., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-854-816-9

Query Match 93.4%; Score 185; DB 10; Length 268;

Best Local Similarity 91.7%; Pred. No. 9.6e-15;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNNTYTLLESQNOEKNEQELLEDKWSLWNMF 36

DB 168 YTSEIYTLLESQNOEKNEQELLEDKWSLWNMF 203

RESULT 14  
US-09-854-816-12  
Sequence 12, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

```

; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: HIV-JRCSE
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-854-816-7

Query Match          94.4%; Score 187; DB 10; Length 268;
Best Local Similarity 94.4%; Pred. No. 5.5e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQNOOEKNEQELLELDKWSLWNMF 36
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Db 168 YNTNTYTLLEESQIOEKNKEQELLELDKWSLWNMF 203

RESULT 9
US-09-854-816-28
; Sequence 28, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Pheasant
; Melissa A. Starovastnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:

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; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-854-816-28

Query Match          94.4%; Score 187; DB 10; Length 269;
Best Local Similarity 94.4%; Pred. No. 5.5e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQNOOEKNEQELLELDKWSLWNMF 36
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Db 169 YTSLYTLLEESQNOOEKNEQELLELDKWSLWNMF 204

RESULT 10
US-09-779-451-47
; Sequence 47, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 36
; TYPE: PPT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-47

Query Match          93.4%; Score 185; DB 10; Length 36;
Best Local Similarity 91.7%; Pred. No. 1.2e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 1 YTSYITLLEESQNOOEKNEQELLELDKWSLWNMF 36

RESULT 11
US-09-779-451-45
; Sequence 45, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-854-816-26

Query Match          96.0%; Score 190; DB 10; Length 268;
Best Local Similarity 94.4%; Pred. No. 2,4e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 168 YTNLYITLLEESONOQEKNEQELLELDKWSLWNNF 203

RESULT 5
US-09-891-609-4
; Sequence 4, Application US/09891609
; Patent No. US20020127238A1
; GENERAL INFORMATION:
; APPLICANT: Stamatacos, Leonidas
; TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
; FILE REFERENCE: 2570-1-002N
; CURRENT APPLICATION NUMBER: US/09/891,609
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,608
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-891-609-4

Query Match          96.0%; Score 190; DB 10; Length 619;
Best Local Similarity 94.4%; Pred. No. 5,8e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YNTTYITLLEESONOQEKNEQELLELDKWSLWNNF 36
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Db 574 YTNLYITLLEESONOQEKNEQELLELDKWSLWNNF 609

RESULT 6
US-09-891-609-2
; Sequence 2, Application US/09891609
; Patent No. US20020127238A1
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; GENERAL INFORMATION:
; APPLICANT: Stamatacos, Leonidas
; TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
; FILE REFERENCE: 2570-1-002N
; CURRENT APPLICATION NUMBER: US/09/891,609
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,608
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-891-609-2

Query Match          96.0%; Score 190; DB 10; Length 646;
Best Local Similarity 94.4%; Pred. No. 6,1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 601 YTNLYITLLEESONOQEKNEQELLELDKWSLWNNF 636

RESULT 7
US-09-476-242-2
; Sequence 2, Application US/09476242
; Patent No. US20020146683A1
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: HARTOG, Karin
; APPLICANT: MARTIN, Eric
; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
; FILE REFERENCE: 1605,002
; CURRENT APPLICATION NUMBER: US/09/476,242
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-476-242-2

Query Match          96.0%; Score 190; DB 10; Length 847;
Best Local Similarity 94.4%; Pred. No. 8,1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 8
US-09-854-816-7
; Sequence 7, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Pheasant
; Melissa A. Starovassnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
```



TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-000-321-11

Query Match 100.0%; Score 198; DB 12; Length 145;  
Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 106 YTNITITLLESQNOQEKNEQELLELDKWSLWNMF 141

RESULT 2  
US-09-854-816-30  
Sequence 30, Application US/09854816  
Patent No. US20020151473A1

## GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasanik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids

TYPE: Amino Acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-854-816-30

Query Match 100.0%; Score 198; DB 10; Length 269;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNITITLLESQNOQEKNEQELLELDKWSLWNMF 36  
|||||  
Db 169 YTNITITLLESQNOQEKNEQELLELDKWSLWNMF 204

RESULT 3

US-09-854-816-31  
Sequence 31, Application US/09854816  
Patent No. US20020151473A1

## GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasanik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids

TYPE: Amino Acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-854-816-31

Query Match 100.0%; Score 198; DB 10; Length 269;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNITITLLESQNOQEKNEQELLELDKWSLWNMF 36  
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Db 169 YTNITITLLESQNOQEKNEQELLELDKWSLWNMF 204

RESULT 4  
US-09-854-816-26

Sequence 26, Application US/09854816

Patent No. US20020151473A1

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasanik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Computen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-3  
Perfect score: 198  
Sequence: 1 YTWITLTLEESQNOEKNEQELLEDKWASLNNMF 36

Scoring table: BLOSUM62  
Gapop 10.0, Capext 0.5

Searched: 362588 seqs, 96450795 residues  
Number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
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  - 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	198	100.0	145 12 US-10-000-321-11	Sequence 11, Appl
2	198	100.0	269 10 US-09-854-816-30	Sequence 30, Appl
3	198	100.0	269 10 US-09-854-816-31	Sequence 31, Appl
4	190	96.0	268 10 US-09-854-816-26	Sequence 26, Appl
5	190	96.0	619 10 US-09-891-609-4	Sequence 4, Appl
6	190	96.0	646 10 US-09-891-609-2	Sequence 2, Appl
7	190	96.0	847 10 US-09-476-242-2	Sequence 2, Appl
8	187	94.4	268 10 US-09-854-816-7	Sequence 7, Appl
9	187	94.4	269 10 US-09-854-816-28	Sequence 28, Appl
10	185	93.4	36 10 US-09-779-451-47	Sequence 47, Appl
11	185	93.4	46 10 US-09-779-451-45	Sequence 45, Appl
12	185	93.4	268 10 US-09-854-816-8	Sequence 8, Appl
13	185	93.4	268 10 US-09-854-816-9	Sequence 9, Appl
14	185	93.4	269 10 US-09-854-816-12	Sequence 12, Appl
15	185	93.4	579 9 US-10-032-162-15	Sequence 15, Appl
16	185	93.4	625 9 US-10-032-162-17	Sequence 17, Appl
17	185	93.4	643 9 US-10-032-162-13	Sequence 13, Appl
18	184	92.9	267 10 US-09-854-816-38	Sequence 38, Appl
19	184	92.9	268 10 US-09-854-816-41	Sequence 41, Appl

20	183	92.4	46 10 US-09-854-816-109	Sequence 109, App
21	183	92.4	269 10 US-09-854-816-6	Sequence 6, Appl
22	181	91.4	268 10 US-09-854-816-13	Sequence 13, Appl
23	181	91.4	269 10 US-09-854-816-42	Sequence 42, Appl
24	180	90.9	233 10 US-09-854-816-50	Sequence 50, Appl
25	179	90.4	268 10 US-09-854-816-39	Sequence 39, Appl
26	178	89.9	267 10 US-09-854-816-11	Sequence 11, Appl
27	178	89.9	269 10 US-09-854-816-33	Sequence 33, Appl
28	177	89.4	269 10 US-09-854-816-20	Sequence 20, Appl
29	177	89.4	269 10 US-09-854-816-37	Sequence 37, Appl
30	177	89.4	269 10 US-09-854-816-43	Sequence 43, Appl
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34	176	88.9	36 9 US-09-493-346-1	Sequence 10, Appl
35	176	88.9	36 10 US-09-796-202-10	Sequence 5, Appl
36	176	88.9	36 10 US-09-779-451-5	Sequence 1, Appl
37	176	88.9	36 10 US-09-834-628-1	Sequence 1, Appl
38	176	88.9	36 10 US-09-854-816-1	Sequence 108, App
39	176	88.9	36 10 US-09-854-816-108	Sequence 176, App
40	176	88.9	37 9 US-09-848-616-176	Sequence 41, Appl
41	176	88.9	46 10 US-09-779-451-41	Sequence 4, Appl
42	176	88.9	56 10 US-09-779-451-4	Sequence 2, Appl
43	176	88.9	177 9 US-10-040-3498-2	Sequence 84, Appl
44	176	88.9	221 9 US-10-059-271-84	Sequence 81, Appl
45	176	88.9	232 9 US-10-059-271-81	

ALIGNMENTS

RESULT 1  
US-10-000-321-11  
; Sequence 11, Application US/10000321  
; Patent No. US20020123039A1

GENERAL INFORMATION:  
APPLICANT: BRUST, Stefan  
KNAPP, Stefan  
GERKEN, Manfred  
GUERTLER, Lutz

TITLE OF INVENTION: Peptides derived from a retrovirus of the HIV group, and their use

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.

COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/000.321  
FILING DATE: 04-Dec-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/131,551  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: SANDERCOCK, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 58315/106/BEAK

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids

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OY 1 YNTTYTLEESONOEKNEOEELLELDKWSLWNF 36  
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Db 169 YNTTYTLEESONOEKNEOEELLELDKWSLWNF 204  
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Job time : 11.1928 secs



Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNMF 36  
DB 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNMF 36

RESULT 10  
US-09-315-304B-1357  
Sequence 1357, Application US/09315304B  
Patent No. 6348368  
GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.  
APPLICANT: Anwer, M. D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1357  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1357

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNMF 36  
DB 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNMF 36

RESULT 11  
US-08-255-208A-3  
Sequence 3, Application US/08255208A  
Patent No. 6440656  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway Jr., Stephen R.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/255,208A

FILING DATE: 07-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNTE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-255-208A-3

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNMF 36  
DB 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNMF 36

RESULT 12  
US-09-570-921-16  
Sequence 16, Application US/09570921  
Patent No. 6453265  
GENERAL INFORMATION:  
APPLICANT: SERRES, PIERRE-FRANCOIS  
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE  
FILE REFERENCE: 106213  
CURRENT APPLICATION NUMBER: US/09/570,921  
CURRENT FILING DATE: 2000-05-15  
PRIOR APPLICATION NUMBER: PCT/FR98/02447  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: FR/97/14387  
PRIOR FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 144  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Human  
US-09-570-921-16

Query Match 100.0%; Score 198; DB 4; Length 138;  
Best Local Similarity 100.0%; Pred. No. 5.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNMF 36  
DB 99 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNMF 134

RESULT 13  
US-08-394-021-11  
Sequence 11, Application US/08394021  
Patent No. 5830634  
GENERAL INFORMATION:  
APPLICANT: BRUST, Stefan  
APPLICANT: KNAPP, Stefan  
APPLICANT: GERKEN, Manfred  
APPLICANT: GUERTLER, Lutz  
TITLE OF INVENTION: Peptides derived from a retrovirus of  
TITLE OF INVENTION: the HIV group, and their use  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner

QY	1 YTNFTIYLLEESQNQEKNQELLEDKWSLNMWF	36
Db	1 YTNTIYTLLLESQNQEKNQELLEDKWSLNMWF	36

RESULT 7  
US-08-485-264A-3  
; Sequence 3, Application US/08485264A

GENERAL INFORMATION:  
 APPLICANT: Bolognesi, Danl P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Peteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
 TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
 NUMBER OF SPOUNCES: 232  
 CORRESPONDENCE ADDRESS:

Query Match	100.0%	Score 198;	DB 4;	length 36;
Best Local Similarity	100.0%;	Pred. No. 1.3e-17;		
Matches 36; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 YTNITYTLLSESQNQEKNEQELLELDKWSALMNF 36  
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Db 1 YTNITYTLLSESQNQEKNEQELLELDKWSALMNF 36

RESULT: 8  
US-09-082-279B-1357  
; Sequence 1357, Application US/0908279B  
; Patent No. 6258752  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anver, Mohamed  
; APPLICANT: Lambert, Dennis

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? TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
? TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
? FILE REFERENCE: 7872-043
? CURRENT APPLICATION NUMBER: US/09/082,279B
? CURRENT FILING DATE: 1998-05-20
? NUMBER OF SEQ. ID NOS: 1515
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 1357
? LENGTH: 36
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Core polypeptide
US-09-082-279B-1357

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Query Match	100.0%;	Score 198;	DB 4;	Length 36;
Best Local Similarity	100.0%;	Pred. No. 1.3e-17;		
Matches 36;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db       1 YTNTIYTLLLESQNQOEKNEQLIELDLKWSASLWNWF 36
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RESULT 9  
US-08-474-349A-3  
; Sequence 3, Application US/08474349A  
; Patent No. 6333395  
SEQUENCE INFORMATION

1 GENERAL INFORMATION:  
2 APPLICANT: Bolognesi, Dani P.  
3 APPLICANT: Matthews, Thomas J.  
4 APPLICANT: Wild, Carl T.  
5 APPLICANT: Barney, Shawn O.  
6 APPLICANT: Lambert, Dennis M.  
7 APPLICANT: Petteway, Stephen R.  
8 APPLICANT: Langlois, Alphonse J.  
9 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
10 TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
11 NUMBER OF SEQUENCES: 517  
12 CORRESPONDENCE ADDRESS:  
13

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-3

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLESQNOOEKNEQELLEIDKWSLWNF 36  
DB 1 YNTYITLLESQNOOEKNEQELLEIDKWSLWNF 36

RESULT 5  
US-08-485-551A-3  
Sequence 3, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-3

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLESQNOOEKNEQELLEIDKWSLWNF 36  
DB 1 YNTYITLLESQNOOEKNEQELLEIDKWSLWNF 36

RESULT 6  
US-08-471-913A-3  
Sequence 3, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-3

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWMMF 36  
Db 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWMMF 36

## RESULT 2

US-08-484-223B-3

; Sequence 3, Application US/08484223B  
; Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pellewey, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie &amp; Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNTE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-484-223B-3

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWMMF 36  
Db 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWMMF 36

## RESULT 3

US-08-919-597-3

; Sequence 3, Application US/08919597  
; Patent No. 6054265

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pellewey, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie &amp; Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,597

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/470,896

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-020

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNTE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-919-597-3

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWMMF 36

## RESULT 4

US-08-475-668A-3

; Sequence 3, Application US/08475668A  
; Patent No. 6060065

GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pellewey, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie &amp; Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds

(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533a-3

Perfect score: 198  
Sequence: 1 YNTTYTTLSESONOQEKNEQLLEIDKWSLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTS.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	36	3	US-08-486-099-3
2	198	100.0	36	3	US-08-484-223B-3
3	198	100.0	36	3	US-08-919-597-3
4	198	100.0	36	3	US-08-475-668A-3
5	198	100.0	36	3	US-08-485-551A-3
6	198	100.0	36	3	US-08-471-913A-3
7	198	100.0	36	4	US-08-485-264A-3
8	198	100.0	36	4	US-09-082-279B-1357
9	198	100.0	36	4	US-08-474-349A-3
10	198	100.0	36	4	US-09-315-304B-1357
11	198	100.0	36	4	US-08-255-208A-3
12	198	100.0	138	4	US-09-570-921-16
13	198	100.0	145	2	US-08-394-021-11
14	198	100.0	145	4	US-09-131-551-11
15	198	100.0	269	4	US-08-965-056-30
16	198	100.0	269	4	US-08-965-056-31
17	198	100.0	610	4	US-09-257-490-12
18	198	100.0	855	4	US-07-956-483-15
19	198	100.0	887	4	US-08-472-240A-6
20	193	97.5	36	1	US-08-073-028-3
21	193	97.5	36	3	US-08-360-107A-3
22	193	97.5	36	4	US-08-554-616-3
23	190	96.0	138	4	US-09-570-921-8
24	190	96.0	268	4	US-08-965-056-26
25	187	94.4	36	4	US-09-082-279B-1051
26	187	94.4	36	4	US-09-315-304B-1051
27	187	94.4	138	4	US-09-570-921-10

28	187	94.4	138	4	US-09-570-921-19	Sequence 19, Appl
29	187	94.4	268	4	US-08-965-056-7	Sequence 7, Appl
30	187	94.4	269	4	US-08-965-056-28	Sequence 28, Appl
31	185	93.4	36	4	US-09-082-279B-856	Sequence 856, App
32	185	93.4	36	4	US-09-315-304B-856	Sequence 856, App
33	185	93.4	138	4	US-09-570-921-12	Sequence 12, Appl
34	185	93.4	268	4	US-08-965-056-8	Sequence 8, Appl
35	185	93.4	268	4	US-08-965-056-9	Sequence 9, Appl
36	185	93.4	269	4	US-08-965-056-12	Sequence 12, Appl
37	185	93.4	855	4	US-07-956-483-14	Sequence 14, Appl
38	185	93.4	887	4	US-08-472-240A-5	Sequence 5, Appl
39	184	92.9	267	4	US-08-965-056-38	Sequence 38, Appl
40	184	92.9	268	4	US-08-965-056-41	Sequence 41, Appl
41	183	92.4	46	4	US-08-965-056-109	Sequence 109, App
42	183	92.4	269	4	US-08-965-056-6	Sequence 6, Appl
43	181	91.4	36	4	US-09-082-279B-642	Sequence 642, App
44	181	91.4	36	4	US-09-315-304B-642	Sequence 642, App
45	181	91.4	268	4	US-08-965-056-13	Sequence 13, App

#### ALIGNMENTS

RESULT 1  
US-08-486-099-3  
; Sequence 3, Application US/08486099  
; Patent No. 6013263  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Paul P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Pellew, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Penne & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,099  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-031  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-486-099-3  
Query Match 100.0%, Score 198, DB 3, Length 36;

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DR Pfam: PF00517; GP41. 1.  
 KW Transmembrane.  
 SO SEQUENCE 866 AA; 98423 MW; E42C8EA2509B056 CRC64;

Query Match  
 Best Local Similarity 94.4%; Score 189; DB 15; Length 866;  
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTTYITLLEESONOEKNEDELLDKWASLWNMF 36  
 DB 648 YTNLYITLLEESONOEKNEDELLDKWALWNMF 683

RESULT 10  
 O9YXN4 PRELIMINARY; PRT; 122 AA.

AC O9YXN4  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein immunodominant region (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RJ97BRP116;  
 RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savcira A.,  
 RA Costa L.J., Teles J.G., Brindeiro R., Schable C., Pieniazek D.,  
 RA Rayfield M.;  
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";  
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF034069; AAC79321.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 122  
 SQ SEQUENCE 122 AA; 14811 MW; F154B211B9D456D5 CRC64;

Query Match  
 Best Local Similarity 94.9%; Score 188; DB 15; Length 122;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTTYITLLEESONOEKNEDELLDKWASLWNMF 36  
 DB 78 YTSTYITLLEAONOEKNEDELLDKWASLWNMF 113

RESULT 11  
 O9EAA2 PRELIMINARY; PRT; 122 AA.

AC O9EAA2  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BX161;  
 RA MEDLINE-20134570; PubMed-10669328;  
 RA Weidie P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,  
 RA Ollivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;  
 RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B  
 RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic  
 RT diversity in the United States.";  
 RL J. Infect. Dis. 181:470-475(2000).  
 DR EMBL: AF190950; AAG02312.1; -;

DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00517; GP41. 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 122  
 SO SEQUENCE 122 AA; 14751 MW; 302E5D7E45ED007D CRC64;

Query Match  
 Best Local Similarity 91.7%; Score 188; DB 15; Length 122;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTTYITLLEESONOEKNEDELLDKWASLWNMF 36  
 DB 78 YTNVYITLLEESONOEKNEDELLDKWASLWNMF 113

RESULT 12  
 O11944 PRELIMINARY; PRT; 849 AA.

AC O11944  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein gp160.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GB8.C1;  
 RC MEDLINE-96100812; PubMed-7483788;  
 RA Vella C., Smith M.H., Farfar G.H., Jones D.H., Daniels R.S.;  
 RT "A molecular and serologic study of the envelope gene of the British  
 RT isolate: HIV-IGB8.";  
 RL Vaccine 13:735-741(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-GB8.C1;  
 RX MEDLINE-98035047; PubMed-9367752;  
 RA Douglas N.W., Munro G.H., Daniels R.S.;  
 RT "HIV/SIV glycoproteins: Structure-Function Relationships.";  
 RL J. Mol. Biol. 273:122-149(1997).  
 DR EMBL: Y13716; CAA4044.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 849 AA; 96612 MW; 3026E6908267F63 CRC64;

Query Match  
 Best Local Similarity 94.9%; Score 188; DB 15; Length 849;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTTYITLLEESONOEKNEDELLDKWASLWNMF 36  
 DB 631 YNTTYITLLEESONOEKNEDELLDKWALWNMF 666

RESULT 13  
 O9YXW9 PRELIMINARY; PRT; 122 AA.

AC O9YXW9  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein immunodominant region (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]

DR Pfam: PF00517, GP41, 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 860 AA; 97739 MW; 1FEB24AAFD7F4216 CRC64;

Query Match  
 Best Local Similarity 94.4%; Score 190; DB 15; Length 860;  
 Pred. No. 1.2e-14;  
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTTYTLLTESQNOEKNEQELLELDKWSLWMP 36  
 DB 642 YTNLIYTLIESQNOEKNEQELLELDKWSLWMP 677

## RESULT 6

OQYP50 PRELIMINARY; PRT; 860 AA.

AC OQYP50:  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope polyprotein.  
 GN ENV.

OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;

RP SEQUENCE FROM N.A.  
 RA Fang G., Weiser B., Chappey C., Vlasosky A., Townsend L., Wang Q.,  
 RA Burger H.;  
 RT "Complete Plasma HIV-1 Sequence: Spl-Promoter Deletion Can Lead to  
 RT Non-Progressive Infection.";  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U69585; AAD10883.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.

DR Pfam: PF00517; GP41; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 860 AA; 97662 MW; A5AC60C558B990BC CRC64;

Query Match  
 Best Local Similarity 94.4%; Score 190; DB 15; Length 860;  
 Pred. No. 1.2e-14;  
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTTYTLLTESQNOEKNEQELLELDKWSLWMP 36  
 DB 642 YTNLIYTLIESQNOEKNEQELLELDKWSLWMP 677

## RESULT 7

OQWJ04 PRELIMINARY; PRT; 863 AA.

AC OQWJ04:  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope polyprotein.  
 GN ENV.

OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;

RP SEQUENCE FROM N.A.  
 RA Fang G., Weiser B., Chappey C., Vlasosky A., Townsend L., Wang Q.,  
 RA Burger H.;  
 RT "Complete Plasma HIV-1 Sequence: Spl-Promoter Deletion Can Lead to  
 RT Non-Progressive Infection.";  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U69592; AAD10939.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 863 AA; 98269 MW; BE12C858E9CEAD11 CRC64;

Query Match  
 Best Local Similarity 94.4%; Score 190; DB 15; Length 863;  
 Pred. No. 1.2e-14;  
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTTYTLLTESQNOEKNEQELLELDKWSLWMP 36  
 DB 645 YTNLIYTLIESQNOEKNEQELLELDKWSLWMP 680

## RESULT 8

OQYP48 PRELIMINARY; PRT; 864 AA.

AC OQYP48:  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope polyprotein.  
 GN ENV.

OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;

RP SEQUENCE FROM N.A.  
 RA Fang G., Weiser B., Chappey C., Vlasosky A., Townsend L., Wang Q.,  
 RA Burger H.;  
 RT "Complete Plasma HIV-1 Sequence: Spl-Promoter Deletion Can Lead to  
 RT Non-Progressive Infection.";  
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U69586; AAD10891.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 864 AA; 98167 MW; 2A0E7AB2A89662F2 CRC64;

Query Match  
 Best Local Similarity 94.4%; Score 190; DB 15; Length 864;  
 Pred. No. 1.2e-14;  
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTTYTLLTESQNOEKNEQELLELDKWSLWMP 36  
 DB 646 YTNLIYTLIESQNOEKNEQELLELDKWSLWMP 681

## RESULT 9

OQELR5 PRELIMINARY; PRT; 866 AA.

AC OQELR5:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Envelope protein.  
 GN ENV.

OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=20442410; PubMed=10984542;  
 RA Cleghorn F.R., Jack N., Carr J.K., Edwards J., Mahabir B., Sill A.,  
 RA McDaniel C.B., Connolly S.M., Goodman D., Bennetts R.O., O'Brien T.R.,  
 RA Weinhold K.J., Bartholomew C., Blattner W.A., Greenberg M.L.;  
 RT "A distinctive clade B HIV type 1 is heterosexually transmitted in  
 RT Trinidad and Tobago.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10532-10537 (2000).

DR EMBL; AF277073; AAC22516.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.

Query Match	Best Local Similarity	Matches	Score	DB	Length
Best Local Similarity	97.0%	97.0%	Score 193;	DB 15;	Length 849;
Matches	34;	Conservative	2;	Mismatches	0;
Indels	0;	Gaps	0;		
<p>RT A molecular and serologic study of the envelope gene of the British isolate: HIV-1 GB8.";</p> <p>RL Vaccine 13:735-741(1995).</p> <p>DR InterPro: IPR000328; Env_Gp41.</p> <p>DR InterPro: IPR000777; Gp120.</p> <p>DR Pfam: PF00516; Gp120; 1.</p> <p>DR Pfam: PF00517; Gp41; 1.</p> <p>KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.</p> <p>SO SEQUENCE 849 AA; 96704 MW; 78F1C47ACA79F3EE CRC64;</p>					
<p>Query Match</p>					
Best Local Similarity	97.4%	97.2%	Score 192;	DB 15;	Length 859;
Matches	35;	Conservative	0;	Mismatches	1;
Indels	0;	Gaps	0;		
<p>OY 1 YNTNTYTLLESQNOEKNEQELLEDKWMASLMNMF 36</p> <p>DB 641 YTNLTLYTLLESQNOEKNEQELLEDKWMASLMNMF 676</p>					
<p>RESULT 5</p>					
ID	Q9YP43	PRELIMINARY;	PRT:	860	AA.
AC	Q9YP43;				
DT	01-MAY-1999 (TREMBlrel. 10, Created)				
DT	01-MAY-1999 (TREMBlrel. 10, Last sequence update)				
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)				
DE	Envelope polyprotein.				
GN	ENV.				
OS	Human immunodeficiency virus type 1.				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11676;				
RA	SEQUENCE FROM N.A.				
RA	Fang G., Weiser B., Chappey C., Vlasosky A., Townsend L., Wang Q.,				
RT	Burger H.;				
RT	"Complete Plasma HIV-1 Sequence: Spl-Promoter Deletion Can Lead to				
RT	Non-Progressive Infection.";				
RL	Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.				
DR	EMBL, 069588; AAD10907.1; "				
DR	InterPro: IPR000328; Env_Gp41.				
DR	InterPro: IPR000777; Gp120.				
DR	Pfam: PF00516; Gp120; 1.				

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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds

(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-3

Perfect score: 198  
Sequence: 1 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	853	15	080161 human immun
2	193	97.5	849	15	091BN3 human immun
3	193	97.5	849	15	09PXE5 human immun
4	192	97.0	859	15	080863 human immun
5	190	96.0	860	15	09YP43 human immun
6	190	96.0	860	15	09YP50 human immun
7	190	96.0	863	15	09WJ04 human immun
8	190	96.0	864	15	09YP48 human immun
9	189	95.5	866	15	09E1R5 human immun
10	188	94.9	122	15	09YXN4 human immun
11	188	94.9	122	15	09EAX2 human immun
12	188	94.9	849	15	011944 human immun
13	187	94.4	122	15	09YXN9 human immun
14	187	94.4	122	15	091J06 human immun
15	187	94.4	848	15	074999 human immun
16	187	94.4	855	15	09E1R7 human immun

17	187	94.4	858	15	080867 human immun
18	187	94.4	858	15	080865 human immun
19	187	94.4	864	15	09E610 human immun
20	186	93.9	122	15	09EAX7 human immun
21	186	93.9	122	15	09EAX2 human immun
22	186	93.9	122	15	091JN5 human immun
23	186	93.9	852	15	092761 human immun
24	186	93.9	852	15	073303 human immun
25	186	93.9	852	15	041546 human immun
26	185	93.4	42	15	069910 human immun
27	185	93.4	122	15	09YX08 human immun
28	185	93.4	123	15	09YXK3 human immun
29	185	93.4	684	15	091K06 human immun
30	185	93.4	841	15	041556 human immun
31	185	93.4	847	15	075760 human immun
32	185	93.4	849	15	077368 human immun
33	185	93.4	849	15	080851 human immun
34	185	93.4	851	15	056110 human immun
35	185	93.4	851	15	080852 human immun
36	185	93.4	855	15	091K00 human immun
37	185	93.4	856	15	09E1S5 human immun
38	185	93.4	856	15	072993 human immun
39	185	93.4	856	15	041539 human immun
40	185	93.4	857	15	073288 human immun
41	185	93.4	857	15	073289 human immun
42	185	93.4	857	15	08U170 human immun
43	185	93.4	859	15	08U185 human immun
44	185	93.4	859	15	08U180 human immun
45	185	93.4	859	15	08U179 human immun

## ALIGNMENTS

RESULT 1  
ID 080161 PRELIMINARY: PRT: 853 AA.  
AC 080161:  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope polypeptide.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92046357; PubMed=1658383;  
RA Cheng-Mayer C., Shioda T., Levy J.A.;  
RT "Host range, replicative, and cytopathic properties of human immunodeficiency virus type 1 are determined by very few amino acid changes in tat and gp120".  
RL J. Virol. 65:6931-6941(1991).  
DR EMBL: L07422; AAA80324.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120: 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 853 AA: 97056 MW: 2181503CFLD14789 CRC64;

Query Match 100.0%; Score 198; DB 15; Length 853;  
Best local similarity 100.0%; Pred. No. 1.3e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNF 36  
DB 635 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNF 670

RESULT 2  
O91BN3



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Query Match	88.9%	Score 176:	DB 1:	Length 861:
NCBI_TaxID=11686;				
[1]				
SEQUENCE FROM N.A.				
Medline=8509333; PubMed=2981635;				
Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.				
"Nucleotide sequence of the AIDS virus, LAV."				
Cell 40:9-17(1985).				
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or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
-----				
EMBL: K02013; AAB59751.1; "				
EMBL: A04321; CAA00352.1; "				
PIR: A03975; VCLJIV.				
HIV: K02013; ENVSBRU.				
InterPro: IPR000328; Env_Gp41.				
InterPro: IPR007772; GP120.				
Pfam: PF00516; GP120.1.				
Pfam: PF00517; Gp41.1.				
AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;				
Signal.				
KW SIGNAL.	1	30		
FT CHAIN	31	516	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT CHAIN	517	861	TRANSMEMBRANE GLYCOPROTEIN.	
FT DISULFID	54	74	BY SIMILARITY.	
FT DISULFID	119	210	BY SIMILARITY.	
FT DISULFID	126	201	BY SIMILARITY.	
FT DISULFID	131	162	BY SIMILARITY.	
FT DISULFID	223	252	BY SIMILARITY.	
FT DISULFID	223	244	BY SIMILARITY.	
FT DISULFID	301	336	BY SIMILARITY.	
FT DISULFID	383	450	BY SIMILARITY.	
FT DISULFID	390	423	BY SIMILARITY.	
FT CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	146	146	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	165	165	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	191	191	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	202	202	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	235	235	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	239	239	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	246	246	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	267	267	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	281	281	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	294	294	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	300	300	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	306	306	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	344	344	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	361	361	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	391	391	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	397	397	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	402	402	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	411	411	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	453	453	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	468	468	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	616	616	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	621	621	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	630	630	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	642	642	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	679	679	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	755	755	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	821	821	N-LINKED (GLCNAC. . .) (POTENTIAL).	
861 AA: 97487 MW: 04DE2B4D4EAFD63A CRC64;				





FT	CARBOHYD	386	386	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	392	392	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	401	401	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	443	443	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	458	458	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	606	606	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	611	611	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	620	620	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	632	632	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	669	669	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
FT	CARBOHYD	745	745	N-LINKED (GLCNAC . . . ) (POTENTIAL) .
SO	SEQUENCE	851 AA:	96644 MW;	D16A3C90857785FL CRC64; N-LINKED (GLCNAC . . . ) (POTENTIAL) .
OY	1 YNTNVTTLLESQNOEKNEDELLELDKWSLMMNF	36		
	11:::			
	633 YTSLHSHLESQNOEKNEDELLELDKWSLMMNF	668		
RESULT 10				
ENV_HV10Y	STANDARD:	PRT,	855 AA.	
AC	P20888:			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).			
OC	Viruses; Retrovird viruses; Retroviridae; Lentivirns.			
OX	NCBI_Taxid=11699;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90148544; PubMed=2559749;			
RA	Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;			
RT	"A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";			
RL	AIDS 3:707-715(1989).			
CC	-I- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A HEALTHY GABONESE INDIVIDUAL.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M26727; AAA83397.1; -			
DR	HIV; M26727; ENVSOVI.			
DR	InterPro: IPR000328; Env GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
KW	AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.			
KW	SIGNAL	1	29	
FT	CHAIN	510	509	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	118	210	BY SIMILARITY.
FT	DISULFID	125	201	BY SIMILARITY.
FT	DISULFID	130	162	BY SIMILARITY.
FT	DISULFID	223	252	BY SIMILARITY.
FT	DISULFID	233	244	BY SIMILARITY.
FT	DISULFID	301	335	BY SIMILARITY.
FT	DISULFID	381	442	BY SIMILARITY.

Query Match	Best local Similarity	86.9%	Score 176;	DB 1;	Length 855;		
Matches	31;	Conservative	86.1%;	Pred. No. 9, 2e-14;	Mismatches 2;	Indels 0;	Gaps 0
QY	1	YNTIYTLLEESQNOEKNEQELLELDKASIMNMF	36	11:			
DB	637	YTHLYTLLEESQNOEKNEQELLELDKAGLMSWF	672				
ENV_HV1B1	STANDARD:	PRT:	856 AA.				
ENV_HV1B1	STANDARD:	PRT:	856 AA.				
AC	P03375:						
DT	21-JUL-1986 (Rel. 01, Created)						
DT	21-JUL-1986 (Rel. 01, Last sequence update)						
DT	15-JUL-1999 (Rel. 38, Last annotation update)						
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].						
DE	ENV.						
OS	Human immunodeficiency virus type 1 (BHD isolate) (HIV-1).						
OC	Vituses; Retroid vituses; Retroviridae; Lentivirus.						
OX	NCBI_TaxID=11678;						
RA	SEQUENCE FROM N.A.						
RA	MEDLINE=8511123; PubMed=2578615;						
RA	Ratner L., Hesselting W., Patarca R., Liyak K.J., Starlich B.R.,						
RA	Josephs S.F., Dotan E.R., Rafalski J.A., Whitehorn E.A.,						
RA	Baumeister K., Ivanoff L., Petewey S.R. Jr., Pearson M.L.,						
RA	Lautebacher J.A., Papas T.S., Grayeb Y., Chang N.T., Gallo R.C.,						
RA	Wong-Staal F.;						
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";						
RL	Nature 313:277-284(1985).						
RP	DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.						
RX	Medline=90285159; PubMed=2355006;						
RT	Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,						
RT	Gregory T.J.;						
RT	"Assignment of intrachain disulfide bonds and characterization of						
RT	potential glycosylation sites of the type 1 recombinant human						
RT	immunodeficiency virus envelope glycoprotein (gp120) expressed in						
RT	Chinese hamster ovary cells.";						
RL	J. Biol. Chem. 265:10373-10382(1990).						
SO	SEQUENCE	855 AA;	97476 MW;	9CF82A607AD62DA	CRC64;		



DR	Pfam: PF00517; GP41; 1.
KW	AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KV	Signal.
FT	SIGNAL 1 29
FT	CHAIN 30 519
FT	CHAIN 520 865
FT	DISULFID 53 73
FT	DISULFID 118 218
FT	DISULFID 125 209
FT	DISULFID 130 157
FT	DISULFID 231 260
FT	DISULFID 241 252
FT	DISULFID 309 343
FT	DISULFID 389 452
FT	DISULFID 396 425
FT	CARBOHYD 87 87
FT	CARBOHYD 129 129
FT	CARBOHYD 136 136
FT	CARBOHYD 139 139
FT	CARBOHYD 156 156
FT	CARBOHYD 193 193
FT	CARBOHYD 194 194
FT	CARBOHYD 197 197
FT	CARBOHYD 198 198
FT	CARBOHYD 203 203
FT	CARBOHYD 210 210
FT	CARBOHYD 247 247
FT	CARBOHYD 254 254
FT	CARBOHYD 275 275
FT	CARBOHYD 289 289
FT	CARBOHYD 302 302
FT	CARBOHYD 308 308
FT	CARBOHYD 314 314
FT	CARBOHYD 344 344
FT	CARBOHYD 351 351
FT	CARBOHYD 367 367
FT	CARBOHYD 397 397
FT	CARBOHYD 403 403
FT	CARBOHYD 407 407
FT	CARBOHYD 413 413
FT	CARBOHYD 418 418
FT	CARBOHYD 455 455
FT	CARBOHYD 471 471
FT	CARBOHYD 620 620
FT	CARBOHYD 625 625
FT	CARBOHYD 634 634
FT	CARBOHYD 646 646
FT	CARBOHYD 825 825
SO	SEQUENCE 865 AA; 97809 MW; 2882B8C314ADCAC CRC64;
.	Query Match 89.9%; Score 178; DB 1; Length 865;
	Best Local Similarity 88.9%; Pred. NO. 5.4e-14;
	Matches 32; Conservative 1; Mismatches 3; Indels 0; Gaps 0
QY	1 YTNITYTLLESQNOEQKNEDELLDLKWASLMMNF 36 
Db	647 YTGILYNLEESQNOEQKNEDELLDLKWANLMNMF 682
RESULT 8	
ENV_HVIJ3	STANDARD; PRT; 867 AA.
ID ENV_HVIJ3	
AC PI2489:	
DT 01-OCT-1989 (Rel. 12, Created)	
DT 01-OCT-1989 (Rel. 12, Last sequence update)	
DT 15-JUN-1999 (Rel. 38, Last annotation update)	
DE Envelope polyprotein GP160 precursor [Contents: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].	
GN ENV.	
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).	
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.	
NCBI TaxID=11694;	
NN [1]	



OY 1 YNTTYTLLLESQNOEKNEQELLEDKWSLMMNF 36  
 DB 634 YTSLYTLLLESQNOEKNEQELLEDKWSLMMNF 669

RESULT 5  
 ENV\_HV1SC STANDARD: PRT: 856 AA.

AC P05878:  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11702;

SEQUENCE FROM N.A.  
 MEDLINE=88219542; PubMed=3369091;  
 RA Guigo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Parrelli K., Wong-Staal F., Gallo R.C., Reitz M.S., Jr.,  
 RT Envelope sequences of two new United States HIV-1 isolates.;  
 RL Virology 164:531-536(1988).  
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.

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CC EMBL: M17450; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: B28922; VCLJSC.  
 DR HIV: M17450; ENV5SC.  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR Aids: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 511 856  
 FT SITE 760 760

EXTERIOR MEMBRANE GLYCOPROTEIN.  
 TRANSMEMBRANE GLYCOPROTEIN.  
 IN-FRAME TERMINATION CODON.

FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 206 BY SIMILARITY.  
 FT DISULFID 125 197 BY SIMILARITY.  
 FT DISULFID 130 160 BY SIMILARITY.  
 FT DISULFID 219 247 BY SIMILARITY.  
 FT DISULFID 228 238 BY SIMILARITY.  
 FT DISULFID 296 330 BY SIMILARITY.  
 FT DISULFID 376 439 BY SIMILARITY.  
 FT DISULFID 383 412 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match 93.4%; Score 185; DB 1; Length 856;  
 Best Local Similarity 91.7%; Pred. No. 7.5e-15;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTTYTLLLESQNOEKNEQELLEDKWSLMMNF 36  
 DB 638 YTSLYTLLLESQNOEKNEQELLEDKWSLMMNF 673

RESULT 6  
 ENV\_HV1WL STANDARD: PRT: 856 AA.

AC P31872:  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (WMJ isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=31678;  
 RN [1]

SEQUENCE FROM N.A.  
 MEDLINE=86218077; PubMed=2423250;  
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,  
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.,  
 RT Identification and characterization of conserved and variable  
 RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of  
 RT Aids.;  
 RL Cell 45:637-648(1986).  
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM  
 CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO  
 CC WAS PERINATALLY INFECTED BY HER MOTHER.  
 DR PIR: A24774; VCLJ3W.  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR Aids: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 511 856  
 FT SITE 760 760

EXTERIOR MEMBRANE GLYCOPROTEIN.  
 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 205 BY SIMILARITY.  
 FT DISULFID 125 196 BY SIMILARITY.  
 FT DISULFID 130 152 BY SIMILARITY.  
 FT DISULFID 218 247 BY SIMILARITY.  
 FT DISULFID 228 239 BY SIMILARITY.  
 FT DISULFID 296 330 BY SIMILARITY.  
 FT DISULFID 376 444 BY SIMILARITY.  
 FT DISULFID 383 417 BY SIMILARITY.

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CC EMBL: M38429; AAB03749.1; -

DR HIV: M38429; ENV5JRCSE.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KW signal.

FT SIGNAL 1 32

FT CHAIN 33 503

FT CHAIN 504 848

FT DISULFID 53 73

FT DISULFID 118 203

FT DISULFID 125 194

FT DISULFID 130 154

FT DISULFID 216 245

FT DISULFID 226 237

FT DISULFID 294 328

FT DISULFID 374 437

FT DISULFID 381 410

FT CARBOHYD 87 87

FT CARBOHYD 134 134

FT CARBOHYD 137 137

FT CARBOHYD 153 153

FT CARBOHYD 157 157

FT CARBOHYD 185 185

FT CARBOHYD 195 195

FT CARBOHYD 228 228

FT CARBOHYD 239 239

FT CARBOHYD 260 260

FT CARBOHYD 274 274

FT CARBOHYD 287 287

FT CARBOHYD 293 293

FT CARBOHYD 299 299

FT CARBOHYD 329 329

FT CARBOHYD 336 336

FT CARBOHYD 352 352

FT CARBOHYD 382 382

FT CARBOHYD 388 388

FT CARBOHYD 392 392

FT CARBOHYD 403 403

FT CARBOHYD 440 440

FT CARBOHYD 453 453

FT CARBOHYD 603 603

FT CARBOHYD 608 608

FT CARBOHYD 617 617

FT CARBOHYD 629 629

FT CARBOHYD 808 808

SO SEQUENCE 848 AA; 96475 MW; 2076751227EC3F3 CRC64;

Query Match

Best Local Similarity 94.4%; Score 187; DB 1; Length 848;

Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CC Viruses; Retrovirdae; Lentivirus.

OX NCBI\_TaxID=11690;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90317906; PubMed=2370688;

RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;

RT "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";

RT J. Virol. 64:4016-4020(1990).

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CC EMBL: M38427; AAA5067.1; -

DR HIV: M38427; ENV5SE33.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KW signal.

FT SIGNAL 1 31

FT CHAIN 32 506

FT CHAIN 507 852

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 156

FT DISULFID 219 248

FT DISULFID 228 240

FT DISULFID 297 331

FT DISULFID 377 439

FT DISULFID 384 412

FT CARBOHYD 87 87

FT CARBOHYD 129 129

FT CARBOHYD 136 136

FT CARBOHYD 141 141

FT CARBOHYD 142 142

FT CARBOHYD 155 155

FT CARBOHYD 159 159

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 242 242

FT CARBOHYD 263 263

FT CARBOHYD 277 277

FT CARBOHYD 290 290

FT CARBOHYD 296 296

FT CARBOHYD 332 332

FT CARBOHYD 339 339

FT CARBOHYD 355 355

FT CARBOHYD 385 385

FT CARBOHYD 391 391

FT CARBOHYD 397 397

FT CARBOHYD 401 401

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 607 607

FT CARBOHYD 612 612

FT CARBOHYD 621 621

FT CARBOHYD 633 633

FT CARBOHYD 812 812

SO SEQUENCE 852 AA; 96663 MW; EE7B8F8D23C9910D CRC64;

Query Match

Best Local Similarity 94.4%; Score 187; DB 1; Length 852;

Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

	Query March	100.0%	Score 198:	DB 1	length 855:
	Best Local Similarity	100.0%:	Pred.	No. 2e-16:	
	Matches 36:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
OY	1 YTNITVTLLESQNOOEKNEDELELDKWASIMNPF	36			
db	637 YTNITVTLLESQNOOEKNEDELELDKWASIMNPF	672			

RP SEQUENCE FROM N.A.  
RX MEDLINE=90347835; Pubmed=2384920;  
RA Cheng-Mayer C., Quitoza M., Tung J.W., Dina D., Levy J.;  
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or  
RL macrophage tropism, cytopathogenicity, and CD4 antigen modulation." J. Virol. 64:4390-4398(1990).

DR EMBL: M65024: AAA45072.1; -.  
DR HIV: M38428; ENVSSFI62.  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.

Query Match 96.0%; Score 190; DB 1; Length 847;  
 Best Local Similarity 94.4%; Pred. No. 1.8e-15;  
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 6.07229 Seconds

(Without alignments)  
245.895 Million cell updates/sec

Title: US-09-623-533a-3

Perfect score: 198  
Sequence: 1 YTNNTYTLLEESQNOQEKNEQELLEDKWASIMWVF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	198	100.0	855	1 ENV_HV1A2	P03378 human immun
2	190	96.0	847	1 ENV_HV1S1	P19550 human immun
3	187	94.4	848	1 ENV_HV1JR	P20871 human immun
4	187	94.4	852	1 ENV_HV1S3	P19549 human immun
5	185	93.4	856	1 ENV_HV1SC	P05878 human immun
6	180	90.9	856	1 ENV_HV1W1	P31872 human immun
7	178	89.9	865	1 ENV_HV1RH	P04579 human immun
8	178	89.9	867	1 ENV_HV1J3	P12489 human immun
9	176	88.9	851	1 ENV_HV1B8	P04582 human immun
10	176	88.9	855	1 ENV_HV1OY	P20888 human immun
11	176	88.9	856	1 ENV_HV1B1	P03375 human immun
12	176	88.9	856	1 ENV_HV1H2	P04578 human immun
13	176	88.9	856	1 ENV_HV1H3	P04624 human immun
14	176	88.9	856	1 ENV_HV1LW	O70626 human immun
15	176	88.9	861	1 ENV_HV1BR	P03377 human immun
16	174	87.9	847	1 ENV_HV1W2	P05880 human immun
17	173	87.4	853	1 ENV_HV1MF	P19551 human immun
18	173	87.4	856	1 ENV_HV1NM	P05877 human immun
19	172	86.9	853	1 ENV_HV1Y2	P35961 human immun
20	172	86.9	853	1 ENV_HV1Z2	P12481 human immun
21	172	86.9	855	1 ENV_HV1Z6	P04580 human immun
22	170	85.9	852	1 ENV_HV1BN	P12488 human immun
23	170	85.9	853	1 ENV_HV1EL	P04581 human immun
24	170	85.9	861	1 ENV_HV1KB	P31819 human immun
25	167	84.3	846	1 ENV_HV1ND	P18799 human immun
26	167	84.3	856	1 ENV_HV1PY	P03376 human immun
27	167	84.3	868	1 ENV_HV1C4	P05879 human immun
28	166	83.8	859	1 ENV_HV1MA	P04583 human immun
29	161	81.3	863	1 ENV_HV1Z8	P05882 human immun
30	156	78.8	854	1 ENV_SIVC2	P17281 chimpanzee
31	150	75.8	856	1 ENV_HV1ZH	P05881 human immun
32	91	46.0	854	1 ENV_SIVAI	O02837 simian immu
33	87	43.9	881	1 ENV_SIVMK	P05884 simian immu

34	87	43.9	882	1 ENV_SIVM1	P05885 simian immu
35	86	43.4	885	1 ENV_SIVS4	P12492 simian immu
36	85	42.9	859	1 ENV_HV2D2	P15831 human immu
37	85	42.9	860	1 ENV_HV2BE	P18094 human immu
38	83	41.9	880	1 ENV_SIVML	P11267 simian immu
39	82	41.4	889	1 ENV_SIVSP	P19503 simian immu
40	81	40.9	859	1 ENV_HV2CA	P24105 human immu
41	81	40.9	877	1 ENV_SIVAG	P27977 simian immu
42	78	39.4	768	1 ENV_SIVAI	P27757 simian immu
43	78	39.4	846	1 ENV_HV2SB	P12449 human immu
44	78	39.4	851	1 ENV_HV2D1	P17755 human immu
45	78	39.4	851	1 ENV_HV2G1	P18040 human immu

## ALIGNMENTS

RESULT 1	ENV_HV1A2	STANDARD:	PRT:	855 AA.
AC	P03378:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, last annotation update)			
DE	Envelope Polyprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).			
OC	Viruses: Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11685;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85090453; PubMed=2578227;			
RA	Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,			
RA	Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,			
RA	Levy J.A., Dina D., Lucht P.A.;			
RT	"Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)."			
RL	Science 227:484-492(1985).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL: K02007; AB59882.1; -.			
DR	PIR: A03976; VCLJAJ2.			
DR	HIV: K02007; ENVSSP2.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120.1.			
DR	Pfam: PF00517; GP41.1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; signal.			
FT	SIGNAL	1	29	
FT	CHAIN	30	509	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHARN	510	855	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	208	BY SIMILARITY.
FT	DISULFID	125	199	BY SIMILARITY.
FT	DISULFID	130	155	BY SIMILARITY.
FT	DISULFID	221	250	BY SIMILARITY.
FT	DISULFID	231	242	BY SIMILARITY.
FT	DISULFID	299	333	BY SIMILARITY.
FT	DISULFID	380	442	BY SIMILARITY.
FT	DISULFID	387	415	BY SIMILARITY.
FT	CARBOHYD	87	415	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).

RESULT 14  
 S70417  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (Fragment  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: patient 3B  
 C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 26-Aug-1999  
 C:Accession: S70417  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildmann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70417  
 A:Status: preliminary  
 A:Molecule type: DNA

Search completed: May 16, 2003, 11:25:05  
Job time : 12.1446 secs

A:Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type E retrovirus env polyprotein

## Query Match

Best Local Similarity 92.4%; Score 183; DB 2; Length 357;  
Pred. No. 1.8e-14;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 36

DB 139 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 174

## RESULT 8

S21998 envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 28

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S21998; S70425

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

A:Title: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi

A:Reference number: S21990

A:Accession: S21998

A:Molecule type: DNA

A:Residues: 1-358 <STE1>

A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb

A:Reference number: S70417; MUID:92144209; PMID:1136940

A:Accession: S70425

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-222, 'X', 224-358 <STE2>

A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183

C:Superfamily: type E retrovirus env polyprotein

## Query Match

Best Local Similarity 91.9%; Score 182; DB 2; Length 358;  
Pred. No. 2.4e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 36

DB 140 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 175

## RESULT 9

S21998 polyprotein P - human immunodeficiency virus type 1 (fragment)

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

C:Accession: C41621

R:Burger, H.; Weiser, B.; Flaherty, K.; Guille, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: C41621

A:Molecule type: DNA

A:Residues: 1-443 <BUR>

A:Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015

A:Note: this virus was isolated from the mother's sexual partner

C:Genetics:

A:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:424-443/Domain: transmembrane #status predicted <TMN>

F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: CD

Query Match 90.9%; Score 180; DB 2; Length 443;  
Best Local Similarity 88.9%; Pred. No. 5.3e-14;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 36

DB 378 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 413

## RESULT 10

VCLJ3W

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WM01)

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997

C:Accession: A24774

R:Starck, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks,

Cell 45, 637-648, 1986

A:Title: Identification and characterization of conserved and variable regions in the

A:Reference number: A24774; MUID:86218077; PMID:2423250

A:Accession: A24774

A:Molecule type: DNA

A:Residues: 1-856 <STA>

A:Cross-references: GB:K03455; GB:M38432; NID:91906382

C:Genetics:

A:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-501/Product: coat protein gp120 #status predicted <GP1>

F:502-847/Product: coat protein gp41 #status predicted <GP2>

F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,

## Query Match

Best Local Similarity 90.9%; Score 180; DB 1; Length 856;  
Pred. No. 1.1e-13;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 36

DB 638 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 673

## RESULT 11

S22006 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999

C:Accession: S70420; S22006

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70420

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-357 <ST2>

A:Cross-references: EMBL:X61354; NID:960190; PIDN:CAA43620.1; PID:960191

A:Experimental source: patient 1

A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polyprotein

## Query Match

Best Local Similarity 88.9%; Score 176; DB 2; Length 357;  
Pred. No. 1.3e-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 36

DB 139 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNMF 174

## RESULT 12

S22002

Query Match 93.4%; Score 185; DB 2; Length 847;  
Best Local Similarity 91.7%; Pred. No. 2.8e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESQNOQEKNEQELLELDKWSLWNNF 36  
DB 629 YTSSEYTLLEESQNOQEKNEQELLELDKWSLWNNF 664

RESULT 3  
S13289  
env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13289  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
C:Accession: S13289  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-847 <OBR>  
C:Superfamily: type E retrovirus env polyprotein

Query Match 93.4%; Score 185; DB 2; Length 847;  
Best Local Similarity 91.7%; Pred. No. 2.8e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESQNOQEKNEQELLELDKWSLWNNF 36  
DB 629 YTSSEYTLLEESQNOQEKNEQELLELDKWSLWNNF 664

RESULT 4  
VCLJSC  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922  
R:Gungo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
Virology 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091  
C:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
E:1-29/Domain: signal sequence #status predicted <ST5>  
E:30-861/Product: env polyprotein #status predicted <EPP>  
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 93.4%; Score 185; DB 1; Length 861;  
Best Local Similarity 91.7%; Pred. No. 2.9e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESQNOQEKNEQELLELDKWSLWNNF 36  
DB 643 YTSYLYTLLEESQNOQEKNEQELLELDKWSLWNNF 678

RESULT 5  
S21994  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 27B  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S21994; S70421  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL data library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
A:Reference number: S21990  
A:Accession: S21994  
A:Molecule type: DNA  
A:Residues: 1-357 <STE1>  
A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:960180  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70421  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
A:Cross-references: EMBL:X61355; NID:960179  
C:Superfamily: type E retrovirus env polyprotein

Query Match 92.9%; Score 184; DB 2; Length 357;  
Best Local Similarity 91.7%; Pred. No. 1.4e-14;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESQNOQEKNEQELLELDKWSLWNNF 36  
DB 139 YTTLYTLLEESQNOQEKNEQELLELDKWSLWNNF 174

RESULT 6  
S21996  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S70422; S21996  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70422  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:91067129  
A:Experimental source: patient 27L  
A>Note: submitted to the EMBL data library, July 1991  
C:Superfamily: type E retrovirus env polyprotein

Query Match 92.9%; Score 184; DB 2; Length 357;  
Best Local Similarity 91.7%; Pred. No. 1.4e-14;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESQNOQEKNEQELLELDKWSLWNNF 36  
DB 139 YTTLYTLLEESQNOQEKNEQELLELDKWSLWNNF 174

RESULT 7  
S21992  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S70424; S21992  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70424  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: EMBL:X61358; NID:960177; PIDN:CAA43628.1; PID:960178  
A:Experimental source: patient 22

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# OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-3

Perfect score: 198

Sequence: 1 YTNITITLLEESQNOEKNEDELLELDKWSLMMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.73:\*

1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	855	1 VCLJA2	env polypeptide pr
2	185	93.4	847	2 T09448	env polypeptide pr
3	185	93.4	847	2 S13289	env polypeptide pr
4	185	93.4	861	1 VCLJSC	env polypeptide pr
5	184	92.9	357	2 S21994	env polypeptide pr
6	184	92.9	357	2 S21996	env polypeptide pr
7	183	92.4	357	2 S21992	env polypeptide pr
8	182	91.9	358	2 S21998	env polypeptide pr
9	180	90.9	443	2 C41621	env polypeptide pr
10	180	90.9	856	1 VCLJ3W	env polypeptide pr
11	176	88.9	357	2 S22006	env polypeptide pr
12	176	88.9	358	2 S22002	env polypeptide pr
13	176	88.9	358	2 S22000	env polypeptide pr
14	176	88.9	358	2 S70417	env polypeptide pr
15	176	88.9	851	2 S33985	env polypeptide pr
16	176	88.9	854	2 S13288	env polypeptide pr
17	176	88.9	856	1 VCLJ3J	env polypeptide pr
18	176	88.9	861	1 VCLJ3I	env polypeptide pr
19	173	87.4	859	1 VCLJMN	env polypeptide pr
20	172	86.9	357	2 S22004	env polypeptide pr
21	172	86.9	445	2 A41621	env polypeptide pr
22	172	86.9	853	1 H44001	env polypeptide pr
23	172	86.9	853	1 S54384	env polypeptide pr
24	172	86.9	855	1 VCLJ3R	env polypeptide pr
25	170	85.9	454	2 B41621	env polypeptide pr
26	170	85.9	729	1 VCLJ3X	env polypeptide pr
27	170	85.9	852	1 VCLJ3B	env polypeptide pr
28	170	85.9	861	1 VCLJ3B	env polypeptide pr
29	169	85.4	852	2 T12016	env polypeptide pr

30	167	84.3	846	1 VCLJND	env polypeptide pr
31	167	84.3	856	1 VCLJVL	env polypeptide pr
32	167	84.3	868	1 VCLJHL	env polypeptide pr
33	166	83.8	859	2 T01672	env polypeptide pr
34	162	81.8	136	2 J00266	env polypeptide pr
35	162	81.8	136	2 J00954	env polypeptide pr
36	156	78.8	854	1 VCLJ3I	env polypeptide pr
37	150	75.8	856	1 A44963	env polypeptide pr
38	146	73.7	357	2 S21990	env polypeptide pr
39	133	67.2	877	2 S49197	env polypeptide pr
40	124	62.6	863	2 A53034	env polypeptide pr
41	87	43.9	881	1 VCLJG3	env polypeptide pr
42	87	43.9	881	2 S03068	env polypeptide pr
43	87	43.9	889	1 VCLJG5	env polypeptide pr
44	86	43.4	151	2 S30448	env polypeptide pr
45	86	43.4	151	2 S30452	env polypeptide pr

## ALIGNMENTS

### RESULT 1

VCLJA2

env polypeptide precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03976

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown

Science 227, 484-492, 1985

A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A:Reference number: A04003; MUID:85090453; PMID:2578227

A:Accession: A03976

A:Molecule type: DNA

A:Residues: 1-855 <S>N>

A:Cross-references: GB:K02007; NID:G328658; PIDN:AB59882.1; PID:G328666

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>

F:510-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,

F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0% Score 198; DB 1; Length 855;

Best Local Similarity 100.0%; Pred. No. 7.9e-16;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNITITLLEESQNOEKNEDELLELDKWSLMMNF 36  
DB 637 YTNITITLLEESQNOEKNEDELLELDKWSLMMNF 672

### RESULT 2

T09448

env polypeptide precursor - human immunodeficiency virus type 1 (strain JRF1)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz

submitted to the EMBL Data Library, July 1996

A:Reference number: 216673

A:Accession: T09448

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-847 <P>N>

A:Cross-references: EMBL:063632; NID:G1465777; PID:G1465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide



AC AAY89136;

XX 23-MAY-2000 (first entry)

DT Core polypeptide fragment T No. 574.

XX Retrovirus: hybrid polypeptide; enhancer: gp41; envelope protein; HIV-1;

KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;

KW anti-fusogenic; differentiation factor; interleukin; interferon;

XX colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX WO959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties

XX comprises enhancer sequence -

XX Disclosure: Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide

XX sequence linked to core polypeptides. The enhancer polypeptides are

XX derived from various retroviral envelope (gp41) protein sequences,

XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the

XX pharmacokinetic properties such as increasing the half-life of any core

XX polypeptide that they are linked to. The core polypeptides are any

XX function as a pharmacologically useful peptide for the treatment or

XX prevention of a disease. The core polypeptides are bioactive peptides

XX selected from a growth factor, cytokine, differentiation factor,

XX interleukin, interferon, colony stimulating factor, hormone or

XX angiogenic factor. The peptides of the invention can be used for

XX inhibiting viral infection and can be used in anti-viral and

XX anti-fusogenic treatments. Sequences AAY8651-Y9005 represent core

XX polypeptide fragments that can be used in the invention. Some sequences

XX among those indicated also comprise enhancer fragments at terminal ends

XX and form hybrid polypeptides.

XX Sequence 36 AA;

XX Query Match 97.0%; Score 191; DB 21; Length 36;

XX Best Local Similarity 97.2%; Pred. No. 3e-17;

XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLEDKWASLWNF 36

Db 1 YTSLSHSLEESONQOEKNEDELLEDKWASLWNF 36

Search completed: May 16, 2003, 11:12:04

Job time : 32.4578 secs

XX Sequence 36 AA;  
SQ  
Query Match 97.0%; Score 191; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTGILHSILIESONQOEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLIHSILIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 13  
AAV88729  
ID AAV88729 standard; peptide; 36 AA.  
AC AAV88729;  
XX  
DT 23-MAY-2000 (first entry)  
Core polypeptide fragment T No. 84.  
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KM colony stimulating factor; hormone; angiogenic factor.  
XX  
OS Unidentified.  
XX  
PN WO9595615-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US11219.  
XX  
PR 20-MAY-1998; 98US-0082279.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
DR WPI: 2000-136792/12.  
XX  
PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence -  
XX  
PS Disclosure; Page 22; 124pp; English.  
The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacologically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAV8651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides.  
SQ Sequence 36 AA;  
QY  
Query Match 97.0%; Score 191; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTGILHSILIESONQOEKNEDELLELDKWSLWNMF 36

DB 1 YTSLIHSILIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 14  
AAV89135  
ID AAV89135 standard; peptide; 36 AA.  
XX  
AC AAV89135;  
XX  
DT 23-MAY-2000 (first entry)  
Core polypeptide fragment T No. 573.  
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KM anti-fusogenic; differentiation factor; interleukin; interferon;  
KM colony stimulating factor; hormone; angiogenic factor.  
XX  
OS Unidentified.  
XX  
PN WO9595615-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US11219.  
XX  
PR 20-MAY-1998; 98US-0082279.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
DR WPI: 2000-136792/12.  
XX  
PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence -  
XX  
PS Disclosure; Page 30; 124pp; English.  
The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacologically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAV8651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides.  
SQ Sequence 36 AA;  
QY  
Query Match 97.0%; Score 191; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTGILHSILIESONQOEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLIHSILIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 15  
AAV89136  
ID AAV89136 standard; peptide; 36 AA.  
XX

XX Sequence 36 AA: 97.0%; Score 191; DB 21; Length 36;  
 SQ Query Match Best Local Similarity 97.2%; Pred. No. 3e-17;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 YTGILHSLEESQNOOEKNEDELLELDKWSLWNMF 36  
 1 YTSILHSLEESQNOOEKNEDELLELDKWSLWNMF 36  
 DB 1 YTSILHSLEESQNOOEKNEDELLELDKWSLWNMF 36

RESULT 11  
 ID AAB14533 standard; peptide: 36 AA.  
 AC AAB14533;  
 XX  
 DT 24-NOV-2000 (first entry)

XX HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).  
 OS Human immunodeficiency virus type 1.  
 XX MO200040616-A1.  
 XX 13-JUL-2000.  
 PD 10-JAN-2000; 2000MO-US00456.  
 PF 08-JAN-1999; 99US-0115404.  
 PR 07-JAN-2000; 2000US-0480336.  
 XX  
 PA (WILD/) WILD C T.  
 XX (WEISS/) WEISS C D.  
 PI Wild CT, Weiss CD;  
 PL WPI; 2000-465959/40.  
 DR  
 XX Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PS coiled-coil solution structure -  
 P3 Claim 13; Page 12; 97pp; English.  
 XX Sequences AAB14532-B14534 and AAB14569-B14602 represent specifically  
 CC claimed peptides derived from the C-helical domain of the gp41  
 CC envelope glycoprotein from a variety of HIV-1 isolates. The invention  
 CC relates to raising a neutralizing antibody response to a broad spectrum  
 CC of HIV (human immunodeficiency virus) strains and isolates, comprising  
 CC the administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the process  
 CC of viral entry into host cells. Such peptides can correspond to or  
 CC mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly a  
 CC combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can  
 CC be alternately linked together to form a peptide which mimics the  
 CC core 6-helix bundle. Administration of the peptide(s) generates a  
 CC humoral response, with the production of antibodies against gp41  
 CC structures involved in viral entry. As these portions of gp41 are well  
 CC conserved, such antibodies may be effective against a broad range of

CC HIV strains and isolates. The peptide compositions may be administered  
 CC as a prophylactic or therapeutic vaccine to generate antibodies which  
 CC reduce or inhibit the ability of HIV to infect uninfected cells. A  
 CC composition comprising polyclonal or monoclonal antibodies can be  
 CC administered to reduce HIV infection of uninfected cells. Antibodies  
 CC raised against entry-relevant gp41 structures may also be used  
 CC therapeutically and as tools to further elucidate the mechanism of HIV  
 CC cell entry.  
 XX  
 SQ Sequence 36 AA: 97.0%; Score 191; DB 21; Length 36;  
 OY Query Match Best Local Similarity 97.2%; Pred. No. 3e-17;  
 DB Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 YTGILHSLEESQNOOEKNEDELLELDKWSLWNMF 36  
 1 YTSILHSLEESQNOOEKNEDELLELDKWSLWNMF 36  
 DB 1 YTSILHSLEESQNOOEKNEDELLELDKWSLWNMF 36

RESULT 12  
 ID AAY88665 standard; peptide: 36 AA.  
 AC AAY88665;  
 XX  
 DT 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 20.  
 DE  
 XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 KW  
 XX Unidentified.  
 OS  
 XX WO959615-A1.  
 XX 25-NOV-1999.  
 PD 20-MAY-1999; 99WO-US11219.  
 PF 20-MAY-1998; 98US-0082279.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI; 2000-136792/12.  
 DR  
 XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 PS Disclosure: Page 21; 124pp; English.  
 XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX OS Human immunodeficiency virus type 1.  
XX PN WO20006622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.  
XX DR WPI; 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX Claim 12; Page 24; 148bp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
XX  
XX Query Match 97.0%; Score 191; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 3e-17; 1; Indels 0; Gaps 0;  
XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 YTGILHSLEESQNOQEKNEQELLELDKWSLWMEF 36  
XX 1 YTSLSHSLEESQNOQEKNEQELLELDKWSLWMEF 36  
XX Db  
XX  
XX RESULT 9  
XX AAB52688  
XX ID AAB52688 standard; Peptide: 36 AA.  
XX  
XX AAB52688;  
XX  
XX 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #66.  
XX PA Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; Inflammatory response up-regulation;  
XX chemoattractant.  
XX KW  
XX OS Human immunodeficiency virus type 1.  
XX PN WO20006622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.  
XX DR WPI; 2000-656493/63.

XX OS Administration of peptide agents with a sequence corresponding to a  
XX PN partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PT antagonist is used to modulate inflammation -  
XX PS Claim 12; Page 25; 148bp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
XX  
XX Query Match 97.0%; Score 191; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 3e-17; 1; Indels 0; Gaps 0;  
XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
XX 1 YTGILHSLEESQNOQEKNEQELLELDKWSLWMEF 36  
XX 1 YTSLSHSLEESQNOQEKNEQELLELDKWSLWMEF 36  
XX Db  
XX  
XX RESULT 10  
XX AAB52818  
XX ID AAB52818 standard; Peptide: 36 AA.  
XX AC AAB52818;  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #97.  
XX PA Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; Inflammatory response up-regulation;  
XX chemoattractant.  
XX KW  
XX OS Human immunodeficiency virus type 1.  
XX PN WO20006622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.  
XX DR WPI; 2000-656493/63.  
XX PT Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PT antagonist is used to modulate inflammation -  
XX PS Claim 14; Page 40; 148bp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.

## RESULT 6

AAV31955

ID AAV31955 standard; Peptide: 36 AA.

XX AAV31955;

DT 21-DEC-1999 (first entry)

DE Synthetic peptide T-20 (DP-178).

XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.

OS Synthetic.

OS Human immunodeficiency virus type 1.

FH Key

FT Modified-site 1 Location/Qualifiers

Modified-site 36 /note= "N-terminal acetyl"

XX Modified-site /note= "C-terminal amide"

XX WO9948513-A1.

XX 30-SEP-1999.

XX 22-MAR-1999; 99WO-US06230.

XX 23-MAR-1998; 98US-0045920.

XX 01-MAY-1998; 98US-0071877.

XX (TRIM-) TRIMERIS INC.

XX Kang M, Bray B, Lichty M, Mader C, Merutka G;

XX WPI: 1999-591038/50.

XX Methods of peptide synthesis, particularly used to produce T-20 or

XX T-20 like peptides

XX Claim 1; Page 102; 120pp; English.

XX The present sequence represents an N- and C-terminal modified

XX peptide, designated T-20 (or DP-178), corresponding to amino acids

XX 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.

XX The invention relates to methods for the synthesis of peptides,

XX in particular T-20 and T-20-like peptides. The method involves

XX synthesizing specific side-chain protected peptide fragment

XX intermediates of T-20 or a T-20-like peptide on a solid support,

XX coupling the protected fragments in solution to form a protected

XX chains to yield the final T-20 or T-20-like peptide. The invention

XX also relates to individual peptide fragments (see AAV31956-73) which

XX act as intermediates in the synthesis of peptides of interest (e.g.

XX T-20), and to particular groups of peptide fragments which act as

XX intermediates in the synthesis of the peptide of interest. The

XX method allows for the large scale, economical production of high

XX purity peptides.

SQ Sequence 36 AA;

Query Match 97.0%; Score 191; DB 20; Length 36;

Best Local Similarity 97.2%; Pred. No. 3e-17; Mismatches 1; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLSIESQNOEKNEQELLELDKWSLWNMF 36

DB 1 YTSLSHSLSIESQNOEKNEQELLELDKWSLWNMF 36

## RESULT 7

AAV31974

ID AAV31974 standard; Peptide: 36 AA.

XX AAV31974;

DT 21-DEC-1999 (first entry)

DE HIV-1 LAI gp41 T-20 peptide.

XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.

OS Human immunodeficiency virus type 1.

XX WO9948513-A1.

XX 30-SEP-1999.

XX 22-MAR-1999; 99WO-US06230.

XX 23-MAR-1998; 98US-0045920.

XX 01-MAY-1998; 98US-0071877.

XX (TRIM-) TRIMERIS INC.

XX Kang M, Bray B, Lichty M, Mader C, Merutka G;

XX WPI: 1999-591038/50.

XX Methods of peptide synthesis, particularly used to produce T-20 or

XX T-20 like peptides

XX Disclosure; Page 9; 120pp; English.

XX The present sequence represents a peptide, designated T-20 (or

XX DP-178), that corresponds to amino acids 638-673 of the

XX transmembrane protein gp41 of HIV-1 LAI isolate. The invention

XX relates to methods for the synthesis of peptides, in particular

XX C- and N-terminal modified T-20 (see AAV31955) and T-20-like peptides.

XX The method involves synthesizing specific side-chain protected

XX peptide fragment intermediates (see AAV31956-73) of T-20 or a

XX T-20-like peptide on a solid support, coupling the protected

XX fragments in solution to form a protected T-20 or T-20-like peptide,

XX followed by deprotection of the side chains to yield the final T-20

XX or T-20-like peptide. The invention also relates to individual

XX peptide fragments which act as intermediates in the synthesis of

XX peptides of interest (e.g. T-20), and to particular groups of

XX peptide fragments which act as intermediates in the synthesis of

XX the peptide of interest. The method allows for the large scale,

XX economical production of high purity peptides.

SQ Sequence 36 AA;

Query Match 97.0%; Score 191; DB 20; Length 36;

Best Local Similarity 97.2%; Pred. No. 3e-17; Mismatches 1; Indels 0; Gaps 0;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLSIESQNOEKNEQELLELDKWSLWNMF 36

DB 1 YTSLSHSLSIESQNOEKNEQELLELDKWSLWNMF 36

## RESULT 8

AAB52655

ID AAB52655 standard; Peptide: 36 AA.

XX AAB52655;

DT 23-FEB-2001 (first entry)

DE T20/DP178 peptide fragment #33.

XX Antinflammatory: T20/DP178; gp41 ectodomain; HIV-1 fusion;

XX formyl peptide receptor family; FPR; Inflammatory response up-regulation;

XX Chemottractant.

RESULT 4  
AAV22912  
ID AAV22912 standard; Peptide: 36 AA.  
XX  
AC AAV22912;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 108 from WO9820036.  
XX  
KM HIV; gp41 protein; constrained helical peptide; HIV infection;  
KM vaccine; antibody; viral membrane fusion; viral infectivity;  
KM ligand affinity purification; protein A replacement;  
KM immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
F WO9820036-A1.  
PD 14-MAY-1998.  
XX  
PF 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH) GENENTECH INC.  
PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
PI Wells JA;  
XX  
DR WPI: 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on termini of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure; Page 233-234; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SQ Sequence 36 AA;  
XX

Query Match 97.0%; Score 191; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 YTGILHSIESQNOQEKNEOELLELDKWSLWNMF 36  
DB 1 YTSLIHSIESQNOQEKNEOELLELDKWSLWNMF 36

RESULT 5  
AAV22805  
ID AAV22805 standard; Peptide: 36 AA.  
XX  
AC AAV22805;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 1 from WO9820036.  
XX  
KM HIV; gp41 protein; constrained helical peptide; HIV infection;  
KM vaccine; antibody; viral membrane fusion; viral infectivity;  
KM ligand affinity purification; protein A replacement;  
KM immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
F WO9820036-A1.  
PD 14-MAY-1998.  
XX  
PF 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH) GENENTECH INC.  
PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
PI Wells JA;  
XX  
DR WPI: 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on termini of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure; Page 143-144; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SQ Sequence 36 AA;  
XX

Query Match 97.0%; Score 191; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 YTGILHSIESQNOQEKNEOELLELDKWSLWNMF 36  
DB 1 YTSLIHSIESQNOQEKNEOELLELDKWSLWNMF 36

PA (UYDU-) UNIV DUKE.  
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Pellewey SR, Wild CT;  
 XX WPI: 1995-036105/05.  
 DR Computer search generated synthetic peptides - are inhibitors of  
 XX HIV transmission  
 PT  
 XX  
 PS Claim 11; Page 132; 182pp; English.  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibits transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.

XX Sequence 36 AA:

Query Match 97.0%; Score 191; DB 16; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 3e-17;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YVGLIHSLEESQNOOEKNEDELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||  
 DB 1 YVSLIHSLEESQNOOEKNEDELLELDKWSLWNMF 36

# RESULT 2

AAR98398  
 ID AAR98398 standard; peptide; 36 AA.

XX AAR98398;

DT 17-FEB-1997 (first entry)

XX DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;

KM ALLMORT5; 107x178x4; PLZIP search motif; viral transmission; HIV;

KM Influenza virus; hepatitis B virus.

XX Human immunodeficiency virus type 1.

PN WO9619495-A1.

PD 27-JUN-1996.

PF 20-DEC-1995; 95WO-US16733.

PR 06-JUN-1995; 95US-0470896.

PR 20-DEC-1994; 94US-0360107.

XX (TRIM-) TRIMERIS INC.

PA (UYDU-) UNIV DUKE.

PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;

PI Matthews TJ, Pellewey SR, Wild CT;

DR WPI: 1996-309517/31.

XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an

PT isolated peptide recognised by an ALLMORT5, 107x178x4 or PLZIP

PT sequence search motif

XX Disclosure; Fig 1; 471pp; English.

CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALLMORT5,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, Influenza virus, or  
 CC hepatitis B virus, to a cell.

XX Sequence 36 AA:

Query Match 97.0%; Score 191; DB 17; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 3e-17;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YVGLIHSLEESQNOOEKNEDELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||  
 DB 1 YVSLIHSLEESQNOOEKNEDELLELDKWSLWNMF 36

# RESULT 3

AAW17011  
 ID AAW17011 standard; peptide; 36 AA.

XX AAW17011;

DT 30-JUN-1997 (first entry)

XX HIV-1 derived peptide useful for treatment of HIV infection.

KM HIV; STV: human; simian immunodeficiency virus; glycoprotein 41;

KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;

KM replication; transmission.

OS Human immunodeficiency virus type 1 LAI isolate.

PN WO9640191-A1.

PD 19-DEC-1996.

PF 06-JUN-1996; 96WO-US09499.

PR 07-JUN-1995; 95US-0481957.

XX (TRIM-) TRIMERIS INC.

PI Johnson RM, Lambert DM;

DR WPI: 1997-099886/09.

XX Compsns. contg. DP-178 or DP-107 in combination with other

PT therapeutic agent - useful for treatment of HIV infection, esp. by

PT inhibiting replication or transmission of HIV.

XX Claim 2; Figure 1; 84pp; English.

CC AAW17011 represents a peptide designated DP-178, a peptide derived

CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The

CC peptide corresponds to residues 638-673 of gp41. DP-178 and its

CC derivatives are used in combination with a therapeutic agent, e.g. a

CC reverse transcriptase, viral protease, cytokine, glycosylation or viral

CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work

CC by inhibiting viral replication or inhibiting transmission. They may

CC also be used in vaccines for protecting against HIV infection.

XX Sequence 36 AA:

Query Match 97.0%; Score 191; DB 18; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 3e-17;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YVGLIHSLEESQNOOEKNEDELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||  
 DB 1 YVSLIHSLEESQNOOEKNEDELLELDKWSLWNMF 36

PR 07-JUN-1993; 93US-0073028



; TITLE OF INVENTION: BEING IMMOBILIZED  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 81  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-81

Query Match 100.0%; Score 179; DB 9; Length 232;  
Best Local Similarity 100.0%; Pred. NO. 3.8e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESQKQKNEQELLELDKQASLWNWF 33  
|||||  
Db 147 LIHSLIEESQKQKNEQELLELDKQASLWNWF 179

RESULT 15  
US-10-059-271-82  
; Sequence 82, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPKE, HEINRICH  
; APPLICANT: BUDDE, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
; TITLE OF INVENTION: BEING IMMOBILIZED  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-82

Query Match 100.0%; Score 179; DB 9; Length 254;  
Best Local Similarity 100.0%; Pred. NO. 4.2e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESQKQKNEQELLELDKQASLWNWF 33  
|||||  
Db 169 LIHSLIEESQKQKNEQELLELDKQASLWNWF 201

Search completed: May 16, 2003, 12:10:24  
Job time : 15.4458 secs

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GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-536

Perfect score: 195

Sequence: 1 YTSIIHSLIESONQOEKNEQELLELDKWSLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.0	851	2 S33985	env polyprotein - huma
2	193	99.0	854	2 S13288	env polyprotein - huma
3	193	99.0	856	1 VCLJH3	env polyprotein pr
4	193	99.0	861	1 VCLJLV	env polyprotein pr
5	184	94.4	443	2 C41621	env polyprotein p
6	184	94.4	856	1 VCLJVL	env polyprotein pr
7	184	94.4	856	1 VCLJ3W	env polyprotein pr
8	184	94.4	861	1 VCLJSC	env polyprotein pr
9	181	92.8	357	2 S21994	env polyprotein pr
10	181	92.8	358	2 S21998	env polyprotein g
11	180	92.3	357	2 S21996	env polyprotein g
12	179	91.8	847	2 T09448	env polyprotein g
13	179	91.8	847	2 S13289	env polyprotein g
14	176	90.3	445	2 A41621	env polyprotein M
15	176	90.3	855	1 VCLJAJ2	env polyprotein pr
16	175	89.7	358	2 S22002	env polyprotein g
17	175	89.7	358	2 S22000	env polyprotein g
18	175	89.7	358	2 S70417	env polyprotein g
19	175	89.7	843	1 H44001	env polyprotein pr
20	175	89.7	852	2 T12016	env polyprotein pr
21	175	89.7	852	1 VCLJMN	env polyprotein pr
22	174	89.2	357	2 S22004	env polyprotein pr
23	172	88.2	357	2 S21992	env polyprotein g
24	172	88.2	853	2 S54384	env polyprotein g
25	172	88.2	855	1 VCLJZR	env polyprotein pr
26	171	87.7	357	2 S22006	env polyprotein g
27	170	87.2	846	1 T01672	env polyprotein pr
28	169	86.7	859	2 T01672	env polyprotein pr
29	168	86.2	852	1 VCLJBR	env polyprotein -

30	166	85.1	729	1 VCLJRX	env polyprotein pr
31	166	85.1	861	1 VCLJKB	env polyprotein pr
32	164	84.1	454	2 B41621	env polyprotein D
33	161	82.6	868	1 VCLJTH4	env polyprotein -
34	158	81.0	136	2 J00266	env polyprotein -
35	158	81.0	136	2 J00954	env polyprotein -
36	151	77.4	856	1 A44963	env polyprotein pr
37	150	76.9	854	1 VCLJST	env polyprotein pr
38	145	74.4	357	2 S21990	env polyprotein pr
39	136	69.7	877	2 S49197	env polyprotein g
40	119	61.0	863	2 A53034	env polyprotein p
41	86	44.1	881	1 VCLJG3	env polyprotein -
42	86	44.1	881	2 S03068	env polyprotein -
43	86	44.1	889	1 VCLJG5	env polyprotein -
44	85	43.6	151	2 S30448	env protein - huma
45	85	43.6	151	2 S30452	env protein - huma

## ALIGNMENTS

### RESULT 1

S33985 env polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F.

Submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <C>

A:Cross-References: EMBL:211530; NID:960192; PID:CAA7628.1; PID:960199

C:Superfamily: type E retrovirus env polyprotein

### Query Match

Best Local Similarity 99.0%; Score 193; DB 2; Length 851;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIIHSLIESONQOEKNEQELLELDKWSLWNMF 36

DB 633 YTSIIHSLIESONQOEKNEQELLELDKWSLWNMF 668

### RESULT 2

S13288 env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Nemaize, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990

A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <O>

C:Superfamily: type E retrovirus env polyprotein

### Query Match

Best Local Similarity 99.0%; Score 193; DB 2; Length 854;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIIHSLIESONQOEKNEQELLELDKWSLWNMF 36

DB 636 YTSIIHSLIESONQOEKNEQELLELDKWSLWNMF 671

### RESULT 3

VCLJH3

```
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberg, J.A.; Papas, T.S.; Grzyb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2576815
A:Accession: A03973
A:Molecule type: DNA
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIS>
F:31-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-86/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 3.3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 638 YTSIHSLIEESONQOEKNEDELLEDKWASLWNMF 673
RESULT 4
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Main-Hodson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIS>
F:31-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-86/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,161,165,191,202,233,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 99.0%; Score 193; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 3.4e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 643 YTSIHSLIEESONQOEKNEDELLEDKWASLWNMF 678
RESULT 5
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
```

```
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: CA1621
R:Burger, H.; Welser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: CA1621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match 94.4%; Score 184; DB 2; Length 443;
Best Local Similarity 91.7%; Pred. No. 1.9e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DB 378 YTSIHSLIEESONQOEKNEDELLEDKWASLWNMF 413
RESULT 6
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Wensing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <WEN>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIS>
F:31-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 94.4%; Score 184; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 4e-14;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 638 YTSIHSLIEESONQOEKNEDELLEDKWASLWNMF 672
RESULT 7
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
```

C:Accession: A24774  
 R:Starch, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; MUID:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STA>  
 A:Cross-references: GB:K03455; GB:M3432; NID:g1906382  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 94.4%; Score 184; DB 1; Length 856;  
 Best local similarity 91.7%; Pred. No. 4e-14;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONQOEKNEQELLELDKASLWNMF 36  
 |||:::|||||  
 Db 638 YTSLYNLIEESONQOEKNEQELLELDKASLWNMF 673

RESULT 8  
 VCLJSC  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #extl\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
 virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-861/Product: env polyprotein #status predicted <Env>  
 F:129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 94.4%; Score 184; DB 1; Length 861;  
 Best local similarity 91.7%; Pred. No. 4e-14;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONQOEKNEQELLELDKASLWNMF 36  
 |||:::|||||  
 Db 643 YTSLYNLIEESONQOEKNEQELLELDKASLWNMF 678

RESULT 9  
 S21994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 27B  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #extl\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21990  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STEL>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140 'X', 142-312, 'X', 314-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:g60179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 92.8%; Score 181; DB 2; Length 357;  
 Best local similarity 88.9%; Pred. No. 3.4e-14;  
 Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONQOEKNEQELLELDKASLWNMF 36  
 |||:::|||||  
 Db 139 YTSLYNLIEESONQOEKNEQELLELDKASLWNMF 174

RESULT 10  
 S21998  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 28  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #extl\_change 01-Dec-2000  
 C:Accession: S21998; S70425  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21998  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STEL>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70425  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222, 'X', 224-358 <STE2>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 92.8%; Score 181; DB 2; Length 358;  
 Best local similarity 88.9%; Pred. No. 3.4e-14;  
 Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONQOEKNEQELLELDKASLWNMF 36  
 |||:::|||||  
 Db 140 YTSLYNLIEESONQOEKNEQELLELDKASLWNMF 175

RESULT 11  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #extl\_change 26-Aug-1999  
 C:Accession: S70422; S21996  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <ST2>  
 A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129  
 A:Experimental source: patient 27L  
 A:Note: Submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polypotein

Query Match 92.3%; Score 180; DB 2; Length 357;  
Best Local Similarity 88.9%; Pred. No. 4.5e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIIHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
DB 139 YTGILYTLIEESONQOEKNEQELLELDKWSLWNMF 174

## RESULT 12

env polypotein - human immunodeficiency virus type 1 (strain JFL)

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
C:Accession: T09448  
R:Paro, S.; Vinters, H.V.; Akash, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,  
submitted to the EMBL Data Library, July 1996  
Reference number: Z16673  
Accession: T09448  
Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-847 <PAN>  
A:Cross-references: EMBL:U63632; NID:q1465777; PID:q1465781  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.8%; Score 179; DB 2; Length 847;  
Best Local Similarity 91.7%; Pred. No. 1.6e-13;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIIHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
DB 629 YTSIYTLIEESONQOEKNEQELLELDKWSLWNMF 664

## RESULT 13

env polypotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13289  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack, J.A.  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
Accession: S13289  
Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-847 <OBR>  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.8%; Score 179; DB 2; Length 847;  
Best Local Similarity 91.7%; Pred. No. 1.6e-13;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIIHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
DB 629 YTSIYTLIEESONQOEKNEQELLELDKWSLWNMF 664

## RESULT 14

A41621

env polypotein M - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypotein  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: A41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: A41621  
A:Molecule type: DNA  
A:Residues: 1-445 <BUR>  
A:Cross-references: GB:M77228; NID:q328627; PIDN:AAB03790.1; PID:q555013  
A:Note: This virus was isolated from the mother  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-253/Product: coat protein gp120 (fragment) #status predicted <GPI>  
F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:426-445/Domain: transmembrane #status predicted <TMN>  
F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding si

Query Match 90.3%; Score 176; DB 2; Length 445;  
Best Local Similarity 86.1%; Pred. No. 1.7e-13;  
Matches 31; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIIHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
DB 380 YTSIYTLIEESONQOEKNEQELLELDKWSLWNMF 415

## RESULT 15

VCUJAZ

env polypotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03976  
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown  
Science 227, 484-492, 1985  
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453; PMID:2578227  
Accession: A03976  
A:Molecule type: DNA  
A:Residues: 1-855 <SAN>  
A:Cross-references: GB:K02007; NID:q328658; PIDN:AAB59882.1; PID:q328666  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:510-855/Product: transmembrane glycoprotein #status predicted <TMN>  
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,  
F:610,624,636,815/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 90.3%; Score 176; DB 1; Length 855;  
Best Local Similarity 86.1%; Pred. No. 3.6e-13;  
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIIHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
DB 637 YTSIYTLIEESONQOEKNEQELLELDKWSLWNMF 672

Search completed: May 16, 2003, 11:25:10  
Job time: 13.1446 secs



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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

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Query Match 99.0%; Score 193; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 5e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36
Db 633 YTSIHSLSIESQNOQEKNEQELLELDKWSLWNMF 668

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RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
AC P03375;
ID ENV_HV1B1
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
NCBI_Taxid=11678;
NCBI_Taxid=11678;
RN [1]
RP MEDLINE=8511123; PubMed=2578615;
RX Rather L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
  Josephs S.F., Dorian E.R., Rafalski J.A., Whitehorn E.A.,
  Baumeister K., Yanoff L., Peteway S.R., Jr., Pearson M.L.,
  Lautenberger J.A., Papas T.S., Ghayab J., Chang N.T., Gallo R.C.,
  Wong-Staal F.;
  "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
  Nature 313:277-284(1985).
RL [2]
RN DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.R., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
  Gregory T.J.;
  "Assignment of intrachain disulfide bonds and characterization of
  potential glycosylation sites of the type 1 recombinant human
  immunodeficiency virus envelope glycoprotein (gp120) expressed in
  Chinese hamster ovary cells.";
  J. Biol. Chem. 265:10373-10382(1990).
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  between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC EMBL: M15654; AAA44205.1;
CC PIR: A03973; VCLRH3.
DR HIV; M15654; ENVSH102.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
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FT DISULFID 296 331
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FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BF61A18931BB27 CRC64;

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Query Match 99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTSIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36
Db 638 YTSIHSLSIESQNOQEKNEQELLELDKWSLWNMF 673

```

```

RESULT 3
ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; O09779;

```



[illegible]

FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>406</td> <td>406</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	406	406	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>448</td> <td>448</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	448	448	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>463</td> <td>463</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	463	463	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>611</td> <td>611</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	611	611	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>616</td> <td>616</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	616	616	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>624</td> <td>624</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	624	624	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>637</td> <td>637</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	637	637	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>674</td> <td>674</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	674	674	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>750</td> <td>750</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	750	750	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>816</td> <td>816</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	816	816	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>856</td> <td>856</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	856	856	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>88</td> <td>88</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	88	88	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>136</td> <td>136</td> <td>N-LINKED (GLCNAC. . .)</td> <td>(POTENTIAL)</td>	136	136	N-LINKED (GLCNAC. . .)	(POTENTIAL)

Query Match: 99.0%; Score 193; DB 1; Length 856;  
 Best local similarity: 97.2%; Pred. No. 5e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIIHSLEESQNOQEKNEQELLELDKWSLMMWF 36  
 638 YTSIIHSLEESQNOQEKNEQELLELDKWSLMMWF 673

RESULT 4  
 ID ENV\_HV1H3 STANDARD; PRT; 856 AA.  
 AC P04624;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85228248; PubMed=2988795;  
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;  
 RT "HIV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";  
 RL Cell 41:979-986(1985).  
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 CC EMBL: M14100; AAA44679.1; -  
 DR HIV: M14100; ENVSHXB3.  
 DR Interpro: IPR000328; Env GP41.  
 DR Interpro: IPR000777; GP120.  
 DR Pfam: PF000516; GP120; 1.  
 DR Pfam: PF000517; GP41; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.  
 FT SIGNAL. 1 30  
 FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 119 205 BY SIMILARITY.  
 FT DISULFID 126 196 BY SIMILARITY.  
 FT DISULFID 131 157 BY SIMILARITY.  
 FT DISULFID 218 247 BY SIMILARITY.  
 FT DISULFID 228 239 BY SIMILARITY.  
 FT DISULFID 296 331 BY SIMILARITY.  
 FT DISULFID 378 445 BY SIMILARITY.  
 FT DISULFID 385 418 BY SIMILARITY.  
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

DR EMBL; U12055; AAA76690.1; - .  
DR GlycosuitedB; Q70626; - .  
DR InterPro; IPR000328; Env\_GP41

OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1)  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11686;  
RN [1]





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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

DR EMBL: M17450; -; NOT\_ANNOTATED\_CDS.

DR PIR: B28922; VCLJSC.

DR HIV: M17450; ENVSSC.

DR InterPro: IPR000328; Env.GP41.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS: Coat protein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL. 1 29

FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.

FT SITE 760 760 IN-FRAME TERMINATION CODON.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 160 BY SIMILARITY.

FT DISULFID 219 247 BY SIMILARITY.

FT DISULFID 228 239 BY SIMILARITY.

FT DISULFID 296 330 BY SIMILARITY.

FT DISULFID 376 439 BY SIMILARITY.

FT DISULFID 383 412 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 856 856 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 856 AA: 97055 MW: DAF4DA600EBA7A08 CRC64;

Query Match 94.4%; Score 184; DB 1; Length 856;  
Best Local Similarity 91.7%; Pred. No. 6.3e-15;  
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLSIESQNOQEKNEOELLELDKWSIIMNF 36  
||||:|||||

Db 638 YTSIIYTLIESQNOQEKNEOELLELDKWSIIMNF 673

RESULT 10  
ENV\_HV1M1 STANDARD; PRT: 856 AA.  
ID AC P31872;  
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein gp160 precursor [contains: exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (HIV-1).

OC Viruses; Retroviridae; Retroviridae; Lentivirus.

OC NCBI\_TaxID=31678;

RP [1]

RN SEQUENCE FROM N.A.

EX MEDLINE=66218077; PubMed=2423250.

RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS";

RL Cell 45:637-648(1986).

CC -; MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

CC PIR: A24774; VCLJ3W.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Glycoprotein; Transmembrane; Signal.

KW SIGNAL. 1 29

KW CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.

FT SITE 760 760 IN-FRAME TERMINATION CODON.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 160 BY SIMILARITY.

FT DISULFID 219 247 BY SIMILARITY.

FT DISULFID 228 239 BY SIMILARITY.

FT DISULFID 296 330 BY SIMILARITY.

FT DISULFID 376 439 BY SIMILARITY.

FT DISULFID 383 412 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 856 856 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 856 AA: 97526 MW: DB68D1E49C404D93 CRC64;

Query Match 94.4%; Score 184; DB 1; Length 856;  
Best Local Similarity 91.7%; Pred. No. 6.3e-15;  
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLSIESQNOQEKNEOELLELDKWSIIMNF 36  
||||:|||||



FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 280 290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 852 AA; 96663 MW; EE7BFB8D23C9910D CRC64;

Query Match 93.3%; Score 182; DB 1; Length 852;  
 Best Local Similarity 88.9%; Pred. No. 1.1e-14;  
 Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESONQOEKNEDELLEDKWASLWNMF 36  
 DB 634 YTSIHTLLESQNOQEKNEDELLEDKWASLWNMF 669

RESULT 13  
 ENV\_HV1S1 STANDARD; PRT; 847 AA.  
 AC P19550:  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 ENV.

Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).  
 Viruses; Retroviridae; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11691;

RP MEDLINE-90347835; PubMed-2384920;  
 RA Cheng-Mayer C., Quirga M., Tung J.W., Dina D., Levy J.;  
 RT "Viral determinants of human immunodeficiency virus type 1 T-cell or  
 RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";  
 RL J. Virol. 64:4390-4398(1990).

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC  
 DR EMBL: M65024; AAA45072.1;  
 DR HIV: M38428; ENV5SF162.  
 DR InterPro: IPR000328; Env GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.

DR Pfam: PF00517; GP41.1;  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 502  
 FT CHAIN 503 847  
 FT DISULFID 53 73  
 FT DISULFID 118 203  
 FT DISULFID 125 194  
 FT DISULFID 130 155  
 FT DISULFID 216 245  
 FT DISULFID 226 237  
 FT DISULFID 294 328  
 FT DISULFID 374 435  
 FT DISULFID 381 408  
 FT CARBOHYD 87 87  
 FT CARBOHYD 135 135  
 FT CARBOHYD 154 154  
 FT CARBOHYD 166 186  
 FT CARBOHYD 186 195  
 FT CARBOHYD 232 232  
 FT CARBOHYD 239 239  
 FT CARBOHYD 329 329  
 FT CARBOHYD 336 336  
 FT CARBOHYD 352 352  
 FT CARBOHYD 382 382  
 FT CARBOHYD 388 388  
 FT CARBOHYD 392 392  
 FT CARBOHYD 398 398  
 FT CARBOHYD 401 401  
 FT CARBOHYD 401 401  
 FT CARBOHYD 438 438  
 FT CARBOHYD 454 454  
 FT CARBOHYD 602 602  
 FT CARBOHYD 607 607  
 FT CARBOHYD 616 616  
 FT CARBOHYD 628 628  
 SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7FF2AB CRC64;

Query Match 92.8%; Score 181; DB 1; Length 847;  
 Best Local Similarity 88.9%; Pred. No. 1.5e-14;  
 Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESONQOEKNEDELLEDKWASLWNMF 36  
 DB 629 YTNLITLLESQNOQEKNEDELLEDKWASLWNMF 664

RESULT 14  
 ENV\_HV1RH STANDARD; PRT; 865 AA.  
 AC P04579;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 ENV.

GN Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).  
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11701;

RP MEDLINE-86218077; PubMed-2423250;  
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,  
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;  
 RT "Identification and characterization of conserved and variable  
 RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of  
 RT AIDS.";  
 RL Cell 45:637-648(1986).







FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 867 AA: 98399 MW; 5F2310146B8E8680 CRC64;

Query Match 90.8%; Score 177; DB 1; Length 867;  
 Best Local Similarity 88.9%; Pred. No. 4, 6e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSIHSILIESONOQEKNEOEELLDKWSLWNF 36  
 |||:|:||||||| ||||| ||||| |||||  
 Db 649 YTSIYTLIESONOQEKNEOEELLDKWSLWNF 684

Search completed: May 16, 2003, 11:13:36  
 Job time : 7.07229 secs



GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-536  
Perfect score: 195  
Sequence: 1 YTSIHSLIEESONQOEKNEOELLELDKWSLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-protent:\*  
12: sp-virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	99.0	645	15	099336 human immun
2	193	99.0	747	15	070607 human immun
3	193	99.0	748	15	070606 human immun
4	193	99.0	752	15	070604 human immun
5	193	99.0	752	15	070605 human immun
6	193	99.0	752	15	070608 human immun
7	193	99.0	851	15	078243 human immun
8	193	99.0	852	15	089797 human immun
9	193	99.0	854	15	085582 human immun
10	193	99.0	856	15	072502 human immun
11	193	99.0	856	15	092877 simian-huma
12	193	99.0	856	15	074599 human immun
13	193	99.0	856	15	074090 human immun
14	189	96.9	838	15	003806 human immun
15	189	96.9	854	15	090178 human immun
16	189	96.9	854	15	078705 human immun

17	189	96.9	854	15	078225 human immun
18	189	96.9	855	15	003805 human immun
19	188	96.4	856	15	0905M7 human immun
20	187	95.9	616	15	0993B0 human immun
21	187	95.9	618	15	0993B2 human immun
22	187	95.9	757	15	090722 human immun
23	187	95.9	848	15	069990 human immun
24	186	95.4	123	15	09YXR3 human immun
25	185	94.9	122	15	090TW0 human immun
26	184	94.4	42	15	069910 human immun
27	184	94.4	443	15	080023 human immun
28	184	94.4	841	15	041556 human immun
29	184	94.4	849	15	077368 human immun
30	184	94.4	849	15	080851 human immun
31	184	94.4	851	15	056110 human immun
32	184	94.4	851	15	080852 human immun
33	184	94.4	856	15	072993 human immun
34	184	94.4	856	15	041539 human immun
35	184	94.4	857	15	080L70 human immun
36	184	94.4	858	15	080L88 human immun
37	184	94.4	858	15	080L85 human immun
38	184	94.4	859	15	080L80 human immun
39	184	94.4	859	15	080L79 human immun
40	184	94.4	859	15	080L77 human immun
41	184	94.4	859	15	080L73 human immun
42	184	94.4	859	15	080850 human immun
43	184	94.4	862	15	080L84 human immun
44	184	94.4	862	15	080L84 human immun
45	184	94.4	862	15	080L83 human immun

## ALIGNMENTS

RESULT 1	099336	PRELIMINARY;	PRT;	645 AA.
AC	099336;			
DT	01-JUN-2001 (TREMREL. 17, Created)			
DT	01-JUN-2001 (TREMREL. 17, Last sequence update)			
DT	01-DEC-2001 (TREMREL. 19, Last annotation update)			
DE	Truncated envelope glycoprotein (Fragment).			
EN	ENV.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=1007;			
RX	MEDLINE=21192672; PubMed=11287644;			
RA	Suman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,			
RA	White S.W., Doherty P.C., Hurwitz J.L.,			
RT	"Localization of CD4 T cell epitope hotspots to exposed strands of			
RT	HIV envelope glycoprotein suggests structural influences on antigen			
RT	processing."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).			
DR	EMBL: AF321563; AAK18810.1;			
DR	InterPro: IPR000328; Env_GPA1.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
KW	Aids; Coat protein; Envelope protein; Glycoprotein; Polypeptide;			
KW	Transmembrane.			
FT	NON_TER			
SO	SEQUENCE			
Query Match	645 AA;	72485 MW;	B076514BE93362EC CRC64;	
Best Local Similarity	99.0%;	Score 193;	DB 15;	Length 645;
Matches	35;	Conservative	97.2%;	Pred. No. 4e-15;
			Mismatches	0;
			Indels	0;
			Gaps	0;
OY	1 YTSIHSLIEESONQOEKNEOELLELDKWSLWMP 36			
DB	607 YTSIHSLIEESONQOEKNEOELLELDKWSLWMP 642			

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RESULT 2
070607 PRELIMINARY: PRT: 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
ENV Envelope glycoprotein (Fragment).
CN
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RX MEDLINE-95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA Mulder K.E.;
  Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12034; AAA76669.1;
  InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245F14 CRC64:

Query Match 99.0%; Score 193; DB 15; Length 747;
Best Local Similarity 97.2%; Pred. No. 4.7e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONOEKNEQELLEDKWASLWNMF 36
Db 633 YTSIHSLEESONOEKNEQELLEDKWASLWNMF 668

RESULT 3
070606 PRELIMINARY: PRT: 748 AA.
AC 070606;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
ENV Envelope glycoprotein (Fragment).
CN
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RX MEDLINE-95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RA Mulder K.E.;
  Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12032; AAA76668.1;
  InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64:
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DR InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA: 84224 MW: 56BEDF186C676948 CRC64:

Query Match 99.0%; Score 193; DB 15; Length 748;
Best Local Similarity 97.2%; Pred. No. 4.7e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONOEKNEQELLEDKWASLWNMF 36
Db 634 YTSIHSLEESONOEKNEQELLEDKWASLWNMF 669

RESULT 4
070604 PRELIMINARY: PRT: 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
ENV Envelope glycoprotein (Fragment).
CN
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RX MEDLINE-95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA Mulder K.E.;
  Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12030; AAA76665.1;
  InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64:

Query Match 99.0%; Score 193; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 4.7e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONOEKNEQELLEDKWASLWNMF 36
Db 638 YTSIHSLEESONOEKNEQELLEDKWASLWNMF 673

RESULT 5
070605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
ENV Envelope glycoprotein (Fragment).
CN
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
```

[1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-LW852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12031; AAA76667.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752  
 SO SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 99.0%; Score 193; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 4.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIESONQOEKNEQELLELDKWSIWMNF 36  
 DB 638 YTSIIHSLIESONQOEKNEQELLELDKWSIWMNF 673

RESULT 6  
 ID 070608 PRELIMINARY; PRT: 752 AA.  
 AC 070608;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752  
 SO SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 4.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSIIHSLIESONQOEKNEQELLELDKWSIWMNF 36  
 DB 638 YTSIIHSLIESONQOEKNEQELLELDKWSIWMNF 673

DB 638 YTSIIHSLIESONQOEKNEQELLELDKWSIWMNF 673

RESULT 7  
 ID 078243 PRELIMINARY; PRT: 851 AA.  
 AC 078243;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Env polypotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
 Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 chronically infected HUT-78 cellular clone.";  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Macchi B., Mangiano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 producer clones from HUT-78 infected with a patient HIV isolate.";  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Borsetti A., Saggio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 productive clone.";  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL: Z11530; CA47628.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 851  
 SO SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 5.3e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIESONQOEKNEQELLELDKWSIWMNF 36  
 DB 633 YTSIIHSLIESONQOEKNEQELLELDKWSIWMNF 668

RESULT 8  
 ID 089797 PRELIMINARY; PRT: 852 AA.  
 AC 089797;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker

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RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW90-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12053; AAA76685.1; -
DR EMBL: U12036; AAA76671.1; -
DR InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120_1.
DR Pfam: PF00517; GP41_1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;
KW Transmembrane.
SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF CRC64;

Query Match          99.0%; Score 193; DB 15; Length 852;
Best Local Similarity 97.2%; Pred. No. 5.3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSIHSLSIESONOENKNEQELLELDKWSLWNMF 36
|||||
634 YTSIHSLSIESONOENKNEQELLELDKWSLWNMF 669

RESULT 9
ID 085582; PRELIMINARY; PRT; 854 AA.
AC 085582;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope polyprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone.";
RT J. Virol. 59:284-291(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RN Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Buckler C.E.;
RN Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92219406; PubMed=1373204;
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
RT gp1 results in loss of killing by CD8+ A24-restricted cytotoxic T
RT lymphocytes.";
RT J. Virol. 66:3151-3154(1992).
DR EMBL: M19921; AAA44992.1; -
DR InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120_1.
DR Pfam: PF00517; GP41_1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;

Query Match          99.0%; Score 193; DB 15; Length 854;
Best Local Similarity 97.2%; Pred. No. 5.3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLSIESONOENKNEQELLELDKWSLWNMF 36
|||||
DB 636 YTSIHSLSIESONOENKNEQELLELDKWSLWNMF 671

RESULT 10
ID 072502; PRELIMINARY; PRT; 854 AA.
AC 072502;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENV polyprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-NL4-3;
RX MEDLINE=96036482; PubMed=7483282;
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
RT from primary virus cultures using the polymerase chain reaction.";
RT J. Virol. 213:80-86(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-NL4-3;
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone.";
RT J. Virol. 59:284-291(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX EMBL: U26942; AAB60578.1; -
RX InterPro: IPR000328; Env-GP41.
RX InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120_1.
DR Pfam: PF00517; GP41_1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
KW CONFLICT 214 H -> L (IN REF. 2).
FT CONFLICT 530 A -> S (IN REF. 2).
FT CONFLICT 739 G -> D (IN REF. 2).
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match          99.0%; Score 193; DB 15; Length 854;
Best Local Similarity 97.2%; Pred. No. 5.3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLSIESONOENKNEQELLELDKWSLWNMF 36
|||||
DB 636 YTSIHSLSIESONOENKNEQELLELDKWSLWNMF 671

RESULT 11
ID 092877; PRELIMINARY; PRT; 856 AA.
AC 092877;
DT 01-NOV-1996 (TREMBLrel. 08, Created)
DT 01-NOV-1996 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99098984; PubMed=9882298;

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RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
RA Stenbeke T., Halloran M., Fenton J.W., Axthelm M.K., Letvin N.L.,
RA Sodroski J.G.;
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
RT responsible for the pathogenicity of a multiply passaged simian-human
RT immunodeficiency virus (SHIV-HXBc2).";
RL J. Virol. 73:976-984(1999).
RP
RN
[2]
SEQUENCE FROM N.A.
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF041850; AAD12142.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120: 1.
DR Pfam: PF00517; GP41: 1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SO SEQUENCE 856 AA; 97151 MW; C50BF038FEB73659 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 856;
Best Local Similarity 97.2%; Pred. No. 5,3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESQNOEKNEDELLDLKWSLWNMF 36
||:|||||
Db 638 YTSIHSLEESQNOEKNEDELLDLKWSLWNMF 673

RESULT 12
ID Q74599 PRELIMINARY; PRT; 856 AA.
AC Q74599.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Env.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=MCK1;
RX MEDLINE=90101366; PubMed=168473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
RT (HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RP
RN
[2]
SEQUENCE FROM N.A.
RA Iwatani Y.;
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: D86068; BAA12995.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120: 1.
DR Pfam: PF00517; GP41: 1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SO SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 856;
Best Local Similarity 97.2%; Pred. No. 5,3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESQNOEKNEDELLDLKWSLWNMF 36
||:|||||
Db 638 YTSIHSLEESQNOEKNEDELLDLKWSLWNMF 673

RESULT 13
ID Q74090

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ID	Q74090	PRELIMINARY;	PRT;	856 AA..
AC	074090;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Env.			
GN	ENV.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A..			
RC	STRAIN=PM213;			
RA	Iwatani Y.;			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: D86069; BAA13003.1; -;			
DR	InterPro: IPR000328; Env.GP41.			
DR	InterPro: IPR000777; GP120.			
DR	PIfam: PF00516; GP120. 1.			
DR	PIfam: PF00517; GP41; 1.			
KW	AIMS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.			
SO	SEQUENCE 856 AA; 97396 MW; FEE3784C423C108C CnC64;			
Query Match		99.0%;	Score 193;	DB 15; Length 856;
Best Local Similarity		97.2%;	Pred. No.5.3e-15;	
Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 YTSIIHSLEFSQNOEKNEQELLELDKASIMNMF 36			
Db	638 YTSIIHSLEFSQNOEKNEQELLELDKASIMNMF 673			
RESULT 14				
ID	Q03806	PRELIMINARY;	PRT;	838 AA.
AC	Q03806;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Envelope polyprotein GP160 precursor [CONTAINS: GP120, GP41].			
GN	ENV.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Reitz M., Popovic M., Gartner S., Gallo R., Reed-Connole E.,			
RA	Beaver B.;			
RL	Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: M68894; AAA44196.1; -;			
DR	InterPro: IPR000328; Env.GP41.			
DR	InterPro: IPR000777; GP120.			
DR	PIfam: PF00516; GP120. 1.			
DR	PIfam: PF00517; GP41; 1.			
KW	AIMS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL 1			
FT	CHAIN ?	493		
FT	CHAIN			EXTERIOR MEMBRANE GLYCOPROTEIN (GP120)
FT	CHAIN	494	838	(BY SIMILARITY).
FT	CHAIN			TRANSMEMBRANE GLYCOPROTEIN (GP41)
FT	DISULFID 53		73	(BY SIMILARITY).
FT	DISULFID 118		216	BY SIMILARITY.
FT	DISULFID 125		184	BY SIMILARITY.
FT	DISULFID 130		145	BY SIMILARITY.
FT	DISULFID 206		235	BY SIMILARITY.

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FT DISULFID 216 227 BY SIMILARITY.
FT DISULFID 284 318 BY SIMILARITY.
FT DISULFID 364 427 BY SIMILARITY.
FT DISULFID 371 400 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 619 619 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 798 798 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 838 AA; 95328 MW; 11044B1CA10CFB4D CRC64;

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Query Match 96.9%; Score 189; DB 15; Length 838;
Best Local Similarity 97.2%; Pred. No. 1.6e-14;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSIHSLSIESQNOEKNQELLEDKWSLWNP 36
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DB 620 YTSIHSLSIESQNOEKNQELLEDKWSLWNP 655

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RESULT 15
OS 090178 PRELIMINARY; PRT; 854 AA.
AC 090178;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
ENVELOPE glycoprotein.
ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95074930; PubMed=7983770;
RA Fang H., Pincus S.H.;
RT "Unique insertion sequence and pattern of CD4 expression in variants
RT selected with immunotoxins from human immunodeficiency virus type 1-
RT infected T cells";
RL J. Virol. 69:75-81(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Fang H., Pincus S.H.;
RT "Spontaneous activation of human immunodeficiency virus type 1 in an
RT immunotoxin-resistant variant T cell line";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070521; AAC28452.1;
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.

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KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

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Query Match 96.9%; Score 189; DB 15; Length 854;
Best Local Similarity 94.4%; Pred. No. 1.6e-14;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSIHSLSIESQNOEKNQELLEDKWSLWNP 36
    |||:|||||:|||||:|||||:|||||:
DB 636 YTSIHSLSIESQNOEKNQELLEDKWSLWNP 671

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Search completed: May 16, 2003, 11:19:48
Job time: 27.3124 secs

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GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533a-536  
Perfect score: 195  
Sequence: 1 YTSIIHSLIESQNOQEKNEQELLELDKWSIWMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2.6/ptodata/1/1aa/PCUTUS.COMB.pep:\*  
6: /cgn2.6/ptodata/1/1aa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.0	36	1 US-08-073-028-1	Sequence 1, Appl
2	193	99.0	36	3 US-08-486-099-1	Sequence 1, Appl
3	193	99.0	36	3 US-09-071-877-1	Sequence 1, Appl
4	193	99.0	36	3 US-08-360-107A-1	Sequence 1, Appl
5	193	99.0	36	3 US-08-484-223B-1	Sequence 1, Appl
6	193	99.0	36	3 US-08-919-597-1	Sequence 1, Appl
7	193	99.0	36	3 US-08-475-668A-1	Sequence 1, Appl
8	193	99.0	36	3 US-08-485-551A-1	Sequence 1, Appl
9	193	99.0	36	3 US-08-471-913A-1	Sequence 1, Appl
10	193	99.0	36	4 US-08-554-616-1	Sequence 1, Appl
11	193	99.0	36	4 US-08-485-264A-1	Sequence 1, Appl
12	193	99.0	36	4 US-09-082-279B-15	Sequence 15, Appl
13	193	99.0	36	4 US-09-082-279B-497	Sequence 497, App
14	193	99.0	36	4 US-09-082-279B-498	Sequence 498, App
15	193	99.0	36	4 US-09-082-279B-603	Sequence 603, App
16	193	99.0	36	4 US-09-082-279B-630	Sequence 630, App
17	193	99.0	36	4 US-09-082-279B-631	Sequence 631, App
18	193	99.0	36	4 US-09-082-279B-705	Sequence 705, App
19	193	99.0	36	4 US-09-082-279B-834	Sequence 834, App
20	193	99.0	36	4 US-09-082-279B-1076	Sequence 1076, App
21	193	99.0	36	4 US-09-082-279B-1121	Sequence 1121, App
22	193	99.0	36	4 US-08-965-056-1	Sequence 1161, App
23	193	99.0	36	4 US-08-965-056-108	Sequence 108, App
24	193	99.0	36	4 US-09-045-920-1	Sequence 1, Appl
25	193	99.0	36	4 US-08-474-349A-1	Sequence 1, Appl
26	193	99.0	36	4 US-08-474-349A-1	Sequence 399, App
27	193	99.0	36	4 US-08-474-349A-399	Sequence 399, App

28	193	99.0	36	4 US-08-474-349A-413	Sequence 413, App
29	193	99.0	36	4 US-09-315-304B-15	Sequence 15, Appl
30	193	99.0	36	4 US-09-315-304B-497	Sequence 497, App
31	193	99.0	36	4 US-09-315-304B-498	Sequence 498, App
32	193	99.0	36	4 US-09-315-304B-603	Sequence 603, App
33	193	99.0	36	4 US-09-315-304B-630	Sequence 630, App
34	193	99.0	36	4 US-09-315-304B-705	Sequence 705, App
35	193	99.0	36	4 US-09-315-304B-834	Sequence 834, App
36	193	99.0	36	4 US-09-315-304B-1076	Sequence 1076, App
37	193	99.0	36	4 US-09-315-304B-1121	Sequence 1121, App
38	193	99.0	36	4 US-09-315-304B-1161	Sequence 1161, App
39	193	99.0	36	4 US-09-315-304B-1469	Sequence 1469, App
40	193	99.0	36	4 US-09-315-304B-1470	Sequence 1470, App
41	193	99.0	36	4 US-09-315-304B-1486	Sequence 1486, App
42	193	99.0	36	4 US-08-255-208A-1	Sequence 1, Appl
43	193	99.0	37	4 US-08-082-279B-771	Sequence 771, App
44	193	99.0	37	4 US-08-082-279B-775	Sequence 775, App
45	193	99.0	37	4 US-08-082-279B-775	Sequence 775, App

## ALIGNMENTS

RESULT 1  
US-08-073-028-1  
Sequence 1, Application US/08073028  
Patent No. 5464933  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073.028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-1  
Query Match 99.0%; Score 193; DB 1; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 YTSIIHSLIESQNOQEKNEQELLELDKWSIWMNF 36  
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Db 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matchews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennile & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNILE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 7,1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lachy, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Merutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

US-09-071-877-1

CURRENT APPLICATION NUMBER: US/09/071,877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO: 1

LENGTH: 36

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-09-071-877-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 7,1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matchews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennile & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNILE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 7,1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLIESQNOEKNEDELLELDKWSLWNNF 36

RESULT 5  
US-08-484-223B-1

Sequence 1, Application US/08484223B  
Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOEKNEDELLELDKWSLWNNF 36  
Db 1 YTSLSHSLIESQNOEKNEDELLELDKWSLWNNF 36

RESULT 6  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOEKNEDELLELDKWSLWNNF 36  
Db 1 YTSLSHSLIESQNOEKNEDELLELDKWSLWNNF 36

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6080065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dant P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1  
Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 YTSIHSLSIESQNOEKNEQELLEDKWASLWNP 36  
Db 1 YTSLSHSLSIESQNOEKNEQELLEDKWASLWNP 36  
RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dant P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1  
Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIHSLSIESQNOEKNEQELLEDKWASLWNP 36  
Db 1 YTSLSHSLSIESQNOEKNEQELLEDKWASLWNP 36  
RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15  
Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 YTSIHSLSIESQNOEKNEQELLEDKWASLWNP 36  
Db 1 YTSLSHSLSIESQNOEKNEQELLEDKWASLWNP 36

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36

## RESULT 13

US-09-082-279B-497

; Sequence 497, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 497

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match 99.0%; Score 193; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 7.1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESQNOOEKNEQELLELDKWSLWNNF 36

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36

## RESULT 14

US-09-082-279B-498

; Sequence 498, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 498

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

Query Match 99.0%; Score 193; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 7.1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESQNOOEKNEQELLELDKWSLWNNF 36

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36

## RESULT 15

US-09-082-279B-603

; Sequence 603, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 603

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 99.0%; Score 193; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 7.1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESQNOOEKNEQELLELDKWSLWNNF 36

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36

Search completed: May 16, 2003, 11:22:13  
Job time: 11.1928 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-536  
Perfect score: 195  
Sequence: 1 YTSLSHSLIESQNOQEKNEDELLEDKWASLWNMF 36

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues  
1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.0	36	9 US-09-874-475-16	Sequence 16, Appl
2	193	99.0	36	9 US-10-116-797-1	Sequence 1, Appl
3	193	99.0	36	9 US-09-493-346-1	Sequence 10, Appl
4	193	99.0	36	10 US-09-796-202-10	Sequence 5, Appl
5	193	99.0	36	10 US-09-779-451-5	Sequence 1, Appl
6	193	99.0	36	10 US-09-834-628-1	Sequence 1, Appl
7	193	99.0	36	10 US-09-854-816-1	Sequence 1, Appl
8	193	99.0	36	10 US-09-854-816-108	Sequence 108, App
9	193	99.0	37	9 US-09-848-616-176	Sequence 176, App
10	193	99.0	46	10 US-09-779-451-41	Sequence 41, Appl
11	193	99.0	56	10 US-09-779-451-41	Sequence 4, Appl
12	193	99.0	177	9 US-10-040-349B-2	Sequence 2, Appl
13	193	99.0	221	9 US-10-059-271-84	Sequence 84, Appl
14	193	99.0	232	9 US-10-059-271-81	Sequence 81, Appl
15	193	99.0	234	9 US-10-059-271-82	Sequence 82, Appl
16	193	99.0	256	9 US-10-059-271-97	Sequence 97, Appl
17	193	99.0	268	10 US-09-854-816-16	Sequence 16, Appl
18	193	99.0	268	10 US-09-854-816-17	Sequence 17, Appl
19	193	99.0	268	10 US-09-854-816-18	Sequence 18, Appl

20	193	99.0	344	9 US-10-040-349B-1	Sequence 1, Appl
21	193	99.0	345	9 US-10-026-741-49	Sequence 49, Appl
22	193	99.0	349	10 US-09-779-451-8	Sequence 8, Appl
23	193	99.0	391	9 US-10-059-271-93	Sequence 93, Appl
24	193	99.0	519	10 US-09-756-551A-8	Sequence 8, Appl
25	193	99.0	853	9 US-10-003-035-33	Sequence 33, Appl
26	193	99.0	856	10 US-09-476-242-1	Sequence 1, Appl
27	193	99.0	861	9 US-10-026-741-103	Sequence 103, App
28	193	99.0	1101	9 US-10-003-035-53	Sequence 53, Appl
29	193	99.0	1186	9 US-10-003-035-55	Sequence 55, Appl
30	190	97.4	36	10 US-09-912-824-1	Sequence 1, Appl
31	190	97.4	268	10 US-09-854-816-19	Sequence 19, Appl
32	189	96.9	268	10 US-09-854-816-13	Sequence 13, Appl
33	187	95.9	1231	9 US-10-059-271-94	Sequence 94, Appl
34	184	94.4	233	10 US-09-854-816-50	Sequence 50, Appl
35	184	94.4	268	10 US-09-854-816-9	Sequence 9, Appl
36	184	94.4	269	10 US-09-854-816-12	Sequence 12, Appl
37	183	93.8	269	10 US-09-854-816-46	Sequence 46, Appl
38	182	93.3	269	10 US-09-854-816-28	Sequence 28, Appl
39	182	93.3	269	10 US-09-854-816-34	Sequence 34, Appl
40	181	92.8	268	10 US-09-854-816-26	Sequence 26, Appl
41	181	92.8	619	10 US-09-891-609-4	Sequence 4, Appl
42	181	92.8	646	10 US-09-891-609-2	Sequence 2, Appl
43	181	92.8	847	10 US-09-476-242-2	Sequence 2, Appl
44	180	92.3	46	10 US-09-854-816-109	Sequence 109, App
45	180	92.3	267	10 US-09-854-816-38	Sequence 38, Appl

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
: Sequence 16, Application US/09874475  
: Publication No. US20020182592A1  
: GENERAL INFORMATION:  
: APPLICANT: Petropoulos, Christos J.  
: APPLICANT: Parkin, Neil T.  
: APPLICANT: Whitcomb, Jeanette  
: APPLICANT: Huang, Wei  
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
: TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS  
: FILE REFERENCE: 2793/65166  
: CURRENT APPLICATION NUMBER: US/09/874,475  
: CURRENT FILING DATE: 2001-06-04  
: NUMBER OF SEQ ID NOS: 16  
: SOFTWARE: PatentIn version 3.1  
: SEQ ID NO 16  
: LENGTH: 36  
: TYPE: PRT  
: ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16

Query Match 99.0% Score 193; DB 9; Length 36;  
Best Local Similarity 97.2% Pred. No. 1e-16; 0: Indels 0: Gaps 0;  
Matches 35; Conservative 1; Mismatches 0

Oy 1 YTSLSHSLIESQNOQEKNEDELLEDKWASLWNMF 36  
Db 1 YTSLSHSLIESQNOQEKNEDELLEDKWASLWNMF 36

RESULT 2  
US-10-116-797-1  
: Sequence 1, Application US/10116797  
: Publication No. US2003004411A1  
: GENERAL INFORMATION:  
: APPLICANT: Olsen, William C.  
: APPLICANT: Maddon, Paul J.  
: TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
: FILE REFERENCE: 64672-A  
: CURRENT APPLICATION NUMBER: US/10/116,797  
: CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36  
|||:|||||  
DB 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36

RESULT 3  
US-09-493-346-1

Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Olson, William C  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36  
|||:|||||  
DB 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36

LT 4  
9-796-202-10

Sequence 10, Application US/09796202  
Patent No. US2002006813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE: NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36  
|||:|||||  
DB 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36

RESULT 5

US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36  
|||:|||||  
DB 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36

RESULT 6  
US-09-834-628-1

Sequence 1, Application US/09834628  
Patent No. US2002011922A1  
GENERAL INFORMATION:  
APPLICANT: YU, YEON-GUN  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36  
|||:|||||  
DB 1 YTSIHSLIEESQNOOEKNEQELLELDKWSLWNNF 36



RESULT 7  
US-09-854-816-1  
Sequence 1, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: DP178  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
9-854-816-1  
Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSIHSLSIESQNOEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLSHSLSIESQNOEKNEDELLELDKWSLWNMF 36  
RESULT 8  
US-09-854-816-108  
Sequence 108, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108  
Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSIHSLSIESQNOEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLSHSLSIESQNOEKNEDELLELDKWSLWNMF 36  
RESULT 9  
US-09-848-616-176  
Sequence 176, Application US/09848616  
Publication No. US20030054010A1  
GENERAL INFORMATION:  
APPLICANT: Seibel, Peter  
APPLICANT: Dunant, Nicolas  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Lechner, Franziska  
TITLE OF INVENTION: Molecular Antigen Array  
FILE REFERENCE: 1700, 0180002  
CURRENT APPLICATION NUMBER: US/09/848,616  
CURRENT FILING DATE: 2001-05-05  
NUMBER OF SEQ ID NOS: 186  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 176  
LENGTH: 37  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DP176c peptide  
US-09-848-616-176  
Query Match 99.0%; Score 193; DB 9; Length 37;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSIHSLSIESQNOEKNEDELLELDKWSLWNMF 36

Db 2 YTSLIHSLIESQNOEKNEQELLELDKWSIWMNF 37

RESULT 10

US-09-779-451-41

Sequence 41, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

Q ID NO 41

LENGTH: 46

TYPE: PRT

US-09-779-451-41

Query Match

Best Local Similarity 99.0%; Score 193; DB 10; Length 46;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIHSLSIESQNOEKNEQELLELDKWSIWMNF 36

Db 11 YTSLIHSLIESQNOEKNEQELLELDKWSIWMNF 46

RESULT 11

US-09-779-451-4

Sequence 4, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT APPLICATION NUMBER: US/09/779,451

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

US-09-779-451-4

Query Match

Best Local Similarity 99.0%; Score 193; DB 10; Length 56;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIHSLSIESQNOEKNEQELLELDKWSIWMNF 36

Db 16 YTSLIHSLIESQNOEKNEQELLELDKWSIWMNF 51

RESULT 12

US-10-040-349B-2

Sequence 2, Application US/10040349B

Publication No. US20030082521A1

GENERAL INFORMATION:

APPLICANT: Brasseur, Robert

APPLICANT: Charlotteaux, Benoit

APPLICANT: Chevalier, Michel

APPLICANT: El Habib, Rphaelle

APPLICANT: Kriell, Tino

TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

FILE REFERENCE: 01-078-A

CURRENT APPLICATION NUMBER: US/10/040,349B

CURRENT FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

US-10-040-349B-2

Query Match

Best Local Similarity 99.0%; Score 193; DB 9; Length 177;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIHSLSIESQNOEKNEQELLELDKWSIWMNF 36

Db 104 YTSLIHSLIESQNOEKNEQELLELDKWSIWMNF 139

RESULT 13

US-10-059-271-84

Sequence 84, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

FILE REFERENCE: ALBRE-22

CURRENT APPLICATION NUMBER: US/10/059,271

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: DE 101 06 295

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

US-10-059-271-84

Query Match

Best Local Similarity 99.0%; Score 193; DB 9; Length 221;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIHSLSIESQNOEKNEQELLELDKWSIWMNF 36

Db 131 YTSLIHSLIESQNOEKNEQELLELDKWSIWMNF 166

RESULT 14

US-10-059-271-81

Sequence 81, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

; TITLE OF INVENTION: BEING IMMOBILIZED  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 81  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-81

Query Match 99.0%; Score 193; DB 9; Length 232;  
Best Local Similarity 97.2%; Pred. No. 7.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36  
|||:|||||  
Db 144 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 179

RESULT 15  
US-10-059-271-82  
; Sequence 82, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPEKE, HEINRICH  
; APPLICANT: BUDD, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-82

Query Match 99.0%; Score 193; DB 9; Length 254;  
Best Local Similarity 97.2%; Pred. No. 8.1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36  
|||:|||||  
Db 166 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 201

Search completed: May 16, 2003, 12:10:25  
Job time : 16.759 secs



GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533a-537  
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Sequence: 1 YTSLYSLIESQNOQEKNEQLDLKWLAMNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
1 number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.\*
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  - 12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.\*
  - 13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.\*
  - 14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.\*
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  - 23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	194	100.0	36	22	ABB00638
2	194	100.0	36	22	ABB02115
3	194	100.0	36	22	AAU13186
4	194	100.0	36	22	AAH77633
5	194	100.0	850	16	AAH67724
6	192	99.0	268	19	AAV22817
7	192	99.0	268	23	ABG68288
8	192	99.0	855	12	AAH14905
9	192	99.0	855	18	AAW1581
10	192	99.0	855	20	AAH88113

11	191	98.5	233	19	AAV22854	SEQ ID NO. 50 from
12	191	98.5	233	23	ABG68325	Envelope protein g
13	191	98.5	268	19	AAV22813	SEQ ID NO. 9 from
14	191	98.5	268	23	ABG68284	Envelope protein g
15	191	98.5	269	19	AAV22816	SEQ ID NO. 12 from
16	191	98.5	269	23	ABG68287	Envelope protein g
17	191	98.5	855	10	AAH94507	Sequence encoded b
18	191	98.5	855	19	AAW43069	HIV-1 gp120 protei
19	190	97.9	269	19	AAV22850	SEQ ID NO. 46 from
20	190	97.9	269	23	ABG68321	Envelope protein g
21	189	97.4	36	16	AAH64364	DP-178 derived fro
22	189	97.4	36	17	AAH98398	DP178 corresponds
23	189	97.4	36	18	AAH17011	HIV-1 derived pept
24	189	97.4	36	19	AAV22912	SEQ ID NO. 108 fro
25	189	97.4	36	19	AAV22805	SEQ ID NO. 1 from
26	189	97.4	36	20	AAV31955	Synthetic peptide
27	189	97.4	36	20	AAV31974	HIV-1 LAI gp41 T-2
28	189	97.4	36	21	AAH52855	T20/DP178 peptide
29	189	97.4	36	21	AAH52858	T20/DP178 peptide
30	189	97.4	36	21	AAH52818	HIV-1 isolate LAI
31	189	97.4	36	21	AAH14533	Core polypeptide f
32	189	97.4	36	21	AAH86655	Core polypeptide f
33	189	97.4	36	21	AAH88729	Core polypeptide f
34	189	97.4	36	21	AAH89135	Core polypeptide f
35	189	97.4	36	21	AAH89136	Core polypeptide f
36	189	97.4	36	21	AAH89242	Core polypeptide f
37	189	97.4	36	21	AAH89424	Core polypeptide f
38	189	97.4	36	21	AAH89692	Core polypeptide f
39	189	97.4	36	21	AAH89735	Core polypeptide f
40	189	97.4	36	21	AAH89777	Core polypeptide f
41	189	97.4	36	21	AAH89982	Core polypeptide f
42	189	97.4	36	21	AAH89983	Core polypeptide f
43	189	97.4	36	21	AAH89983	Core polypeptide f
44	189	97.4	36	22	AAU70179	HIV viral envelope
45	189	97.4	36	22	AAU70741	HX82 transmembrane

ALIGNMENTS

RESULT 1	ABB00638	standard; Peptide; 36 AA.
ID	ABB00638	
AC	ABB00638	
XX		
DT	03-JAN-2002	(first entry)
DE	Viral DP178/107-like region peptide T720.	
XX		
KW	Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;	
KW	virulence; heptad repeat region; transmembrane protein; gp121; HRI; HR2;	
KW	infection.	
XX		
OS	Virididae.	
XX		
FT	Key	Location/Qualifiers
FT	Modified-site	1
FT	Modified-site	/note="N-terminal is substituted by ac"
FT	Modified-site	36
FT	Modified-site	/note="C-terminal amide"
XX		
PN	WO200164013-A2.	
XX		
PD	07-SEP-2001.	
XX		
PF	07-FEB-2001; 2001WO-US03988.	
XX		
PR	29-FEB-2000; 2000US-0515965.	
XX		
PA	(TRIM-) TRIMERIS INC.	
XX		
PI	Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;	





ID	ABG68288 standard; Protein: 268 AA.	
XX	ABG68288;	
XX	07-OCT-2002 (first entry)	
XX	Envelope protein gp41 from HIV clade B strain #7.	
XX	HIV: glycoprotein: gp41; antigen; helical conformation;	
XX	virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;	
XX	viral envelope protein; vaccine; virucide; anti-HIV.	
XX	Human immunodeficiency virus type 1 clade B.	
XX	US6271198-B1.	
XX	07-AUG-2001.	
XX	05-NOV-1997; 97US-0965056.	
XX	16-JUN-1997; 97US-049787P.	
XX	06-NOV-1996; 96US-0743698.	
XX	16-JUN-1997; 97US-0876698.	
XX	(GETH ) GENENTECH INC.	
XX	Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasmnik MA;	
XX	Wells JA;	
XX	WPI: 2002-487624/52.	
XX	New cyclic peptides from human immune deficiency virus gp41, useful for	
XX	treatment or prevention of HIV infection, are constrained to have	
XX	alpha-helical conformation	
XX	Disclosure: Column 147-150; 175pp; English.	
XX	The invention relates to cyclic peptides (A) with a constrained helical	
XX	conformation, derived from gp41 (glycoprotein 41, a viral envelope	
XX	protein) protein of human immunodeficiency virus (HIV). The cyclic	
XX	peptides have formulas given in the specification part of which are	
XX	derived from a consensus sequence of gp41 derived from HIV clades A, B,	
XX	C, D, E or O. The peptides are used to cause induction of a specific	
XX	immune response, resulting in antibodies that prevent virus-induced	
XX	membrane fusion. The peptides are used to treat subjects with, or at risk	
XX	of, HIV infection, either as antilution/anti-infection agents or,	
XX	preferably where associated with a carrier, as an immunogen (including as	
XX	vaccine) to raise antibodies. The antibodies may be used for diagnosis or	
XX	prevention/treatment of HIV infection (i.e. acquired immunodeficiency	
XX	syndrome, AIDS), e.g. prevention of mother-to-child transmission or in	
XX	cases of health care accidents. The peptides can be based on specific HIV	
XX	strains, e.g. breakthrough isolates of HIV that have developed during	
XX	vaccine trials, so a combination of them should cover a wide range of	
XX	protection. The present sequence is gp41 protein from a particular	
XX	HIV clade used to derive a consensus sequence of gp41.	
XX	Sequence 268 AA.	
XX	Query Match: 99.0%; Score 192; DB 23; Length 268;	
XX	Best Local Similarity 97.2%; Pred. No. 4.7e-16;	
XX	Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0.0	
XX	1 YTSITYSLIEESQNOOEKNECELELDKASIMNMF 36	
XX	168 YTSITYSLIEESQNOOEKNECELELDKASIMNMF 203	
XX	RESULT 8	
XX	AAR14905	
XX	AAR14905 standard; Protein: 855 AA.	
XX	AAR14905;	



```

DT 17-DEC-2001 (updated)
DT 05-FEB-1992 (first entry)
XX
DE HIV-1 BA-L clone-encoded env protein.
XX
KW human immunodeficiency virus; United States; MN isolate; AIDS;
XX viral envelope protein.
XX
OS Human immunodeficiency virus-1;
XX
PN USN7599491-N.
XX
PD 15-OCT-1991.
XX
PF 17-OCT-1990; 90US-0183830.
XX
PR 17-OCT-1990; 90US-0599491.
XX
PA (USSH ) NAT INST OF HEALTH.
XX
PS Reitz M;
XX
DR WPI: 1991-346752/47.
DR N-PSDB; AAQ14753.
XX
PT US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are
XX useful in therapeutics, vaccines and diagnostic tests
XX
PS Example 3; Fig 9; 61pp; English.
XX
CC A HindIII fragment of unintegrated viral DNA representing the HIV-1
CC (Ba-L) genome was cloned by standard techniques into lambda phage
CC Charon 28 DNA from total DNA of peripheral blood macrophages
CC infected with and producing HIV-1 (Ba-L). A positive clone was
CC selected by hybridisation using a HIV-1 envelope probe. This clone,
CC designated Ba-L1, contained the entire env gene. The insert was
CC subcloned and sequenced and the amino acid sequence deduced from
CC it.
CC (Note: Revised entry submitted to correct the patent number format of
CC US Government-owned NTIS applications to prevent clashes with ongoing US
CC granted patent numbers. For further information please visit the Derwent
CC web site at www.derwent.com/dwpl/updates/ntis-us.html.)
XX
SO Sequence 855 AA:

Query Match 99.0%; Score 192; DB 12; Length 855;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSIYSLIESONOQEKNEQELLEDKWSLWNMF 36
|||:|||||:|||||:|||||:|||||:|||||:
636 YTSIYSLIESONOQEKNEQELLEDKWSLWNMF 671

RESULT 9
AAW11581
ID AAW11581 standard; Protein; 855 AA.
XX
AC AAW11581;
XX
DT 25-MAR-1997 (first entry)
XX
DE Human Immunodeficiency Virus-1 strain BA-L envelope protein.
XX
KW Acquired immune deficiency syndrome; AIDS; envelope protein;
XX env gene; vaccine.
XX
OS Human immunodeficiency virus type 1 (strain BA-L).
XX
PN US5576000-A.
XX
PD 19-NOV-1996.

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PF 17-OCT-1990; 90US-0599491.
XX
PR 17-OCT-1990; 90US-0599491.
PR 25-FEB-1993; 93US-0022835.
PR 15-FEB-1993; 95US-0388809.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Franchini G, Gallo RC, Gartner S, Lori FC, Markham PD;
PI Popovic M, Reitz MS;
XX
DR WPI: 1997-011206/01.
DR N-PSDB; AAT58551.
XX
PT New isolated envelope protein of HIV-1 strain BA-L and recombinant
XX equivalents - useful as immunogens for vaccines and antibody prodn.,
XX typical of US clinical isolates
XX
PS Claim 1; Fig 9; 86pp; English.
XX
CC A HindIII fragment of unintegrated viral DNA representing the BA-L
CC genome was cloned into lambda phage Charon 28 DNA from total DNA of
CC peripheral blood lymphocytes infected with and producing HIV-1(BA-L).
CC A positive clone was selected by hybridisation using a HIV-1 env
CC probe. This clone, designated BA-L1, was found to contain the
CC entire gene for the envelope protein on a 2.8 kb HindIII-XbaI
CC fragment and a 0.4 kb EcoRI-HindIII fragment. When cloned together
CC these fragments comprise the env gene, as well as the coding regions
CC for rev and the rev-responsive element of env, both necessary for
CC efficient expression in eukaryotic cells. The claimed recombinantly
CC produced envelope protein can be used as an immunogen for raising
CC antibodies against HIV.
XX
SO Sequence 855 AA:

Query Match 99.0%; Score 192; DB 18; Length 855;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSIYSLIESONOQEKNEQELLEDKWSLWNMF 36
|||:|||||:|||||:|||||:|||||:|||||
636 YTSIYSLIESONOQEKNEQELLEDKWSLWNMF 671

RESULT 10
AAW88113
ID AAW88113 standard; Protein; 855 AA.
XX
AC AAW88113;
XX
DT 09-APR-1999 (first entry)
XX
DE Env protein of the BA-L strain of Human immunodeficiency virus type 1.
XX
KW HIV-1; HIV-1 strain BA-L; env protein; vaccine;
XX immunotherapy; HIV infection; immunogen; HIV-1 diagnosis.
XX
OS Human immunodeficiency virus type 1.
XX
FH Key Location/Qualifiers
FT MISC-difference 11 /note="Gln encoded by CG"
XX
PD 09-FEB-1999.
XX
PF 14-MAY-1996; 96US-0647714.
XX
PR 17-OCT-1990; 90US-0599491.
PR 25-FEB-1993; 93US-0022835.
PR 15-FEB-1995; 95US-0388809.
PR 14-MAY-1996; 96US-0647714.

```

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA Franchini G, Gallo RC, Gartner S, Lori FC, Markham PD;  
 PI Popovic M, Reitz MS;  
 XX WPI: 1999-152779/13.  
 DR N-PSDB: AAX04767.  
 PT DNA encoding env protein of the human immune deficiency virus  
 PT isolate Ba-L - useful for producing protein for use in vaccines, as  
 PT assay reagent and to generate antibodies  
 PS Example 1; Fig 9A-C; 87pp; English.  
 CC The present sequence represents the envelope protein of the BA-L  
 CC (ATCC 40880) strain of Human immunodeficiency virus type 1 (HIV-1)  
 CC strain MN-ST1. BA-L is more typical of United States isolates of  
 CC HIV-1 than previously known strains. Recombinant, complete env protein  
 CC of the BA-L strain is used as a vaccine component and for immunotherapy  
 CC of existing HIV infections, to detect HIV-specific antibodies, e.g. in  
 CC donated blood, and as an immunogen to raise specific antibodies, for  
 CC HIV-1 diagnosis.  
 SQ Sequence 855 AA;  
 SO  
 Query Match 99.0%; Score 192; DB 20; Length 855;  
 Best Local Similarity 97.2%; Pred. No. 1.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLIYSLIEESQNOEKNEOELLFDKWSLWMPF 36  
 DB 636 YTSIYSLIEESQNOEKNEOELLFDKWSLWMPF 671  
 RESULT 11  
 ID AAY22854 standard; Protein: 233 AA.  
 AC AAY22854;  
 XX  
 DT 19-AUG-1999 (first entry)  
 DE SEQ ID NO. 50 from WO9820036.  
 KM HIV: gp41 protein; constrained helical peptide; HIV infection;  
 KM vaccine; antibody; viral membrane fusion; viral infectivity;  
 KM ligand affinity purification; protein A replacement;  
 KM immunoglobulin purification; epitope mimic.  
 OS Human immunodeficiency virus.  
 PN WO9820036-A1.  
 PD 14-MAY-1998.  
 PF 05-NOV-1997; 97WO-US20069.  
 PR 16-JUN-1997; 97US-0876698.  
 PR 06-NOV-1996; 96US-0743698.  
 PA (GETH ) GENENTECH INC.  
 PI Wells JA;  
 PI Wells JA;  
 DR WPI: 1998-286866/25.  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa-peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection

PS Claim 11; Page 192-193; 279pp; English.  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 SQ Sequence 233 AA;  
 SO  
 Query Match 98.5%; Score 191; DB 19; Length 233;  
 Best Local Similarity 97.2%; Pred. No. 5.4e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLIYSLIEESQNOEKNEOELLFDKWSLWMPF 36  
 DB 168 YTSIYSLIEESQNOEKNEOELLFDKWSLWMPF 203  
 RESULT 12  
 ID ABG68325 standard; Protein: 233 AA.  
 AC ABG68325;  
 XX  
 DT 07-OCT-2002 (first entry)  
 DE Envelope protein gp41 from HIV clade B strain #44.  
 KM HIV: glycoprotein; gp41; antigen; helical conformation;  
 KM virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;  
 KM viral envelope protein; vaccine; virucide; anti-HIV.  
 OS Human immunodeficiency virus type 1 clade B.  
 PN US6271198-B1.  
 PD 07-AUG-2001.  
 PF 05-NOV-1997; 97US-0965056.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 06-NOV-1996; 96US-0743698.  
 PR 16-JUN-1997; 97US-0876698.  
 PA (GETH ) GENENTECH INC.  
 PI Bralsted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 DR WPI: 2002-487624/52.  
 PT New cyclic peptides from human immune deficiency virus gp41, useful for  
 PT treatment or prevention of HIV infection, are constrained to have  
 PT alpha-helical conformation  
 PS Disclosure: Column 207-208; 175pp; English.





GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-537  
Perfect score: 194  
Sequence: 1 YTSLIYSLIEESONQOEKNEDELLDKWASLWMMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues  
1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	98.5	443	2 C41621	env polypeptide p
2	191	98.5	856	1 VCLJ3W	env polypeptide pr
3	191	98.5	861	1 VCLJSC	env polypeptide pr
4	189	97.4	851	2 S33985	env polypeptide -
5	189	97.4	854	2 S13288	env protein - huma
6	189	97.4	856	1 VCLJH3	env polypeptide pr
7	189	97.4	861	1 VCLJLV	env polypeptide pr
8	188	96.9	357	2 S21994	envelope protein g
9	188	96.9	358	2 S21998	envelope protein g
10	187	96.4	357	2 S21996	envelope protein g
11	184	94.8	847	2 T09448	envelope glycoprot
12	184	94.8	847	2 S13289	env protein - huma
13	183	94.3	445	2 A41621	env polypeptide M
14	182	93.8	358	2 S22002	envelope protein g
15	182	93.8	358	2 S22000	envelope protein g
16	182	93.8	358	2 S70417	envelope protein g
17	182	93.8	852	2 T12016	envelope glycoprot
18	182	93.8	859	1 VCLJMN	env polypeptide pr
19	181	93.3	357	2 S22004	envelope protein g
20	181	93.3	855	1 VCLJAL	env polypeptide pr
21	180	92.8	856	1 VCLJVL	env polypeptide pr
22	179	92.3	853	2 S34384	envelope polypept
23	179	92.3	855	1 VCLJZR	env polypeptide pr
24	178	91.8	357	2 S22006	envelope protein g
25	178	91.8	843	1 H44001	env polypeptide pr
26	177	91.2	846	1 VCLJND	env polypeptide pr
27	175	90.2	357	2 S21992	envelope protein g
28	175	90.2	852	1 VCLJBR	env polypeptide pr
29	173	89.2	729	1 VCLJKB	env polypeptide pr

30	173	89.2	861	1 VCLJKB	env polypeptide pr
31	172	88.7	859	2 T01672	envelope polypept
32	169	87.1	454	2 B41621	env polypeptide D
33	168	86.6	868	1 VCLJH4	env polypeptide -
34	165	85.1	136	2 J00266	envelope polypept
35	165	85.1	136	2 J00266	envelope polypept
36	155	79.9	854	1 VCLJSI	env polypeptide pr
37	154	79.4	856	1 A44963	env polypeptide pr
38	152	78.4	357	2 S21990	envelope protein g
39	141	72.7	877	2 S49197	envelope protein p
40	124	63.9	863	2 A53034	gag polypeptide -
41	86	44.3	881	1 VCLJG3	env polypeptide -
42	86	44.3	881	1 S03068	env protein - huma
43	86	44.3	889	1 VCLJG5	env polypeptide -
44	85	43.8	151	2 S30448	env protein - huma
45	85	43.8	151	2 S30452	env protein - huma

## ALIGNMENTS

RESULT 1  
C41621  
env polypeptide p - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polypeptide  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Guila, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi  
A:Reference number: A41621; M01D:92107924; PMID:1763038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:G328631; PIDN:AA803792.1; PID:G555015  
A:Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP2>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:424-443/Domain: transmembrane #status predicted <TMN>  
F:223,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:  
Query Match 98.5% Score 191; DB 2; Length 443;  
Best Local Similarity 97.2% Pred. No. 1.9e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLIYSLIEESONQOEKNEDELLDKWASLWMMF 36  
DB 378 YTSLIYSLIEESONQOEKNEDELLDKWASLWMMF 413  
RESULT 2  
VCLJ3W  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
C:Accession: A24774  
R:Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks,  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the  
A:Reference number: A24774; M01D:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:G1906382  
C:Genetics:

```

A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-50/Product: coat protein gp120 #status predicted <GP1>
F:507-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459
Query Match          98.5%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 3,9e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY      1 YTSLYSLIEESONQOEKNEDELLELDKMASLWMP 36
Db-    638 YTSLYSLIEESONQOEKNEDELLELDKMASLWMP 673
RESULT 3
VCLJSC
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
Alternate names: coat polyprotein
Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
R:Gungo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal, P.; Gallo, R.C. Retroviruses, pp. 161-172. In: AIDS, Vol. 1, New York: Raven Press, 1987.
A>Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3365091
A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-861/Product: env polyprotein #status predicted <PPP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396
Query Match          98.5%; Score 191; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 3,9e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Caps 0;
OY      1 YTSLYSLIEESONQOEKNEDELLELDKMASLWMP 36
Db       643 YTSLYSLIEESONQOEKNEDELLELDKMASLWMP 678
ULT 4
S33985
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C:Accession: S33985
R:Carlini, F.
Submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199
C:Superfamily: type E retrovirus env polyprotein
Query Match          97.4%; Score 189; DB 2; Length 851;
Best Local Similarity 97.2%; Pred. No. 6,8e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY      1 YTSLYSLIEESONQOEKNEDELLELDKMASLWMP 36
Db       633 YTSLYSLIEESONQOEKNEDELLELDKMASLWMP 668

```

RESULT 5

S13288

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 97.4%; Score 189; DB 2; Length 854;

Best Local Similarity 97.2%; Pred. No. 6.8e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLIYSLIEESONQOEKNEDELLEDKWASLWMMF 36

Db 636 YTSLIHSLIEESONQOEKNEDELLEDKWASLWMMF 671

RESULT 6

VCLJH3

env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03973

R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starck, B.; Josephs, S.F.; D

enberg, J.A.; Papas, T.S.; Ghayour, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A:Reference number: A93353; MUID:85111123; PMID:2578615

A:Accession: A03973

A:Molecule type: DNA

A:Residues: 1-856 <RAT>

A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-51/Product: exterior membrane glycoprotein #status predicted <EXT>

F:512-856/Product: transmembrane glycoprotein #status predicted <TM>

F:88-136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,

F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 97.4%; Score 189; DB 1; Length 856;

Best Local Similarity 97.2%; Pred. No. 6.8e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLIYSLIEESONQOEKNEDELLEDKWASLWMMF 36

Db 638 YTSLIHSLIEESONQOEKNEDELLEDKWASLWMMF 673

RESULT 7

VCLJIV

env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03975

R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.

Cell 40, 9-17, 1985

A:Title: Nucleotide sequence of the AIDS virus, LAV.

```

A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAI>
A:Cross-references: GB:K02013; NID:g3326417; PIDN:AAH59751.1; PID:g3326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
E:1-30/Domain: signal sequence #status predicted <Sig>
E:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
E:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,416,421,426,430,435,440,445,450,455,460,465,470,475,480,485,490,495,500,505,510,515,520,525,530,535,540,545,550,555,560,565,570,575,580,585,590,595,600,605,610,615,620,625,630,635,640,645,650,655,660,665,670,675,680,685,690,695,700,705,710,715,720,725,730,735,740,745,750,755,760,765,770,775,780,785,790,795,800,805,810,815,820,825,830,835,840,845,850,855,860,865
F:616,621,630,642,679,755,821/Binding site: carboxydrate (Asn) (covalent) #status predicted
Query Match 97.4%; Score 189; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. NO. 6.9e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 YTSLSYSLIEESONOEKNEDELLDLKWSLWNF 36
|||||:|||||:|||||:|||||:|||||:|||||:
643 YTSLSYSLIEESONOEKNEDELLDLKWSLWNF 678

```

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RESULT 8
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate Z7B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuler, H., Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HTV-1 in blood and cerebrospinal fluid as determined by polymerase chain reaction PCR
A:Reference number: S21994
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STEL>
A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:960180
R:Steuler, H., Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-140,'X','142-312','X','314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:960179
superfamily: type E retrovirus env polyprotein

Query Match          96.9%; Score 188; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.3e-15;
Matches   34; Conservative    2; Mismatches     0; Indels      0; Gaps       0;

QY         1 YTSLSYSLESQNQEKNDELELDKWKASIMNF 36
            ||::|||:|||||::::|:|||||||:|||||||
Db        139 YTTLTYLTIESNQNEKEDELLEDKWASIMNF 174

RESULT 9
S21998
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 28
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21998; S70425
R:Steuler, H., Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HTV-1 in blood and cerebrospinal fluid as determined by polymerase chain reaction PCR
A:Reference number: S21990
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <STEL>
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A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAAA3630.1; PID:960183
R:Strular, H.; Storch-Hagenlocher, B.; Milderann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and ce
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70425
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-222, 'X', 224-358 <STE2>
A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAAA3630.1; PID:960183
C:Superfamily: type E retrovirus env polypeptide

Query Match          96.9%; Score 188; DB 2; Length 358;
Best Local Similarity 94.4%; Pred. No. 3.3e-15;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy      1  YTSLYISLIEESONOQEKNEDELLELDKMASLNMF 36
        |||||:||||:||||:||||:||||:||||:||||:
Db      140 YTSLYITLIEESONOQEKNEDELLELDKMASLNMF 175

```

[illegible]







RESULT 2			
ID	ENV_HV1M1	STANDARD;	PRT; 856 AA.
AC	ENV_HV1M1		
DT	P31872;		
DT	01-JUL-1993 (Rel. 26, Created)		
DT	01-JUL-1993 (Rel. 26, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
ENV.			
CS	Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_Taxid=31678;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=66218077; PubMed=2423250;		
RA	Starotch B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.		
RA	Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;		
RT	"Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";		
RL	Cell 45:637-648(1986).		
CC	-1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.		
CC			
CC	PIR; A24774; VCLJ3W.		
DR	Interpro: IPR000328; Env_GP41.		
DR	Interpro: IPR000777; GP120.		
DR	Pfam: PF00516; GP120; 1.		
DR	Pfam: PF00517; GP41; 1.		
KW	AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;		
KT	Signal.		
KT	1		29

RESULT 3	ENV_HV1B8	STANDARD:	PRT:	851 AA.
ID	ENV_HV1B8			
AC	P04582;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentiviruses.			
OX	NCBI_TaxID=11684;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85111123; PubMed=2578615;			
RA	Reiner L., Haseline W., Patarca R., Livak K.J., Starcich B.R.,			
RA	Josephs S.F., Doran E.R., Ratafski J.A., Whitehorn E.A.,			
RA	Baumeister K., Ivanoff L., Pettenay S.R. Jr., Pearson M.L.,			
RA	Lautenberger J.A., Paps T.S., Ghayeb J., Chang N.T., Gallo R.C.,			
RT	Wong-Staal F.;			
RL	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
CC	Nature 313:227-284(1985).			
CC				
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DR EMBL, K02011; AAA44661.1; -  
 DR HIV, K02011; ENVSBH8.  
 DR GlycosultedB: P04582; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.

FT SIGNAL 1 30  
 FT CHAIN 31 506  
 FT CHAIN 507 851  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
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 FT DISULFID 378 440  
 FT DISULFID 385 413  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
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 FT CARBOHYD 356 356  
 FT CARBOHYD 366 366  
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 FT CARBOHYD 458 458  
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 FT CARBOHYD 620 620  
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 FT CARBOHYD 669 669  
 FT CARBOHYD 745 745  
 FT CARBOHYD 811 811  
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 SO SEQUENCE

Query Match 97.4%; Score 189; DB 1; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 1.1e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLSEESNOOEKNEDELLEDKWASLWNMF 36  
 DB 633 YTSLSLSEESNOOEKNEDELLEDKWASLWNMF 668

ENV\_HV1S3 STANDARD; PRT; 852 AA.  
 AC P19549; 01-FEB-1991 (rel. 17, Created)

DT 01-FEB-1991 (rel. 17, last sequence update)  
 DT 16-OCT-2001 (rel. 40, last annotation update)  
 DE Envelope polypeptide Gp160 precursor [Contains: Exterior membrane  
 DE glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OC NCBI\_Taxid=11690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90317906; PubMed=2370688;  
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;  
 RT "Human immunodeficiency virus type 1 cellular host range,  
 RT replication, and cytopathicity are linked to the envelope region of  
 RT the viral genome";  
 RL J. Virol. 64:4016-4020(1990).  
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DR EMBL, M38427; AAA45067.1; -  
 DR HIV, M38427; ENVSEF33.  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.

FT SIGNAL 1 31  
 FT CHAIN 32 506  
 FT CHAIN 507 852  
 FT DISULFID 53 73  
 FT DISULFID 118 206  
 FT DISULFID 125 197  
 FT DISULFID 130 156  
 FT DISULFID 219 248  
 FT DISULFID 229 240  
 FT DISULFID 297 331  
 FT DISULFID 377 439  
 FT DISULFID 384 412  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 142 142  
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 FT CARBOHYD 189 189  
 FT CARBOHYD 198 198  
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 FT CARBOHYD 290 290  
 FT CARBOHYD 296 296  
 FT CARBOHYD 332 332  
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 FT CARBOHYD 621 621  
 FT CARBOHYD 633 633

FT CAROHD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 852 AA; 96663 MW; EE7BBFD23C9910D CRC64;  
 Query Match 97.4%; Score 189; DB 1; Length 852;  
 Best Local Similarity 94.4%; Pred. No. 1.1e-15;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYSLIEESQNOEKNQOELELDKWSLWNMF 36  
 DB 634 YTSLYSLIEESQNOEKNQOELELDKWSLWNMF 669

RESULT 5  
 ENV\_HV1B1 STANDARD: PRT; 856 AA.  
 ID ENV\_HV1B1  
 AC P03375;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 OS ENV.  
 OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).  
 OC Viruses: Retrovirus; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11678;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=8511123; PubMed=2578615;  
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Peteway S.R., Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Chrayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;  
 RA "Complete nucleotide sequence of the AIDS virus, HTLV-III.";  
 RA Nature 313:277-284 (1985).  
 RL [2]  
 RN [2]  
 RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.  
 RA MEDLINE=90285159; PubMed=2355006;  
 RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N., Gregory T.J.;  
 RA "Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in Chinese hamster ovary cells";  
 RL J. Biol. Chem. 265:10373-10382 (1990).  
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 CC -----  
 CC EMBL: M15654; AAA44205.1; -  
 DR PIR: A03973; VCLJH3.  
 DR HIV; M15654; ENVSBH102.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 1 511  
 FT CHAIN 512 856  
 FT CHAIN 857 966  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331

FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CAROHD 88 88  
 FT CAROHD 136 136  
 FT CAROHD 141 141  
 FT CAROHD 146 146  
 FT CAROHD 156 156  
 FT CAROHD 160 160  
 FT CAROHD 186 186  
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 FT CAROHD 625 625  
 FT CAROHD 637 637  
 FT CAROHD 674 674  
 FT CAROHD 750 750  
 FT CAROHD 816 816  
 SQ SEQUENCE 856 AA; 97224 MW; 0BFB1A18931BB27 CRC64;

Query Match 97.4%; Score 189; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 1.1e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYSLIEESQNOEKNQOELELDKWSLWNMF 36  
 DB 638 YTSLYSLIEESQNOEKNQOELELDKWSLWNMF 673

RESULT 6  
 ENV\_HV1B2 STANDARD: PRT; 856 AA.  
 ID ENV\_HV1B2  
 AC P04578; 009779;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 OS ENV.  
 OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).  
 OC Viruses: Retrovirus; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11706;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=87299196; PubMed=3040055;  
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;  
 RA "Complete nucleotide sequences of functional clones of the AIDS virus";  
 RA AIDS Res. Hum. Retroviruses 3:57-69 (1987).  
 RL [2]  
 RN [2]  
 RP REVISIONS.  
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;  
 RA Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.  
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DR EMBL: K03455; AAB50262.1; -  
 DR EMBL: AF038399; AAB99976.1; -  
 DR EMBL: AF038319; AAC82596.1; -  
 DR HIV: K03455; ENVSHXB2.  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
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 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
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 FT CARBOHYD 156 156  
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 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 FT CARBOHYD 856 AA; 97212 MW; 6FABI6AF85107FE0 CR64;  
 SQ SEQUENCE

Query Match 97.4%; Score 189; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 1.1e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLIEESONQOEKNEQELLELDKWSLWNP 36  
 DB 638 YTSLSLIEESONQOEKNEQELLELDKWSLWNP 673

RESULT 7  
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 ID ENV\_HY1H3 STANDARD; PRT; 856 AA.

AC P04624;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).  
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxId=11707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85228248; PubMed=2988795;  
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,  
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;  
 RT "HIV-III env gene products synthesized in E. coli are recognized by  
 RT antibodies present in the sera of AIDS patients.";  
 RL Cell 41:979-986(1985).  
 CC -----  
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DR EMBL: M14100; AAA44679.1; -  
 DR HIV: M14100; ENVSHXB3.  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
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 FT CARBOHYD 406 406  
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 FT CARBOHYD 624 624

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FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 3373C68B84C1AFC CRC64;

Query Match
Best Local Similarity 97.4%; Score 189; DB 1; Length 856;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSEESONQOEKNEDELLEDKWASLWNMF 36
Db 638 YTSLSLSEESONQOEKNEDELLEDKWASLWNMF 673

RESULT 8
ENV_HV1LM STANDARD; PRT; 856 AA.
ID ENV_HV1LM 070626;
AC 15-JUL-1998 (Rel. 36, Created)
DE 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=82634;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RT Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1153(1994).

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CC -----
CC EMBL: U12055; AAAT6690.1; -
CC DR glycosultedb: 070626; -
CC DR InterPro: IPR000328; Env_GP41.
CC DR InterPro: IPR000777; GP120.
CC Pfam: PF00517; GP120; 1.
DR Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
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FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CE7E6687 CRC64;

Query Match
Best Local Similarity 97.4%; Score 189; DB 1; Length 856;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSEESONQOEKNEDELLEDKWASLWNMF 36
Db 638 YTSLSLSEESONQOEKNEDELLEDKWASLWNMF 673

RESULT 9
ENV_HV1BR STANDARD; PRT; 861 AA.
ID ENV_HV1BR 070626;
AC P03377;
DE 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099333; PubMed=2981635;
RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RT "Nucleotide sequence of the AIDS virus, LAV.";
RL Cell 40:9-17(1985).

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: K02013; AAB59751.1; -
CC DR EMBL: A04321; CAA00352.1; -
CC DR PIR: A03975; VCLIV.
CC DR HIV; K02013; ENV5BRU.
CC DR InterPro: IPR000328; Env_GP41.
CC DR InterPro: IPR000777; GP120.
CC Pfam: PF00517; GP120; 1.
DR Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30

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FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 861 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 210 BY SIMILARITY.
FT DISULFID 126 201 BY SIMILARITY.
FT DISULFID 131 162 BY SIMILARITY.
FT DISULFID 223 252 BY SIMILARITY.
FT DISULFID 233 244 BY SIMILARITY.
FT DISULFID 301 336 BY SIMILARITY.
FT DISULFID 383 450 BY SIMILARITY.
FT DISULFID 390 423 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 630 630 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 755 755 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 821 821 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 861 AA: 97487 MW: 04DE2BAD4E4FD63A CRC64:

Query Match
Best Local Similarity 97.4%: Score 189; DB 1; Length 861;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLIYSLIEESQNOEKNEDELLELDKWSLIMNF 36
||||:||||:||||:||||:||||:||||:||||:
DB 643 YTSLIHSLIEESQNOEKNEDELLELDKWSLIMNF 678

RESULT 10
ENV_HV1S1 STANDARD: PRT: 847 AA.
AC P19550:
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirinae.
OX NCBI_Taxid=11691;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA "Cheng-Wayer C., Outroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
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RL J. Virol. 64:4390-4398(1990).
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CC or send an email to license@isb.ch).
CC -----
DR EMBL: M65024; AAA5072.1;
DR HIV: M38428; ENVSEF162.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 338 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA: 96135 MW: 0A901317ED7FE2AB CRC64:

Query Match
Best Local Similarity 96.9%: Score 188; DB 1; Length 847;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 YTSLIYSLIEESQNOEKNEDELLELDKWSLIMNF 36
||||:||||:||||:||||:||||:||||:||||:
DB 629 YTNLIYTLIEESQNOEKNEDELLELDKWSLIMNF 664

RESULT 11
ENV_HV1MF STANDARD: PRT: 853 AA.
ID ENV_HV1MF
AC P19551:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```

SQ	SEQUENCE	853 AA;	96912 MW;	3377593B6F22ABA CRC64;
QY	Query March	Best Local Similarity	94.4%;	Pred. No. 2,7e-15;
D0	Matches 34;	Conservative	2;	Mismatches 0; Indels 0; Gaps 0;
ID	1 YTSLYSLIESQNQQEKNEQELLELDKWSIMWNF	36		
DB	636 YTSLSHSLIDESQNQQEKNQEELLELDKWSIMWNF	671		
RESULT 12				
ID	ENV_HV1W2	STANDARD;	PRT;	847 AA.
AC	P05880;			
DT	01-NOV-1988 (Rel. 09, Created)			
DT	01-NOV-1988 (Rel. 09, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope polyprotein gp160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (WM02 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11705;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86235450; PubMed=3012778;			
RA	Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D., Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.; "Genetic variation in HTLV-II/LAV over time in patients with AIDS or at risk for AIDS." Science 232:1548-1553(1986).			
RT	-I-			
SC	MISCELLANEOUS: ISOLATES WMU1, WMU2, AND WMU3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.			
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CC	or send an email to license@isb-sib.ch).			
DR	EMBL: M12507; AAB12990.1; -.			
DR	HIV: M12507; ENVSMWJ2.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	29	
FT	CHAIN	30	501	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	502	847	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	202	BY SIMILARITY.
FT	DISULFID	125	193	BY SIMILARITY.
FT	DISULFID*	130	152	BY SIMILARITY.
FT	DISULFID	215	244	BY SIMILARITY.
FT	DISULFID	225	236	BY SIMILARITY.
FT	DISULFID	293	326	BY SIMILARITY.
FT	DISULFID	372	435	BY SIMILARITY.
FT	DISULFID	379	408	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAG. . . ) (POTENTIAL).
FT	CARBOHYD	134	134	N-LINKED (GLCNAG. . . ) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAG. . . ) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAG. . . ) (POTENTIAL).
FT	CARBOHYD	155	155	N-LINKED (GLCNAG. . . ) (POTENTIAL).
FT	CARBOHYD	183	183	N-LINKED (GLCNAG. . . ) (POTENTIAL).
FT	CARBOHYD	184	184	N-LINKED (GLCNAG. . . ) (POTENTIAL).
FT	CARBOHYD	194	194	N-LINKED (GLCNAG. . . ) (POTENTIAL).
FT	CARBOHYD	231	231	N-LINKED (GLCNAG. . . ) (POTENTIAL).



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FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 847 AA; 96466 MW; CD1E33D73A5BCAE CRC64;

Query Match 95.4%; Score 185; DB 1; Length 847;
Best Local Similarity 94.4%; Pred. No. 3.5e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLYSLIESQNOEKNEQELLELDKWSLWMNF 36
Db 629 YTSLYSLIESQNOEKNEQELLELDKWSLWMNF 664

RESULT 13
ENV_HV1J3 STANDARD; PRT; 867 AA.
ID ENV_HV1J3
AC P12489;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RP MEDLINE=89352108; PubMed=2669897;
RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
"Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria."
RA AIDS Res. Hum. Retroviruses 5:411-419(1989).
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CC -----
CC EMBL: M21138; AAB03526.1; -
CC HIV; M21138; ENV5JH3.
DR InterPro: IPR000328; ENV_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.

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FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 388 457 BY SIMILARITY.
FT DISULFID 395 430 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 867 AA; 98399 MW; 5F231014B8B8680 CRC64;

Query Match 94.8%; Score 184; DB 1; Length 867;
Best Local Similarity 94.4%; Pred. No. 4.8e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLYSLIESQNOEKNEQELLELDKWSLWMNF 36
Db 649 YTSLYSLIESQNOEKNEQELLELDKWSLWMNF 684

RESULT 14
ENV_HV1MN STANDARD; PRT; 856 AA.
ID ENV_HV1MN
AC P05877;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP MEDLINE=88219542; PubMed=3169091;
RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
"Envelope sequences of two new United States HIV-1 isolates."
RL Virology 164:531-536(1988).
CC -i- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC -----
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-537  
Perfect score: 194  
Sequence: 1 YTSLLYSLEISQNOQEKNEQELLELDKRWASIMWVF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	194	100.0	848	15	069990 human immun
2	192	99.0	838	15	003806 human immun
3	192	99.0	854	15	078225 human immun
4	192	99.0	855	15	003805 human immun
5	191	98.5	42	15	069910 human immun
6	191	98.5	443	15	080023 human immun
7	191	98.5	841	15	041556 human immun
8	191	98.5	849	15	077368 human immun
9	191	98.5	849	15	080851 human immun
10	191	98.5	851	15	056110 human immun
11	191	98.5	851	15	080852 human immun
12	191	98.5	856	15	072993 human immun
13	191	98.5	856	15	041539 human immun
14	191	98.5	857	15	080170 human immun
15	191	98.5	858	15	080190 human immun
16	191	98.5	858	15	080188 human immun

17	191	98.5	859	15	080185 human immun
18	191	98.5	859	15	080180 human immun
19	191	98.5	859	15	080179 human immun
20	191	98.5	859	15	080177 human immun
21	191	98.5	859	15	080173 human immun
22	191	98.5	859	15	080850 human immun
23	191	98.5	862	15	080184 human immun
24	191	98.5	862	15	080183 human immun
25	191	98.5	862	15	080182 human immun
26	191	98.5	862	15	080178 human immun
27	191	98.5	862	15	080174 human immun
28	191	98.5	868	15	080186 human immun
29	190	97.9	848	15	069988 human immun
30	189	97.4	123	15	09YXR3 human immun
31	189	97.4	645	15	0993A6 human immun
32	189	97.4	747	15	070607 human immun
33	189	97.4	748	15	070606 human immun
34	189	97.4	752	15	070604 human immun
35	189	97.4	752	15	070605 human immun
36	189	97.4	752	15	070608 human immun
37	189	97.4	851	15	078243 human immun
38	189	97.4	852	15	069992 human immun
39	189	97.4	852	15	089797 human immun
40	189	97.4	854	15	085582 human immun
41	189	97.4	854	15	072502 human immun
42	189	97.4	855	15	09E1R7 human immun
43	189	97.4	856	15	092877 human immun
44	189	97.4	856	15	074599 human immun
45	189	97.4	856	15	074090 human immun

## ALIGNMENTS

RESULT 1  
ID 069990 PRELIMINARY: PRT; 848 AA.  
AC 069990;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DT Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=651;  
RX MEDLINE=96190564; PubMed=8627686;  
RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S., Karlsson G., Sodroski J., Morgado M., Galvao-Castro B., von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M., Hahn B.H.;  
RA Molecular cloning and analysis of functional envelope genes from human immunodeficiency virus type 1 sequence subtypes A through G. The WHO and NIAID Networks for HIV Isolation and Characterization.";  
RT J. Virol. 70:1651-1657(1996).  
RL [2]  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=651;  
RX MCEVILLY M.M.;  
RA Submitted (Apr-1994) to the EMBL/Genbank/DBJ databases.  
DR EMBL; U08442; AA04065.1;  
DR InterPro; IPR000328; Env\_Gp41.  
DR InterPro; IPR000777; Gp120.  
DR Pfam; PF00516; Gp120; 1.  
DR Pfam; PF00517; Gp41; 1.

```

FT CARBOHYD      598      598      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD      607      607      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD      619      619      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD      798      798      N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE      838 AA; 95328 MW; 11044B1CA10CFB4D CRC64;

Query Match
Best Local Similarity 97.2%; Score 192; DB 15; Length 838;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSYSLIESQNQEKNQELLELDKWSLWMPF 36
   |||:|||||||:|||||||:|||||||:|||||||:
Db 636 YTSIYSYLIESQNQEKNQELLELDKWSLWMPF 671

RESULT 4
ID Q03805 PRELIMINARY; PRT; 855 AA.
AC Q03805;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Envelope polypeptide GP160 precursor [CONTAINS: GP120; GP41].
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Beiter B.; Popovic M., Gartner S., Gallo R., Reed-Connole E.,
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL, M68893; AAA44191.1;
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120. 1.

Query Match
Best Local Similarity 97.2%; Score 192; DB 15; Length 854;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 854 AA; 97186 MW; 005FC81B5CBDFD8 CRC64;

Query Match
Best Local Similarity 97.2%; Score 192; DB 15; Length 854;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSYSLIESQNQEKNQELLELDKWSLWMPF 36
   |||:|||||||:|||||||:|||||||:|||||||:
Db 636 YTSIYSYLIESQNQEKNQELLELDKWSLWMPF 671

RESULT 3
ID Q78225 PRELIMINARY; PRT; 854 AA.
AC Q78225;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Env protein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-B4-1;
RC MEDLINE-91289160; PubMed-1905842;
RX Huang S.S., Boyle T.J., Lyerly H.K., Cullen B.R.;
RT Identification of the envelope V3 loop as the primary determinant of
RT cell tropism in HIV-1;
RL Science 253:71-74(1991);
RL EMBL, M63929; AAA75116.1;
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120. 1.
DR Pfam: PF00517; GP41. 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 854 AA; 97186 MW; 005FC81B5CBDFD8 CRC64;
```

DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.  
 FT SIGNAL 1 ?  
 FT CHAIN 509 855 EXTERIOR MEMBRANE GLYCOPROTEIN (GP120).  
 FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN (GP41).  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 209 BY SIMILARITY.  
 FT DISULFID 125 200 BY SIMILARITY.  
 FT DISULFID 130 160 BY SIMILARITY.  
 FT DISULFID 222 251 BY SIMILARITY.  
 FT DISULFID 232 243 BY SIMILARITY.  
 FT DISULFID 300 334 BY SIMILARITY.  
 FT DISULFID 380 443 BY SIMILARITY.  
 FT DISULFID 387 416 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 855 AA; 96988 MW; EC631A3B84180C8D CRC64;  
 Query Match 99.0%; Score 192; DB 15; Length 855;  
 Best Local Similarity 97.2%; Pred. No. 2, 7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 1 YTSLYSLIEESONOEKNEQELLELDKASLWNMF 36  
 DB 636 YTSIYSLIEESONOEKNEQELLELDKASLWNMF 671  
 RESULT 5  
 ID 069910 PRELIMINARY: PRT: 42 AA.  
 AC 069910;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE GP41 (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9421161; PubMed=7512731;  
 RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,  
 RA Keller P.M., Shaw A.R., Emini E.A.;  
 RT "Neutralization of divergent human immunodeficiency virus type 1  
 variants and primary isolates by IAM-41-2F5, an anti-gp41 human

RT monoclonal antibody.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).  
 DR EMBL: U06740; AAA19153.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 42 42  
 SQ SEQUENCE 42 AA; 5248 MW; 613EB1B2DBB31A722 CRC64;  
 Query Match 98.5%; Score 191; DB 15; Length 42;  
 Best Local Similarity 97.2%; Pred. No. 1, 6e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 1 YTSLYSLIEESONOEKNEQELLELDKASLWNMF 36  
 DB 7 YTSLYSLIEESONOEKNEQELLELDKASLWNMF 42  
 RESULT 6  
 ID 080023 PRELIMINARY: PRT: 443 AA.  
 AC 080023;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Env protein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92107924; PubMed=1763038;  
 RA Burger H., Weiser B., Flaherty K., Gulla J., Nguyen P.N., Gibbs R.A.;  
 RT "Evolution of human immunodeficiency virus type 1 nucleotide sequence  
 diversity among close contacts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11236-11240(1991).  
 DR EMBL: M77230; AAB03792.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 443 443  
 SQ SEQUENCE 443 AA; 50195 MW; 428E1A864E4D5DCD CRC64;  
 Query Match 98.5%; Score 191; DB 15; Length 443;  
 Best Local Similarity 97.2%; Pred. No. 1, 8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 1 YTSLYSLIEESONOEKNEQELLELDKASLWNMF 36  
 DB 378 YTSIYSLIEESONOEKNEQELLELDKASLWNMF 413  
 RESULT 7  
 ID 041556 PRELIMINARY: PRT: 841 AA.  
 AC 041556;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C17;  
 RX MEDLINE=98105804; PubMed=9445059;





RT "Evidence for the spread of immune-escape HIV-1 subtype B in the  
RT Korean population."  
RT Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AJ417426; CAD10138.1; -  
SO SEQUENCE 851 AA; 96667 MW; 2CAA47A865B9CFAD CRC64;

Query Match 98.5%; Score 191; DB 15; Length 851;  
Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIYSLIEESONQOEKNEOELLELDKNASLWNMF 36  
DB 633 YTSLIYSLIEESONQOEKNEOELLELDKNASLWNMF 668

RESULT 12

ID 072993 PRELIMINARY; PRT: 856 AA.  
AC 072993;  
01-NOV-1996 (TREMBlrel. 01, Created)  
01-NOV-1996 (TREMBlrel. 01, last sequence update)  
01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE Env protein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9628454; PubMed=8679299;  
RA Guillon C., Bedin F., Fouchier R.A., Schutemaker H., Gruters R.A.;  
RT "Completion of nucleotide sequences of non-synctium-inducing and  
RT syncytium-inducing HIV type 1 variants isolated from the same  
RT patient."  
RL AIDS Res. Hum. Retroviruses 11:1537-1541(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Guillon C., Bedin F., Fouchier R.A.M., Schutemaker H., Gruters R.A.;  
RT Submitted (AUG-1995) to the EMBL/Genbank/DBJ databases.  
DR EMBL: U34664; AAC54649.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SO SEQUENCE 856 AA; 96685 MW; BD1B19EE6B182DE0 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIYSLIEESONQOEKNEOELLELDKNASLWNMF 36  
DB 638 YTSLIYSLIEESONQOEKNEOELLELDKNASLWNMF 673

RESULT 13

ID 041539 PRELIMINARY; PRT: 856 AA.  
AC 041539;  
01-JAN-1998 (TREMBlrel. 05, Created)  
01-JAN-1998 (TREMBlrel. 05, last sequence update)  
01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C10;  
RX MEDLINE=98105804; PubMed=9445059;  
RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,

RA Walker B.D., Neumann A.U., Vermund S.H., Westlock J., Jackson S.,  
RA Fenamore E., Cao Y., Gao F., Kalam S., Kunstan K.J., McDonald D.,  
RA Williams N., Trkola A., Moore J.P., Wolinsky S.M.;  
RT "Immunological and virological analyses of persons infected by human  
RT immunodeficiency virus type 1 while participating in trials of  
RT recombinant gp120 subunit vaccines."  
RL J. Virol. 72:1552-1576(1998).  
DR EMBL: U84800; AAC58827.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT NON\_TER  
SO SEQUENCE 856 AA; 97545 MW; 7971B750E9ADFEA8 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIYSLIEESONQOEKNEOELLELDKNASLWNMF 36  
DB 638 YTSLIYSLIEESONQOEKNEOELLELDKNASLWNMF 673

RESULT 14

ID 080L70 PRELIMINARY; PRT: 857 AA.  
AC 080L70;  
01-MAR-2002 (TREMBlrel. 20, Created)  
01-MAR-2002 (TREMBlrel. 20, last sequence update)  
01-JUN-2002 (TREMBlrel. 21, last annotation update)  
DE GP160 protein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zheng N.N., Vella C., Easterbrook P.J., Daniels R.S.;  
RT "Selection on isolation of HIV-1 in peripheral blood mononuclear cells  
RT and Herpesvirus saimiri transformed T-cells is comparable."  
RT Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AJ418516; CAD10926.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
SO SEQUENCE 857 AA; 97590 MW; 3FE27F181D19DB31 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 857;  
Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIYSLIEESONQOEKNEOELLELDKNASLWNMF 36  
DB 639 YTSLIYSLIEESONQOEKNEOELLELDKNASLWNMF 674

RESULT 15

ID 080L90 PRELIMINARY; PRT: 858 AA.  
AC 080L90;  
01-MAR-2002 (TREMBlrel. 20, Created)  
01-MAR-2002 (TREMBlrel. 20, last sequence update)  
01-JUN-2002 (TREMBlrel. 21, last annotation update)  
DE GP160 protein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Zheng N.N., Vella C., Easterbrook P.J., Daniels R.S.;  
 RT "Selection on isolation of HIV-1 in peripheral blood mononuclear cells  
 and Herpesvirus saimiri transformed T-cells is comparable."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ418496; CAD10906.1; -;  
 DR InterPro; IPR000328; Env\_Gp41.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 SQ SEQUENCE 858 AA; 97600 MW; 444D6861F6C0355 CRC64;  
 Query Match 98.5%; Score 191; DB 15; Length 858;  
 Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Job completed: May 16, 2003, 11:19:48  
 Time : 26.3124 secs

AC AAY89136;

XX 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 574.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX WO9959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX MPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

XX Disclosure; Page 30; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

SU Sequence 36 AA;

Query Match 98.0%; Score 192; DB 21; Length 36;

Best Local Similarity 97.2%; Pred. No. 6.5e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIESONQOEKNEOELLELDKASLNNWF 36

DB 1 YTSLIHTLIESONQOEKNEOELLELDKASLNNWF 36

Search completed: May 16, 2003, 11:12:06  
 Job time : 32.4578 secs



XX Sequence 36 AA;  
SQ  
Query Match 98.0%; Score 192; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6.5e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 11  
AAB14533  
ID AAB14533 standard; peptide; 36 AA.  
AC AAB14533;  
XX  
XX  
DT 24-NOV-2000 (first entry)

HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).  
KW HIV-1; gp41 C-helical domain;  
KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
KW core 6-helix bundle; viral entry inhibition; immunogenic;  
KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
KW envelope glycoprotein; prophylaxis; therapy.  
XX  
XX  
OS Human immunodeficiency virus type 1.  
XX  
XX  
PN WO200040616-A1.  
XX  
XX  
PD 13-JUL-2000.  
XX  
XX  
PE 10-JAN-2000; 2000MO-US00456.  
XX  
XX  
PR 08-JAN-1999; 990S-0115404.  
PR 07-JAN-2000; 2000US-0480336.  
XX  
XX  
PA (WIID/) WIID C T.  
PA (WEIS/) WEIS C D.  
XX  
XX  
PI W1LD CT, Weiss CD;  
XX  
DR WPI; 2000-465959/40.  
XX  
XX  
PT Raising neutralizing antibody response to human immunodeficiency virus,  
PT comprises administering a polypeptide capable of forming a stable  
PT coiled-coil solution structure -  
PS Claim 13, Page 12; 97pp; English.

Sequences AAB14532-B14534 and AAB14569-B14602 represent specifically  
CC claimed peptides derived from the C-helical domain of the gp41  
CC envelope glycoprotein from a variety of HIV-1 isolates. The invention  
CC relates to raising a neutralising antibody response to a broad spectrum  
CC of HIV (human immunodeficiency virus) strains and isolates, comprising  
CC the administration of a peptide which corresponds to or mimics highly  
CC conserved portions of gp41 which are important in mediating the process  
CC of viral entry into host cells. Such peptides can correspond to or  
CC mimic the coiled coil solution structure of the N-helical domain  
CC (the heptad repeat region), or can correspond or mimic the C-helical  
CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
CC or the gp41 core 6-helix bundle, which is formed by the interaction  
CC of the N- and C-helical domains of three gp41 proteins. The peptides  
CC can be administered either singly or as a combination (particularly a  
CC combination of N-helical and C-helical peptides), and can be  
CC multimerised. For example, N- and C-helical domain peptides can  
CC be alternately linked together to form a peptide which mimics the  
CC core 6-helix bundle. Administration of the peptide(s) generates a  
CC humoral response, with the production of antibodies against gp41  
CC structures involved in viral entry. As these portions of gp41 are well  
CC conserved, such antibodies may be effective against a broad range of

CC HIV strains and isolates. The peptide compositions may be administered  
CC as a prophylactic or therapeutic vaccine to generate antibodies which  
CC reduce or inhibit the ability of HIV to infect uninfected cells. A  
CC composition comprising polyclonal or monoclonal antibodies can be  
CC administered to reduce HIV infection of uninfected cells. Antibodies  
CC raised against entry-relevant gp41 structures may also be used  
CC therapeutically and as tools to further elucidate the mechanism of HIV  
CC cell entry.  
XX  
XX  
SQ Sequence 36 AA;  
XX  
XX  
Query Match 98.0%; Score 192; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6.5e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 12  
AA88665  
ID AA88665 standard; peptide; 36 AA.  
XX  
XX  
AC AA88665;  
XX  
XX  
DT 23-MAY-2000 (first entry)  
XX  
XX  
DE Core polypeptide fragment T No. 20.  
XX  
XX  
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX  
XX  
OS Unidentified.  
XX  
XX  
PN WO95959615-A1.  
XX  
XX  
PD 25-NOV-1999.  
XX  
XX  
PE 20-MAY-1999; 99MO-US11219.  
XX  
XX  
PR 20-MAY-1998; 980S-0082279;  
XX  
XX  
PA (TRIM-) TRIMERS INC.  
XX  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
XX  
DR WPI; 2000-136792/12.  
XX  
XX  
PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence -  
PS Disclosure; Page 21; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AA88651-990055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.

```

XX OS Human immunodeficiency virus type 1.
XX PN WO200066622-A1.
XX PD 09-NOV-2000.
XX PF 05-MAY-2000; 2000WO-US12371.
XX PR 05-MAY-1999; 99US-0132686.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.
XX DR WPI: 2000-656493/63.
XX PT Administration of peptide agents with a sequence corresponding to a
XX PP partial-length T20/DP178 or T21/DP107 formyl peptide receptor
XX PR antagonist is used to modulate inflammation -
XX PD
XX Claim 12; Page 24; 148pp; English.
XX
XX The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a
XX CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is
XX CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a
XX CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178
XX CC interacts with members of the formyl peptide receptor (FPR) family and
XX CC thereby up-regulates an inflammatory response, and acts as a potent
XX CC chemotactic and activator of human peripheral blood phagocytes
XX CC (but not T cells). The present peptide can be used to modulate an
XX CC inflammatory response in a subject.
XX SQ Sequence 36 AA:
XX
XX Query Match 98.0%; Score 192; DB 21; Length 36;
XX Best Local Similarity 97.2%; Pred. No. 6.5e-17;
XX Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0
XX
XX 1 YTSLIHTLIESQNOQEKNEQELLELDKWSLWNMF 36
XX |||||:|||||:|||||:|||||:|||||
XX Db 1 YTSLIHTLIESQNOQEKNEQELLELDKWSLWNMF 36
XX
XX RESULT 9
XX AAB52688
XX ID AAB52688 standard; Peptide; 36 AA.
XX
XX AAB52688;
XX
XX 23-FEB-2001 (first entry)
XX DE T20/DP178 peptide fragment #66.
XX
XX Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;
XX KW formyl peptide receptor family; FPR; Inflammatory response up-regulation;
XX XM chemottractant.
XX
XX Human immunodeficiency virus type 1:
XX OS
XX PN WO200066622-A1.
XX PD 09-NOV-2000.
XX PF 05-MAY-2000; 2000WO-US12371.
XX PR 05-MAY-1999; 99US-0132686.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.
XX DR WPI: 2000-656493/63.

```

PX	Administration of peptide agents with a sequence corresponding to a
PT	partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor
PT	antagonist is used to modulate inflammation -
XX	
PS	Claim 12; Page 25; 148bp; English.
CC	
CC	The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a
CC	helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is
CC	located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a
CC	critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178
CC	interacts with members of the formyl peptide receptor (FPR) family and
CC	thereby up-regulates an inflammatory response, and acts as a potent
CC	chemoattractant and activator of human peripheral blood phagocytes
CC	(but not T cells). The present peptide can be used to modulate an
CC	inflammatory response in a subject.
SQ	
	Sequence 36 AA:
	Query Match 98.0%; Score 192; DB 21; Length 36;
	Best Local Similarity 97.2%; Pred. No. 6.5e-17;
	Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
OY	
Dn	1 YTSLSHTLFEESONOEKNEDELLEDDKWASLMNMF 36           :           :           :           1 YTSLSHTLFEESONOEKNEDELLEDDKWASLMNMF 36
RESULT 10	
AAB52818	
ID	AAB52818 standard; Peptide: 36 AA.
XX	
AC	AAB52818;
XX	
DT	23-FEB-2001 (first entry)
XX	
DE	T20/Dp178 peptide fragment #97.
KW	Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;
KM	formyl peptide receptor family; FPR; inflammatory response up-regulation;
KW	chemoattractant.
OS	
XS	Human immunodeficiency virus type 1.
PN	WO200066622-A1.
PD	
XX	09-NOV-2000.
PF	
XX	05-MAY-2000; 2000MO-US12371.
PR	
XX	05-MAY-1999; 99US-0132686.
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
XX	
XX	WPI: 2000-656493/63.
DR	
XX	
PT	Adminstration of peptide agents with a sequence corresponding to a
PT	partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor
PT	antagonist is used to modulate inflammation -
XX	
PS	Claim 14; Page 40; 148bp; English.
CC	
CC	The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a
CC	helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is
CC	located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a
CC	critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178
CC	interacts with members of the formyl peptide receptor (FPR) family and
CC	thereby up-regulates an inflammatory response, and acts as a potent
CC	chemoattractant and activator of human peripheral blood phagocytes
CC	(but not T cells). The present peptide can be used to modulate an
CC	inflammatory response in a subject

ID	AAV31974	standard; Peptide: 36 AA.
AC	AAV31974;	
XX		
XX	21-DEC-1999	(first entry)
DT		
XX		
XX	HIV-1 LAI gp41 T-20 peptide.	
DE		
XX		
XX	T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.	
KW		
XX		
OS	Human immunodeficiency virus type 1.	
XX		
XX	MO5948513-A1.	
PN		
PD	30-SEP-1999.	
XX		
XX	22-MAR-1999;	99WO-US06230.
PE		
XX		
PR	23-MAR-1998;	98US-0045920.
XX		
PR	01-MAY-1998;	98US-0071877.
XX		
PA	(TRIM-) TRIMERIS INC.	
XX		
PI	Kang M, Bray B, Lichty M, Mader C, Merutka G;	
DR	WPI: 1999-591038/50.	
XX		
PT	Methods of peptide synthesis, particularly used to produce T-20 or	
XX	T-20 like peptides	
XX		
PS	Disclosure: Page 9; 120pp; English.	
XX		
CC	The present sequence represents a peptide, designated T-20 (or	
CC	DP-178), that corresponds to amino acids 638-673 of the	
CC	transmembrane protein gp41 of HIV-1 LAI isolate. The invention	
CC	relates to methods for the synthesis of peptides, in particular	
CC	C- and N-terminal modified T-20 (see AAV31955) and T-20-like peptides.	
CC	The method involves synthesizing specific side-chain protected	
CC	peptide fragment intermediates (see AAV31956-73) of T-20 or a	
CC	T-20-like peptide on a solid support, coupling the protected	
CC	fragments in solution to form a protected T-20 or T20-like peptide,	
CC	followed by deprotection of the side chains to yield the final T-20	
CC	or T-20-like peptide. The invention also relates to individual	
CC	peptide fragments which act as intermediates in the synthesis of	
CC	peptides of interest (e.g. T-20), and to particular groups of	
CC	peptide fragments which act as intermediates in the synthesis of	
CC	the peptide of interest. The method allows for the large scale,	
CC	economical production of high purity peptides.	
XX		
XX		
SQ	Sequence	36 AA;
XX		
Query Match	98.0%;	Score 192;
Best Local Similarity	97.2%;	Pred. No. 6,5e-17;
Matches	35;	Conservative 1;
	Mismatches 0;	Indels 0;
	Gaps 0	
Oy	1	YTSLIHTLEESONOEKKEOELLELDKASLWNMF 36
	:     :     :     :	
Db	1	YTSLIHTLEESONOEKKEOELLELDKASLWNMF 36
RESULT 8		
ID	AAV32655	
AC	AAV32655;	
XX		
XX	23-FEB-2001	(first entry)
DT		
XX		
DE	T20/Dp178 peptide fragment #33.	
XX		
XX		
KW	Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;	
XX	chemokine receptor family; FPR; inflammatory response up-regulation;	
KW	chemokine receptor family; FPR; inflammatory response up-regulation;	

XX	RESULT 4
XX	AYY22912
ID	AYY22912 standard; peptide; 36 AA.
XX	
AC	AYY22912;
DT	19-AUG-1999 (first entry)
XX	
DE	SEQ ID NO. 108 from WO9820036.
XX	
KM	HIV; gp41 protein; constrained helical peptide; HIV infection;
KM	vaccine; antibody; viral membrane fusion; viral infectivity;
KM	ligand affinity purification; protein A replacement;
KM	immunoglobulin purification; epitope mimic.
XX	
OS	Human immunodeficiency virus.
XX	
●	WO9820036-A1.
XX	
PF	14-MAY-1998.
XX	
PF	05-NOV-1997; 97MO-US20069.
XX	
PR	16-JUN-1997; 97US-0876698.
PR	06-NOV-1996; 96US-0743698.
XX	
PA	(GETH ) GENENTECH INC.
PI	Bristed A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA,
PI	Wells JA;
XX	
DR	WPI; 1998-286866/25.
XX	
PT	Production of constrained helical peptide(s) by linking side chains
PT	on termini of octapeptide - derived from human immunodeficiency
PT	virus gp41 protein, useful in vaccines for treatment and prevention
PT	of infection
PS	
XX	Disclosure; Page 233-234; 279pp; English.
XX	
CC	Peptides AYY22805-Y22917 are derived from Human immunodeficiency virus
CC	(HIV). Specifically, AYY22810-Y22910 are derived from gp41 proteins
CC	of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and
CC	AAY22903 represent consensus sequences of various sections of the gp41
CC	protein). Sequences derived from the peptides are used to produce
CC	constrained helical peptides of the invention. The constrained helical
CC	peptide is produced by synthesizing an octapeptide in which both terminal
●	amino acids have a side-chain that includes a group able to form an amide
●	bond, and cyclizing the octapeptide by reacting the specified side-chain
CC	residues with a difunctional linker to produce two amide bonds.
CC	The constrained helical peptides are used to treat or prevent HIV
CC	infection, especially as vaccines that generate antibodies that
CC	prevent viral membrane fusion or infectivity. Vaccines may contain
CC	constrained helical peptides derived from several different strains of
CC	HIV. The antibodies are also useful for diagnosing HIV infection. Other
CC	uses for the constrained helical peptides are in affinity purification
CC	of ligands (particularly where complete binding protein is not readily
CC	available), e.g. replacements for protein A in immunoglobulin
CC	purification); as epitope mimics for antibody production; for isolation
CC	of synthetic antibody clones from phage display libraries, or as stable
CC	forms of "floppy" peptides or proteins.
XX	
Sequence	36 AA:
Query Match	98.0%; Score 192; DB 19; Length 36;
Best Local Similarity	97.2%; Pred. No. 6,5e-17;
Matches	35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
0Y	1 YTSLSHTLIEESONQOEKNEDELLEDKKASLMNMF 36
	:     :     :     :     :     :
DB	1 YTSLHSLEIESONOQEKNEDELLEDKKASLMNMF 36

Query Match	Best Local Similarity	98.0%: Score 192; DB 19;	Length 36;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
1 YTSLHTLIESONQOEKNEDELFLDKWASLWNNF 36	1 YTSLHTLIESONQOEKNEDELFLDKWASLWNNF 36		
1 YTSLHTLIESONQOEKNEDELFLDKWASLWNNF 36	1 YTSLHTLIESONQOEKNEDELFLDKWASLWNNF 36		



The sequences given in AAR6938-008 represent peptides which exhibit antifusogenic activity antiviral capability and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. These peptides are recognised by the ALMO15, CC107x18x4 and PLZIP search motifs. These peptides may be used to inhibit the transmission of a virus, pref. HIV, influenza virus, or hepatitis B virus, to a cell.

Sequence 36 AA:

Query Match 98.0%; Score 192; DB 17; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,5e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIESQNOEKNEDELLELDKWSLMMNF 36  
|||||:|||||:|||||:|||||:|||||:  
Db 1 YTSLIHTLIESQNOEKNEDELLELDKWSLMMNF 36

RESULT 3  
AAM17011  
ID AAM17011 standard; peptide: 36 AA.  
AC AAM17011;  
XX 30-JUN-1997 (first entry)  
DE HIV-1 derived peptide useful for treatment of HIV infection.  
KW HIV; SIV: simian immunodeficiency virus; glycoprotein 41;  
KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
KW replication; transmission.  
XX Human immunodeficiency virus type 1 LAI isolate.  
OS  
XX  
PN W03640191-A1.  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US09499.  
XX  
PR 07-JUN-1995; 95US-0481957.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Johnson RM, Lambert DM;  
XX  
DR WPI; 1997-099886/09.  
XX  
PT Compins. contg. DP-178 or DP-107 in combination with other  
PT therapeutic agent - useful for treatment of HIV infection, esp. by  
PT inhibiting replication or transmission of HIV.  
XX  
PS Claim 2; Figure 1; 84pp; English.  
XX  
CC AAM17011 represents a peptide designated DP-178, a peptide derived  
CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
CC derivatives are used in combination with a therapeutic agent, e.g. a  
CC reverse transcriptase, viral protease, cytokine, glycosylation or viral  
CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
CC by inhibiting viral replication or inhibiting transmission. They may  
CC also be used in vaccines for protecting against HIV infection.  
XX  
SQ Sequence 36 AA:  
  
Query Match 98.0%; Score 192; DB 18; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,5e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIESQNOEKNEDELLELDKWSLMMNF 36  
|||||:|||||:|||||:|||||:|||||:  
Db 1 YTSLIHTLIESQNOEKNEDELLELDKWSLMMNF 36



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: TITLE OF INVENTION: BEING IMMOBILIZED
: FILE REFERENCE: ALBRE-22
: CURRENT APPLICATION NUMBER: US/10/059,271
: CURRENT FILING DATE: 2002-01-31
: PRIOR APPLICATION NUMBER: DE 101 06 295
: PRIOR FILING DATE: 2001-02-02
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 81
: LENGTH: 232
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: peptide
US-10-059-271-81

```

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Query Match          96.9%; Score 190; DB 9; Length 232;
Best Local Similarity 97.2%; Pred. No. 1.5e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 YTSLIHRLIESQNOQEKNEQELLELDKWSLWNMF 36
|||||
Db 144 YTSLIHSLIEFSQNOQEKNEQELLELDKWSLWNMF 179

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RESULT 15
US-10-059-271-82
: Sequence 82, Application US/10059271
: Publication No. US20030082208A1
: GENERAL INFORMATION:
: APPLICANT: REPEKE, HEINRICH
: APPLICANT: BUDEDE, ECKHARD
: APPLICANT: NICOLAUS, STEFFAN
: TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
: TITLE OF INVENTION: BEING IMMOBILIZED
: FILE REFERENCE: ALBRE-22
: CURRENT APPLICATION NUMBER: US/10/059,271
: CURRENT FILING DATE: 2002-01-31
: PRIOR APPLICATION NUMBER: DE 101 06 295
: PRIOR FILING DATE: 2001-02-02
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 82
: LENGTH: 254
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: peptide
US-10-059-271-82

```

```

Query Match          96.9%; Score 190; DB 9; Length 254;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 YTSLIHRLIESQNOQEKNEQELLELDKWSLWNMF 36
|||||
Db 166 YTSLIHSLIEFSQNOQEKNEQELLELDKWSLWNMF 201

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Search completed: May 16, 2003, 12:10:25  
Job time : 15.759 secs

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Db      2  YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 37
RESULT 10
US-09-779-451-41
; Sequence 41, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; ID NO 41
; LENGTH: 46
; TYPE: PRF
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-41
Query Match          96.9%; Score 190; DB 10; Length 46;
Best Local Similarity 97.2%; Pred. No. 2.7e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 36
Db      11 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 46
RESULT 11
US-09-779-451-4
; Sequence 4, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 56
; TYPE: PRF
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-4
Query Match          96.9%; Score 190; DB 10; Length 56;
Best Local Similarity 97.2%; Pred. No. 3.3e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 36
Db      16 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 51
RESULT 12
US-10-040-349B-2
; Sequence 2, Application US/10040349B
; Publication No. US20030082521A1
; GENERAL INFORMATION:
; APPLICANT: Brasseur, Robert
```

```
; APPLICANT: Charlotiaux, Benoit
; APPLICANT: Chevalier, Michel
; APPLICANT: El Hadid, Raphaelle
; APPLICANT: Krell, Tino
; TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
; FILE REFERENCE: 01-078-A
; CURRENT FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 177
; TYPE: PRF
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(177)
; OTHER INFORMATION: polypeptide derived from gp41 LAI
US-10-040-349B-2
Query Match          96.9%; Score 190; DB 9; Length 177;
Best Local Similarity 97.2%; Pred. No. 1.1e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 36
Db      104 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 139
RESULT 13
US-10-059-271-84
; Sequence 84, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 221
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-84
Query Match          96.9%; Score 190; DB 9; Length 221;
Best Local Similarity 97.2%; Pred. No. 1.4e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 36
Db      131 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 166
RESULT 14
US-10-059-271-81
; Sequence 81, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
```

RESULT 7  
US-09-854-816-1  
Sequence 1, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Pheilan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: DP178  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
09-854-816-1  
Query Match 96.9%; Score 190; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2,1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTSLHRLIEESONQOEKNEDELLEDKWASLWNWF 36  
DB 1 YTSLHSLIEESONQOEKNEDELLEDKWASLWNWF 36  
RESULT 8  
US-09-854-816-108  
Sequence 108, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Pheilan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108  
Query Match 96.9%; Score 190; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2,1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTSLHRLIEESONQOEKNEDELLEDKWASLWNWF 36  
DB 1 YTSLHSLIEESONQOEKNEDELLEDKWASLWNWF 36  
RESULT 9  
US-09-848-616-176  
Sequence 176, Application US/09848616  
Publication No. US20030054010A1  
GENERAL INFORMATION:  
APPLICANT: Seibel, Peter  
APPLICANT: Dunant, Nicolas  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Lechner, Franziska  
TITLE OF INVENTION: Molecular Antigen Array  
FILE REFERENCE: 1700.0180002  
CURRENT APPLICATION NUMBER: US/09/848,616  
CURRENT FILING DATE: 2001-05-05  
NUMBER OF SEQ ID NOS: 186  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 176  
LENGTH: 37  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: DP178c peptide  
US-09-848-616-176  
Query Match 96.9%; Score 190; DB 9; Length 37;  
Best Local Similarity 97.2%; Pred. No. 2,1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTSLHRLIEESONQOEKNEDELLEDKWASLWNWF 36  
DB 1 YTSLHSLIEESONQOEKNEDELLEDKWASLWNWF 36

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 96.9%; Score 190; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEQELLELDKWSLWNF 36  
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DB 1 YTSLIHSLIEESONOQEKNEQELLELDKWSLWNF 36

## RESULT 3

US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1

## GENERAL INFORMATION:

APPLICANT: Olson, William C  
APPLICANT: Maddon, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
TITLE OF INVENTION: Infection  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 96.9%; Score 190; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEQELLELDKWSLWNF 36  
|||||  
DB 1 YTSLIHSLIEESONOQEKNEQELLELDKWSLWNF 36

## RESULT 4

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1

GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPM/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)-(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 96.9%; Score 190; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEQELLELDKWSLWNF 36  
|||||  
DB 1 YTSLIHSLIEESONOQEKNEQELLELDKWSLWNF 36

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEQELLELDKWSLWNF 36  
|||||  
DB 1 YTSLIHSLIEESONOQEKNEQELLELDKWSLWNF 36

## RESULT 5

US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1

## GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 96.9%; Score 190; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEQELLELDKWSLWNF 36  
|||||  
DB 1 YTSLIHSLIEESONOQEKNEQELLELDKWSLWNF 36

## RESULT 6

US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US2002011922A1

GENERAL INFORMATION:  
APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 96.9%; Score 190; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEQELLELDKWSLWNF 36  
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DB 1 YTSLIHSLIEESONOQEKNEQELLELDKWSLWNF 36

Query Match 96.9%; Score 190; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEQELLELDKWSLWNF 36  
|||||  
DB 1 YTSLIHSLIEESONOQEKNEQELLELDKWSLWNF 36

GenCore version 5.1.4\_p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-538  
Perfect score: 196  
Sequence: 1 YTSLIHRIEESQNOEKNEQELLELDKWSLWNNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	96.9	36	9	US-09-874-475-16
2	190	96.9	36	9	US-10-116-797-1
3	190	96.9	36	9	US-09-493-346-1
4	190	96.9	36	10	US-09-796-202-10
5	190	96.9	36	10	US-09-779-451-5
6	190	96.9	36	10	US-09-834-628-1
7	190	96.9	36	10	US-09-854-816-1
8	190	96.9	36	10	US-09-854-816-108
9	190	96.9	37	9	US-09-848-616-176
10	190	96.9	46	10	US-09-779-451-41
11	190	96.9	56	10	US-09-779-451-4
12	190	96.9	177	9	US-10-040-349B-2
13	190	96.9	221	9	US-10-059-271-84
14	190	96.9	232	9	US-10-059-271-81
15	190	96.9	254	9	US-10-059-271-82
16	190	96.9	256	9	US-10-059-271-97
17	190	96.9	268	10	US-09-854-816-16
18	190	96.9	268	10	US-09-854-816-17
19	190	96.9	268	10	US-09-854-816-18

20	190	96.9	344	9	US-10-040-349B-1	Sequence 1, Appli
21	190	96.9	345	9	US-10-026-741-49	Sequence 49, Appl
22	190	96.9	345	10	US-09-779-451-8	Sequence 8, Appli
23	190	96.9	391	9	US-10-059-271-93	Sequence 93, Appl
24	190	96.9	519	10	US-09-756-551A-8	Sequence 8, Appli
25	190	96.9	853	9	US-10-003-035-33	Sequence 33, Appl
26	190	96.9	856	10	US-09-476-242-1	Sequence 1, Appli
27	190	96.9	861	9	US-10-026-741-103	Sequence 103, App
28	190	96.9	1101	9	US-10-003-035-53	Sequence 53, Appl
29	190	96.9	1186	9	US-10-003-035-55	Sequence 55, Appl
30	187	95.4	36	10	US-09-912-824-1	Sequence 1, Appli
31	187	95.4	268	10	US-09-854-816-19	Sequence 19, Appl
32	185	94.4	233	10	US-09-854-816-50	Sequence 50, Appl
33	184	93.9	268	10	US-09-854-816-9	Sequence 9, Appli
34	184	93.9	269	10	US-09-854-816-12	Sequence 12, Appl
35	184	93.9	1231	9	US-10-059-271-94	Sequence 94, Appl
36	182	92.9	268	10	US-09-854-816-13	Sequence 13, Appl
37	182	92.9	269	10	US-09-854-816-28	Sequence 28, Appl
38	181	92.3	268	10	US-09-854-816-26	Sequence 26, Appl
39	181	92.3	619	10	US-09-891-609-4	Sequence 4, Appli
40	181	92.3	646	10	US-09-891-609-2	Sequence 2, Appli
41	181	92.3	847	10	US-09-476-242-2	Sequence 2, Appli
42	180	91.8	46	10	US-09-854-816-109	Sequence 109, App
43	180	91.8	267	10	US-09-854-816-38	Sequence 38, Appl
44	180	91.8	268	10	US-09-854-816-41	Sequence 41, Appl
45	180	91.8	269	10	US-09-854-816-6	Sequence 6, Appli

## ALIGNMENTS

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RESULT 1
US-09-874-475-16
; Sequence 16, Application US/09874475
; Publication No. US20020182592A1
; GENERAL INFORMATION:
; APPLICANT: Petropoulos, Christos J.
; APPLICANT: Parkin, Neil T.
; APPLICANT: Whitcomb, Jeanette
; APPLICANT: Huang, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE
; TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS
; FILE REFERENCE: 2793/65166
; CURRENT APPLICATION NUMBER: US/09/874,475
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Fusion Inhibitor Peptide
US-09-874-475-16

Query Match          96.9%; Score 190; DB 9; Length 36;
Best Local Similarity 97.2%; Pred. No. 2.1e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 YTSLIHRIEESQNOEKNEQELLELDKWSLWNNF 36
Db 1 YTSLIHRIEESQNOEKNEQELLELDKWSLWNNF 36

RESULT 2
US-10-116-797-1
; Sequence 1, Application US/10116797
; Publication No. US20030044411A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672-A
; CURRENT APPLICATION NUMBER: US/10/116,797
; CURRENT FILING DATE: 2002-10-15

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Db 1 YTSLIHSLIESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 13

US-09-082-279B-497

; Sequence 497, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 497

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match 96.9%; Score 190; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLIESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 14

US-09-082-279B-498

; Sequence 498, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 498

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

Query Match 96.9%; Score 190; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLIESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 15

US-09-082-279B-603

; Sequence 603, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 603

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 96.9%; Score 190; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLIESONQOEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:22:13  
Job time: 10.1928 secs

RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1  
Query Match 96.9%; Score 190; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOQEKNDLELDKNASLWNMF 36  
Db 1 YTSLHSLIEESONOQEKNDLELDKNASLWNMF 36

RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1

Query Match 96.9%; Score 190; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOQEKNDLELDKNASLWNMF 36  
Db 1 YTSLHSLIEESONOQEKNDLELDKNASLWNMF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Gutnile, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15

Query Match 96.9%; Score 190; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOQEKNDLELDKNASLWNMF 36  
Db 1 YTSLHSLIEESONOQEKNDLELDKNASLWNMF 36

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
8-475-668A-1

Query Match 96.9%; Score 190; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5,5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOENKNEQELLELDKWSLWNNF 36  
DB 1 YTSLHSLIEESONOENKNEQELLELDKWSLWNNF 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Daniel P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 96.9%; Score 190; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5,5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOENKNEQELLELDKWSLWNNF 36  
DB 1 YTSLHSLIEESONOENKNEQELLELDKWSLWNNF 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Daniel P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 96.9%; Score 190; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5,5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOENKNEQELLELDKWSLWNNF 36  
DB 1 YTSLHSLIEESONOENKNEQELLELDKWSLWNNF 36

Db 1 YTSLSHLSIESQNOQEKNEQELLEDLKWASLWNMF 36

RESULT 5  
US-08-484-223B-1  
Sequence 1, Application US/08484223B

PATENT No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TRANSMISSION  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-484-223B-1

Query Match 96.9%; Score 190; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLEDLKWASLWNMF 36

Db 1 YTSLSHLSIESQNOQEKNEQELLEDLKWASLWNMF 36

RESULT 6

US-08-919-597-1

Sequence 1, Application US/08919597

PATENT No. 6054265

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petleway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TRANSMISSION

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,597

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/470,896

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-020

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-919-597-1

Query Match 96.9%; Score 190; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESQNOQEKNEQELLEDLKWASLWNMF 36

Db 1 YTSLSHLSIESQNOQEKNEQELLEDLKWASLWNMF 36

RESULT 7

US-08-475-668A-1

Sequence 1, Application US/08475668A

PATENT No. 6060065

GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petleway, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TRANSMISSION

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

Db 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWMP 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 96.9%; Score 190; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWMP 36

Db 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWMP 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichty, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Merutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

Db 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWMP 36

CURRENT APPLICATION NUMBER: US/09/071,877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 1

LENGTH: 36

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-09-071-877-1

Query Match 96.9%; Score 190; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWMP 36

Db 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWMP 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 96.9%; Score 190; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWMP 36

GenCore version 5.1.4\_P5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533a-538

Perfect score: 196  
Sequence: 1 YTSILHRLIEESQNOEKNEDELLDKWASLMMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190	96.9	36	1	US-08-073-028-1
2	190	96.9	36	3	US-08-486-099-1
3	190	96.9	36	3	US-09-071-877-1
4	190	96.9	36	3	US-08-360-107A-1
5	190	96.9	36	3	US-08-484-223B-1
6	190	96.9	36	3	US-08-919-597-1
7	190	96.9	36	3	US-08-475-668A-1
8	190	96.9	36	3	US-08-485-551A-1
9	190	96.9	36	3	US-08-471-912A-1
10	190	96.9	36	4	US-08-554-616-1
11	190	96.9	36	4	US-08-485-264A-1
12	190	96.9	36	4	US-09-082-279B-15
13	190	96.9	36	4	US-09-082-279B-497
14	190	96.9	36	4	US-09-082-279B-498
15	190	96.9	36	4	US-09-082-279B-603
16	190	96.9	36	4	US-09-082-279B-630
17	190	96.9	36	4	US-09-082-279B-631
18	190	96.9	36	4	US-09-082-279B-705
19	190	96.9	36	4	US-09-082-279B-834
20	190	96.9	36	4	US-09-082-279B-1076
21	190	96.9	36	4	US-09-082-279B-1121
22	190	96.9	36	4	US-09-082-279B-1161
23	190	96.9	36	4	US-08-965-056-1
24	190	96.9	36	4	US-08-965-056-108
25	190	96.9	36	4	US-09-045-920-1
26	190	96.9	36	4	US-08-474-349A-1
27	190	96.9	36	4	US-08-474-349A-399

28	190	96.9	36	4	US-08-474-349A-413	Sequence 413, App
29	190	96.9	36	4	US-09-315-304B-15	Sequence 15, Appl
30	190	96.9	36	4	US-09-315-304B-497	Sequence 497, App
31	190	96.9	36	4	US-09-315-304B-498	Sequence 498, App
32	190	96.9	36	4	US-09-315-304B-603	Sequence 603, App
33	190	96.9	36	4	US-09-315-304B-630	Sequence 630, App
34	190	96.9	36	4	US-09-315-304B-631	Sequence 631, App
35	190	96.9	36	4	US-09-315-304B-705	Sequence 705, App
36	190	96.9	36	4	US-09-315-304B-834	Sequence 834, App
37	190	96.9	36	4	US-09-315-304B-1076	Sequence 1076, Ap
38	190	96.9	36	4	US-09-315-304B-1121	Sequence 1121, Ap
39	190	96.9	36	4	US-09-315-304B-1161	Sequence 1161, Ap
40	190	96.9	36	4	US-09-315-304B-1469	Sequence 1469, Ap
41	190	96.9	36	4	US-09-315-304B-1470	Sequence 1470, Ap
42	190	96.9	36	4	US-09-315-304B-1486	Sequence 1486, Ap
43	190	96.9	36	4	US-09-315-304B-1511	Sequence 1511, Ap
44	190	96.9	36	4	US-08-255-208A-1	Sequence 1, Appli
45	190	96.9	37	4	US-09-082-279B-771	Sequence 771, App

## ALIGNMENTS

RESULT 1  
US-08-073-028-1  
; Sequence 1, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Penite & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNTE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-073-028-1  
Query Match 96.9%; Score 190; DB 1; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTSILHRLIEESQNOEKNEDELLDKWASLMMWF 36  
|||||

Query Match	94.9%	Score 186;	DB 15;	Length 854;
Best Local Similarity	94.4%	Pred. No. 3.6e-14;		
Matches	34;	Conservative 1;	Mismatches 1;	Indels 0;
			Gaps 0;	

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QY      1 YTSLIHRLIEESQNOQEKNEQELLLEDDKWSLWNMF 36
          ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db      636 YTSLIHSLIEESQNOQEEENEQELLEDDKWSLWNMF 671

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RESULT 15  
078705

ID	Q78705	PRELIMINARY;	PRT;	854	AA
AC	Q78705.				

DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Envelope glycoprotein gp120.
GN	ENV.
OS	Human immunodeficiency virus type 1.
	Viruses: Retroid viruses; Retroviridae; Lentivirus
	NCBI_TaxID=11676;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96013815; PubMed=7474132;  
 RA Duensing T.D., Fang H., Dordard D.W., Pincus S.H.;  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 RT resistant cell lines chronically infected with human immunodeficiency  
 RT virus type 1.";  
 RL J. Virol. 69:7122-7131(1995).  
 DR EMBL, L42371; AAA96826.1; -.  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 854 AA; 97199 MW; 5B9512216533E256 CRC64;

Query Match	94.98;	Score 186;	DB 15;	Length 854;
Best Local Similarity	94.48;	Pred. No. 3.6e-14;		
Matches 34;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0

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OY      1 YTSLHRLIEESQNOQEKNEQELLLEDDKWSLWNWF 36
        ||||| ||||| : ||||| ||||| ||||| |||||
Db      636 YTSLHSLIEESQNOQEEENEQELLLEDDKWSLWNWF 671

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Search completed: May 16, 2003, 11:19:49
time : 27.3124 secs
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RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
RA Steenbeke T., Halloran M., Fenton J.W., Axthelm M.K., Letvin N.L.,  
RA Sodroski J.G.;  
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
RT responsible for the pathogenicity of a multiply passaged simian-human  
RT immunodeficiency virus (SHIV-HXB2).";  
RL J. Virol. 73:976-984(1999).  
RN  
RP SEQUENCE FROM N.A.  
RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF041850; AAD12142.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA: 97151 MW: C50BE0386FB73659 CRC64;

Query Match 96.9%; Score 190; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOQEKNEQELLELDKWSLMMNF 36  
DB 638 YTSLIHSLIESQNOQEKNEQELLELDKWSLMMNF 673

## RESULT 12

ID 074599 PRELIMINARY; PRT; 856 AA.  
AC 074599;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.;  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates.";  
RL J. Virol. 74:103-116(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RA Iwataani Y.;  
RN Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
DR EMBL: D86068; BAA12995.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA: 97287 MW: 238042A234C56685 CRC64;

Query Match 96.9%; Score 190; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOQEKNEQELLELDKWSLMMNF 36  
DB 638 YTSLIHSLIESQNOQEKNEQELLELDKWSLMMNF 673

## RESULT 13

OY 074090

ID 074090 PRELIMINARY; PRT; 856 AA.  
AC 074090;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM213;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.;  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates.";  
RL J. Virol. 74:103-116(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM213;  
RA Iwataani Y.;  
RN Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
DR EMBL: D86069; BAA13003.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA: 97396 MW: FE3E784C423C108C CRC64;

Query Match 96.9%; Score 190; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOQEKNEQELLELDKWSLMMNF 36  
DB 638 YTSLIHSLIESQNOQEKNEQELLELDKWSLMMNF 673

## RESULT 14

ID 090178 PRELIMINARY; PRT; 854 AA.  
AC 090178;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95074930; PubMed=7983770;  
RA Fang H., Pincus S.H.;  
RT "Unique insertion sequence and pattern of CD4 expression in variants  
RT selected with immunotoxins from human immunodeficiency virus type 1-  
RT infected T cells.";  
RL J. Virol. 69:75-81(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Fang H., Pincus S.H.;  
RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
RT immunotoxin-resistant variant T cell line.";  
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF070521; AAC28452.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 854 AA: 96885 MW: 0808F3AED27C693B CRC64;



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RT Infected with HIV type 1 (HTLV type IIB).
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-EM90-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12053; AAA76685.1; -.
DR EMBL; U12036; AAA76671.1; -.
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Envelope protein; glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF.CRC64;

Query Match 96.9%; Score 190; DB 15; Length 852;
Best Local Similarity 97.2%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 YTSLIHRLIEESONOQEKNEDELLELDKWSLWNF 36
|||||
DB 634 YTSLIHSLIEESONOQEKNEDELLELDKWSLWNF 669

RESULT 9
085582 PRELIMINARY: PRT; 854 AA.
AC 085582;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Envelope polyprotein.
GN ENV.
RT Human immunodeficiency virus type 1.
OS Viruses; Retrovirdae; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
OX [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A., Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated retrovirus in human and nonhuman cells transfected with an infectious molecular clone."
RT J. Virol. 59:284-291(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Buckler C.E., Willey R.L., McCoy J.;
RN [3]
RP Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RA Buckler C.E.;
RN [4]
RP Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RX MEDLINE=92219406; PubMed=1373204;
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on gp41 results in loss of killing by CD8+ A2A-restricted cytotoxic T lymphocytes."
RL J. Virol. 66:3151-3154(1992).
DR EMBL; M19921; AAA44992.1; -.
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A.CRC64;

Query Match 96.9%; Score 190; DB 15; Length 854;
Best Local Similarity 97.2%; Pred. No. 1.2e-14;

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Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEDELLELDKWSLWNF 36
|||||
DB 636 YTSLIHSLIEESONOQEKNEDELLELDKWSLWNF 671

RESULT 10
072502 PRELIMINARY: PRT; 854 AA.
AC 072502;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE ENV polyprotein.
GN ENV.
RT Human immunodeficiency virus type 1.
OS Viruses; Retrovirdae; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
OX [1]
RN SEQUENCE FROM N.A.
RX STRAIN-NLA-3;
RX MEDLINE=96036482; PubMed=7483282;
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K., Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes from primary virus cultures using the polymerase chain reaction."
RL Virology 213:80-86(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-NLA-3;
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A., Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated retrovirus in human and nonhuman cells transfected with an infectious molecular clone."
RL J. Virol. 59:284-291(1986).
DR EMBL; 026942; AAB60578.1; -.
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT CONFLICT 214 H -> L (IN REF. 2).
FT CONFLICT 530 A -> S (IN REF. 2).
FT CONFLICT 739 G -> D (IN REF. 2).
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220.CRC64;

Query Match 96.9%; Score 190; DB 15; Length 854;
Best Local Similarity 97.2%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEDELLELDKWSLWNF 36
|||||
DB 636 YTSLIHSLIEESONOQEKNEDELLELDKWSLWNF 671

RESULT 11
092877 PRELIMINARY: PRT; 856 AA.
AC 092877;
DT 01-NOV-1998 (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9908984; PubMed=9882298;

```

RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 GN Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12031; AAA76667.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 NON\_TER 752  
 SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.9%; Score 190; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 36  
 DB 638 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 673

RESULT 6  
 ID 070608 PRELIMINARY; PRT; 752 AA.  
 AC 070608;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 GN Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 NON\_TER 752  
 SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E88 CRC64;

Query Match 96.9%; Score 190; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 36  
 DB 638 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 673

DB 638 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 673

RESULT 7  
 ID 078243 PRELIMINARY; PRT; 851 AA.  
 AC 078243;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Env polyprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
 Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 chronically infected HUT-78 cellular clone.";  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RX Federico M., Tilti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Macchi B., Mangiano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 producer clones from HUT-78 infected with a patient HIV isolate.";  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RA Tilti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Borsetti A., Saglio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 productive clone.";  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL: Z11530; CA47628.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 96.9%; Score 190; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 36  
 DB 633 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 668

RESULT 8  
 ID 089797 PRELIMINARY; PRT; 852 AA.  
 AC 089797;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-OCT-2001 (TRENBLREL. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker

## RESULT 2

070607 PRELIMINARY: PRT: 747 AA.  
 AC 070607;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U12034; AAA76669.1;  
 DR InterPro; IPR000328; Env\_Gp41.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 747  
 SQ SEQUENCE 747 AA: 84250 MW; 732E836A52245F14 CRC64;

Query Match 96.9%; Score 190; DB 15; Length 747;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONQOEKNEDELLDKWASLWNMF 36  
 Db 633 YTSLSHLSIESONQOEKNEDELLDKWASLWNMF 668

RESULT 3  
 070606 PRELIMINARY: PRT: 748 AA.  
 AC 070606;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U12033; AAA76668.1;  
 DR InterPro; IPR000328; Env\_Gp41.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 752  
 SQ SEQUENCE 752 AA: 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.9%; Score 190; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEDELLDKWASLWNMF 36  
 Db 638 YTSLSHLSIESONQOEKNEDELLDKWASLWNMF 673

RESULT 5  
 070605 PRELIMINARY: PRT: 752 AA.  
 AC 070605;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;

DR InterPro; IPR000328; Env\_Gp41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 748  
 SQ SEQUENCE 748 AA: 84224 MW; 56BEDF186C67694B CRC64;

Query Match 96.9%; Score 190; DB 15; Length 748;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEDELLDKWASLWNMF 36  
 Db 634 YTSLSHLSIESONQOEKNEDELLDKWASLWNMF 669

## RESULT 4

070604 PRELIMINARY: PRT: 752 AA.  
 AC 070604;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U12030; AAA76666.1;  
 DR InterPro; IPR000328; Env\_Gp41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 752  
 SQ SEQUENCE 752 AA: 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.9%; Score 190; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEDELLDKWASLWNMF 36  
 Db 638 YTSLSHLSIESONQOEKNEDELLDKWASLWNMF 673

RESULT 5  
 070605 PRELIMINARY: PRT: 752 AA.  
 AC 070605;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-538  
Perfect score: 196  
Sequence: 1 YTSLIHRLIESONQOEKNEQELLDKWSLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mmc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.proteint:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriophage:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	96.9	645	15	0993A6 human immun
2	190	96.9	747	15	070607 human immun
3	190	96.9	748	15	070606 human immun
4	190	96.9	752	15	070604 human immun
5	190	96.9	752	15	070605 human immun
6	190	96.9	752	15	070608 human immun
7	190	96.9	851	15	078243 human immun
8	190	96.9	852	15	089797 human immun
9	190	96.9	854	15	085582 human immun
10	190	96.9	854	15	072502 human immun
11	190	96.9	856	15	092877 simian-huma
12	190	96.9	856	15	074599 human immun
13	190	96.9	854	15	074090 human immun
14	186	94.9	854	15	090178 human immun
15	186	94.9	854	15	078705 human immun
16	185	94.4	443	15	080023 human immun

17	185	94.4	856	15	0905M7 human immun
18	184	93.9	42	15	069910 human immun
19	184	93.9	616	15	0993B0 human immun
20	184	93.9	618	15	0993B2 human immun
21	184	93.9	757	15	090722 human immun
22	184	93.9	841	15	041556 human immun
23	184	93.9	848	15	069990 human immun
24	184	93.9	849	15	077368 human immun
25	184	93.9	849	15	080851 human immun
26	184	93.9	851	15	056110 human immun
27	184	93.9	851	15	080852 human immun
28	184	93.9	856	15	072993 human immun
29	184	93.9	856	15	041539 human immun
30	184	93.9	857	15	080170 human immun
31	184	93.9	859	15	080185 human immun
32	184	93.9	859	15	080180 human immun
33	184	93.9	859	15	080179 human immun
34	184	93.9	859	15	080177 human immun
35	184	93.9	859	15	080173 human immun
36	184	93.9	859	15	080850 human immun
37	184	93.9	862	15	080184 human immun
38	184	93.9	862	15	080183 human immun
39	184	93.9	862	15	080182 human immun
40	184	93.9	862	15	080178 human immun
41	184	93.9	862	15	080174 human immun
42	184	93.9	868	15	080186 human immun
43	183	93.4	858	15	071974 human immun
44	183	93.4	859	15	092937 human immun
45	182	92.9	122	15	09YX08 human immun

## ALIGNMENTS

RESULT 1  
ID 0993A6 PRELIMINARY: PRT: 645 AA.  
AC 0993A6;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RA MEDLINE=21192672; PubMed=11287644;  
RX Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4 T cell epitope hotspots to exposed strands of  
HIV envelope glycoprotein suggests structural influences on antigen  
processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
RL EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;  
KW Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 645 AA: 72485 MW: B076514BE93362EC CRC64;

Query Match 96.9%; Score 190; DB 15; Length 645;  
Best Local Similarity 97.2%; Pred. No. 8.8e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESONQOEKNEQELLDKWSLWMP 36  
DB 607 YTSLIHRLIESONQOEKNEQELLDKWSLWMP 642

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FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 867 AA: 98399 MW: 5F2310146B8E8680 CRC64;

Query Match 90.3%; Score 177; DB 1; Length 867;  
 Best Local Similarity 91.7%; Pred. No. 4, 8e-14;  
 Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOQEKNEOELELLELDKMASLWNF 36  
 ||||:|||||||  
 DB 649 YTSLIYTLIESQNOQEKNEOELELLELDKMASLWNF 684

Search completed: May 16, 2003, 11:13:37  
 Job time : 7.07229 secs



FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SEQUENCE 856 AA; 97339 MW; 5FCDBJDC3C1209B3 CRC64;

Query Match Best Local Similarity 92.3%; Score 181; DB 1; Length 856;  
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLHRLIEESQNOOEKNEOELLELDKWSLWNP 35  
DB 638 YTSLHSLIEESQNOOEKNEOELLELDKWSLWNP 672

RESULT 13  
ENV\_HV122 STANDARD; PRT; 853 AA.

AC P12487;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11683;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Theodore T., Buckler-White A.;  
P1 Submitted (NOV-1988) to the HIV data bank.

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DR EMBL; M2639; AAA45370.1; -  
DR HIV; M2639; ENV5226.  
DR InterPro; IPR000328; ENV\_GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
KW Signal.  
FT SIGNAL 1 31 BY SIMILARITY.  
FT CHAIN 32 508 EXTENSOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 53 73 BY SIMILARITY.  
FT DISULFID 118 206 BY SIMILARITY.  
FT DISULFID 125 197 BY SIMILARITY.  
FT DISULFID 130 154 BY SIMILARITY.

FT DISULFID 219 248 BY SIMILARITY.  
FT DISULFID 229 240 BY SIMILARITY.  
FT DISULFID 297 330 BY SIMILARITY.  
FT DISULFID 376 442 BY SIMILARITY.  
FT DISULFID 383 415 BY SIMILARITY.  
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 853 AA; 97043 MW; 849B0B8CAFF7008 CRC64;

Query Match Best Local Similarity 91.8%; Score 180; DB 1; Length 853;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLHRLIEESQNOOEKNEOELLELDKWSLWNP 36  
DB 635 YTSLHRLIEESQNOOEKNEOELLELDKWSLWNP 670

RESULT 14  
ENV\_HV126 STANDARD; PRT; 855 AA.

AC P04580;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11708;  
RN [1]

RP SEQUENCE FROM N.A.  
RA MEDLINE=87248097; PubMed=3036660;  
RA Strinivasan A., Anand R., Ranganathan P., Feorino P.,  
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,  
RA Sanchez-Pescador R.;  
RT "Molecular characterization of human immunodeficiency virus from  
RT Zaire: nucleotide sequence analysis identifies conserved and variable  
RT domains in the envelope gene.";  
RL Gene 52:71-82(1987).

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ENV_HV1S1	STANDARD:	PRT:	847 AA.
AC	ENV_HV1S1		
AD	ENV_HV1S1		
AE	ENV_HV1S1		
AF	ENV_HV1S1		
AG	ENV_HV1S1		
AH	ENV_HV1S1		
AI	ENV_HV1S1		
AJ	ENV_HV1S1		
AK	ENV_HV1S1		
AL	ENV_HV1S1		
AM	ENV_HV1S1		
AN	ENV_HV1S1		
AO	ENV_HV1S1		
AP	ENV_HV1S1		
AQ	ENV_HV1S1		
AR	ENV_HV1S1		
AS	ENV_HV1S1		
AT	ENV_HV1S1		
AV	ENV_HV1S1		
AW	ENV_HV1S1		
AX	ENV_HV1S1		
AY	ENV_HV1S1		
AZ	ENV_HV1S1		
BA	ENV_HV1S1		
BB	ENV_HV1S1		
BC	ENV_HV1S1		
BD	ENV_HV1S1		
BE	ENV_HV1S1		
BF	ENV_HV1S1		
BG	ENV_HV1S1		
BH	ENV_HV1S1		
BI	ENV_HV1S1		
BJ	ENV_HV1S1		
BK	ENV_HV1S1		
BL	ENV_HV1S1		
BM	ENV_HV1S1		
BN	ENV_HV1S1		
BO	ENV_HV1S1		
BP	ENV_HV1S1		
BQ	ENV_HV1S1		
BR	ENV_HV1S1		
BS	ENV_HV1S1		
BT	ENV_HV1S1		
BU	ENV_HV1S1		
BV	ENV_HV1S1		
BW	ENV_HV1S1		
BX	ENV_HV1S1		
BY	ENV_HV1S1		
BZ	ENV_HV1S1		
CA	ENV_HV1S1		
CB	ENV_HV1S1		
CC	ENV_HV1S1		
CD	ENV_HV1S1		
CE	ENV_HV1S1		
CF	ENV_HV1S1		
CG	ENV_HV1S1		
CH	ENV_HV1S1		
CI	ENV_HV1S1		
CJ	ENV_HV1S1		
CK	ENV_HV1S1		
CL	ENV_HV1S1		
CM	ENV_HV1S1		
CN	ENV_HV1S1		
CO	ENV_HV1S1		
CP	ENV_HV1S1		
CQ	ENV_HV1S1		
CR	ENV_HV1S1		
CS	ENV_HV1S1		
CT	ENV_HV1S1		
CU	ENV_HV1S1		
CV	ENV_HV1S1		
CW	ENV_HV1S1		
CX	ENV_HV1S1		
CY	ENV_HV1S1		
CZ	ENV_HV1S1		
DA	ENV_HV1S1		
DB	ENV_HV1S1		
DC	ENV_HV1S1		
DD	ENV_HV1S1		
DE	ENV_HV1S1		
DF	ENV_HV1S1		
DG	ENV_HV1S1		
DH	ENV_HV1S1		
DI	ENV_HV1S1		
DJ	ENV_HV1S1		
DK	ENV_HV1S1		
DL	ENV_HV1S1		
DM	ENV_HV1S1		
DN	ENV_HV1S1		
DO	ENV_HV1S1		
DP	ENV_HV1S1		
DQ	ENV_HV1S1		
DR	ENV_HV1S1		
DS	ENV_HV1S1		
DT	ENV_HV1S1		
DU	ENV_HV1S1		
DV	ENV_HV1S1		
DW	ENV_HV1S1		
DX	ENV_HV1S1		
DY	ENV_HV1S1		
DZ	ENV_HV1S1		
EA	ENV_HV1S1		
EB	ENV_HV1S1		
EC	ENV_HV1S1		
ED	ENV_HV1S1		
EE	ENV_HV1S1		
EF	ENV_HV1S1		
EG	ENV_HV1S1		
EH	ENV_HV1S1		
EI	ENV_HV1S1		
EJ	ENV_HV1S1		
EK	ENV_HV1S1		
EL	ENV_HV1S1		
EM	ENV_HV1S1		
EN	ENV_HV1S1		
EO	ENV_HV1S1		
EP	ENV_HV1S1		
EQ	ENV_HV1S1		
ER	ENV_HV1S1		
ES	ENV_HV1S1		
ET	ENV_HV1S1		
EU	ENV_HV1S1		
EV	ENV_HV1S1		
EW	ENV_HV1S1		
EX	ENV_HV1S1		
EY	ENV_HV1S1		
EZ	ENV_HV1S1		
FA	ENV_HV1S1		
FB	ENV_HV1S1		
FC	ENV_HV1S1		
FD			

SQ	SEQUENCE	847 AA;	96135 MW;	0A901317FD/FF2AB CRC64;
	Query Match		92.3%;	Score 181; DB 1; Length 847;
	Best Local Similarity		91.7%;	Pred. No.1.5e-14;
Matches	33; Conservative	2; Mismatches	1; Indels	0; Gaps
OY	1 YTSLHRLIEESQNOEKNEDELLELDKWSIWMNF	36		
DB	629 YTNLIYLTILEESONOEKNEDLELDKWSIWMNF	664		
RESULT 12				
ENV_HVLPV	STANDARD:	PRT,	856 AA.	
ID	ENV_HVLPV			
AC	P03376;			
DT	21-JUL-1986 (Rel. 01, Created)			
DR	21-JUL-1986 (Rel. 01, Last sequence update)			
DI	15-JUL-1999 (Rel. 38, last annotation update)			
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirinae.			
OX	NCBI_TaxID=11700;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85111157; PubMed=2982104;			
RA	Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A., Capon D.J.;			
RT	"Nucleic acid structure and expression of the human AIDS lymphadenopathy retrovirus.";			
RL	Nature 313:450-458(1985).			
CC	-----			
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CC	-----			
DR	EMBL; K02083; AAB59873.1;			
DR	PIR; X01762; CAA25903.1; ALT_SEQ.			
DR	PIR; A03974; VCLJVL.			
DR	HIV_K02083; ENVS_PV22.			
DR	InterPro; IPR000328; Env_GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120_1.			
KW	Pfam; PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	511	EXTEIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	512	856	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	226	331	BY SIMILARITY.
FT	DISULFID	378	445	BY SIMILARITY.
FT	DISULFID	385	418	BY SIMILARITY.
FT	CARBOHYD	88	136	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	116	136	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	197	197	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	230	230	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	234	234	N-LINKED (GLCNAC . . . ) (POTENTIAL).
FT	CARBOHYD	241	241	N-LINKED (GLCNAC . . . ) (POTENTIAL).

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FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
FT SITE 760 760 IN-FRAME TERMINATION CODON.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 219 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 439 BY SIMILARITY.
FT DISULFID 383 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600E8A7A08 CRC64;

Query Match 93.9%; Score 184; DB 1; Length 856;
Best Local Similarity 94.4%; Pred. No. 6,6e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOQEKNEOELLELDKWSLWMWF 36
Db 638 YTSLIYTLIESQNOQEKNEOELLELDKWSLWMWF 673

ENV_HV133 STANDARD; PRT; 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range."

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RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome."
RL J. Virol. 64:4016-4020(1990).
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CC -----
DR EMBL: M38427; AAA45067.1;
DR HIV; M38427; ENVSEF33.
DR InterPro: IPR000328; ENV_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane;
KW Signal.
FT CHAIN 1 31 BY SIMILARITY.
FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C910D CRC64;

Query Match 92.9%; Score 182; DB 1; Length 852;
Best Local Similarity 91.7%; Pred. No. 1.2e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOQEKNEOELLELDKWSLWMWF 36
Db 634 YTSLIYTLIESQNOQEKNEOELLELDKWSLWMWF 669

RESULT 11

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97188 MW; 3373C68B84C1AFC CRC64;

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Query Match          96.9%; Score 190; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTSLHRLIEESQNOEKNEQELLELDKASLWNMF 36
Db 638 YTSLSHLSIEESQNOEKNEQELLELDKASLWNMF 673

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RESULT 5
ENV_HV11M STANDARD; PRT; 856 AA.
ID ENV_HV11M
AC 070626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
   Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
   infected with HIV type 1 (HIV type 111B).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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   or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U12055; AAA76690.1; -
CC DR GlycoSuiteDB; O70626; -
CC DR InterPro; IPR000328; Env_GP41.

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DR DR GlycoSuiteDB; O70626; -
DR DR InterPro; IPR000328; Env_GP41.

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DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
   Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
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FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

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Query Match          96.9%; Score 190; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTSLHRLIEESQNOEKNEQELLELDKASLWNMF 36
Db 638 YTSLSHLSIEESQNOEKNEQELLELDKASLWNMF 673

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RESULT 6
ENV_HV1BR STANDARD; PRT; 861 AA.
ID ENV_HV1BR
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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```

OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

```

Query Match	Best Local Similarity	Score	DB 1:	Length	DB 2:	Score	DB 3:	Length	DB 4:	Score	DB 5:	Length	DB 6:	Score	DB 7:	Length	DB 8:	Score	DB 9:	Length	DB 10:	Score	DB 11:	Length	DB 12:	Score	DB 13:	Length	DB 14:	Score	DB 15:	Length	DB 16:	Score	DB 17:	Length	DB 18:	Score	DB 19:	Length	DB 20:	Score	DB 21:	Length	DB 22:	Score	DB 23:	Length	DB 24:	Score	DB 25:	Length	DB 26:	Score	DB 27:	Length	DB 28:	Score	DB 29:	Length	DB 30:	Score	DB 31:	Length	DB 32:	Score	DB 33:	Length	DB 34:	Score	DB 35:	Length	DB 36:	Score	DB 37:	Length	DB 38:	Score	DB 39:	Length	DB 40:	Score	DB 41:	Length	DB 42:	Score	DB 43:	Length	DB 44:	Score	DB 45:	Length	DB 46:	Score	DB 47:	Length	DB 48:	Score	DB 49:	Length	DB 50:	Score	DB 51:	Length	DB 52:	Score	DB 53:	Length	DB 54:	Score	DB 55:	Length	DB 56:	Score	DB 57:	Length	DB 58:	Score	DB 59:	Length	DB 60:	Score	DB 61:	Length	DB 62:	Score	DB 63:	Length	DB 64:	Score	DB 65:	Length	DB 66:	Score	DB 67:	Length	DB 68:	Score	DB 69:	Length	DB 70:	Score	DB 71:	Length	DB 72:	Score	DB 73:	Length	DB 74:	Score	DB 75:	Length	DB 76:	Score	DB 77:	Length	DB 78:	Score	DB 79:	Length	DB 80:	Score	DB 81:	Length	DB 82:	Score	DB 83:	Length	DB 84:	Score	DB 85:	Length	DB 86:	Score	DB 87:	Length	DB 88:	Score	DB 89:	Length	DB 90:	Score	DB 91:	Length	DB 92:	Score	DB 93:	Length	DB 94:	Score	DB 95:	Length	DB 96:	Score	DB 97:	Length	DB 98:	Score	DB 99:	Length	DB 100:	Score	DB 101:	Length	DB 102:	Score	DB 103:	Length	DB 104:	Score	DB 105:	Length	DB 106:	Score	DB 107:	Length	DB 108:	Score	DB 109:	Length	DB 110:	Score	DB 111:	Length	DB 112:	Score	DB 113:	Length	DB 114:	Score	DB 115:	Length	DB 116:	Score	DB 117:	Length	DB 118:	Score	DB 119:	Length	DB 120:	Score	DB 121:	Length	DB 122:	Score	DB 123:	Length	DB 124:	Score	DB 125:	Length	DB 126:	Score	DB 127:	Length	DB 128:	Score	DB 129:	Length	DB 130:	Score	DB 131:	Length	DB 132:	Score	DB 133:	Length	DB 134:	Score	DB 135:	Length	DB 136:	Score	DB 137:	Length	DB 138:	Score	DB 139:	Length	DB 140:	Score	DB 141:	Length	DB 142:	Score	DB 143:	Length	DB 144:	Score	DB 145:	Length	DB 146:	Score	DB 147:	Length	DB 148:	Score	DB 149:	Length	DB 150:	Score	DB 151:	Length	DB 152:	Score	DB 153:	Length	DB 154:	Score	DB 155:	Length	DB 156:	Score	DB 157:	Length	DB 158:	Score	DB 159:	Length	DB 160:	Score	DB 161:	Length	DB 162:	Score	DB 163:	Length	DB 164:	Score	DB 165:	Length	DB 166:	Score	DB 167:	Length	DB 168:	Score	DB 169:	Length	DB 170:	Score	DB 171:	Length	DB 172:	Score	DB 173:	Length	DB 174:	Score	DB 175:	Length	DB 176:	Score	DB 177:	Length	DB 178:	Score	DB 179:	Length	DB 180:	Score	DB 181:	Length	DB 182:	Score	DB 183:	Length	DB 184:	Score	DB 185:	Length	DB 186:	Score	DB 187:	Length	DB 188:	Score	DB 189:	Length	DB 190:	Score	DB 191:	Length	DB 192:	Score	DB 193:	Length	DB 194:	Score	DB 195:	Length	DB 196:	Score	DB 197:	Length	DB 198:	Score	DB 199:	Length	DB 200:	Score	DB 201:	Length	DB 202:	Score	DB 203:	Length	DB 204:	Score	DB 205:	Length	DB 206:	Score	DB 207:	Length	DB 208:	Score	DB 209:	Length	DB 210:	Score	DB 211:	Length	DB 212:	Score	DB 213:	Length	DB 214:	Score	DB 215:	Length	DB 216:	Score	DB 217:	Length	DB 218:	Score	DB 219:	Length	DB 220:	Score	DB 221:	Length	DB 222:	Score	DB 223:	Length	DB 224:	Score	DB 225:	Length	DB 226:	Score	DB 227:	Length	DB 228:	Score	DB 229:	Length	DB 230:	Score	DB 231:	Length	DB 232:	Score	DB 233:	Length	DB 234:	Score	DB 235:	Length	DB 236:	Score	DB 237:	Length	DB 238:	Score	DB 239:	Length	DB 240:	Score	DB 241:	Length	DB 242:	Score	DB 243:	Length	DB 244:	Score	DB 245:	Length	DB 246:	Score	DB 247:	Length	DB 248:	Score	DB 249:	Length	DB 250:	Score	DB 251:	Length	DB 252:	Score	DB 253:	Length	DB 254:	Score	DB 255:	Length	DB 256:	Score	DB 257:	Length	DB 258:	Score	DB 259:	Length	DB 260:	Score	DB 261:
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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

```

```

Query Match 96.9%; Score 190; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 YTSLIHRLIEESONOQKNEQLELDKWSLWNNF 36
DB 633 YTSLIHSLIEESONOQKNEQLELDKWSLWNNF 668

```

```

RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
   Viruses: Retrovirdae; Retroviridae; Lentiviridae;
   NCBI_TaxID=11678;
RA MEDLINE=8511123; PubMed=2578615;
RA Rafter L., Haseltine W., Patarca R., Liyak K.J., Starich B.R.,
RA Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Peteway S.R.Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RT Nature 313:277-284 (1985).
RL [2]
RN DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
  potential glycosylation sites of the type 1 recombinant human
  immunodeficiency virus envelope glycoprotein (gp120) expressed in
  Chinese hamster ovary cells."
RT J. Biol. Chem. 265:10373-10382 (1990).
CC -----
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```

CC EMBL; M15654; AAA4205.1;
CC PIR; A03973; VCLJH3.
DR HIV; M15654; ENVSH102.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931BB27 CRC64;

```

```

Query Match 96.9%; Score 190; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 YTSLIHRLIEESONOQKNEQLELDKWSLWNNF 36
DB 638 YTSLIHSLIEESONOQKNEQLELDKWSLWNNF 673

```

```

RESULT 3
ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;

```



GenCore version 5.1.4-P5.4578  
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OM protein - protein search, using SW model

Run on: May 16, 2003, 10:53:39 ; Search time 6.07229 Seconds

(without alignments)  
245.895 Million cell updates/sec

Title: US-09-623-533A-538

Perfect score: 196

Sequence: 1 YTSLIHRLIESQNOQEKNEQELLELDKWSLIMWF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	190	96.9	851	ENV_HV1B8	P04582 human immun
2	190	96.9	856	ENV_HV1B1	P03375 human immun
3	190	96.9	856	ENV_HV1B2	P04578 human immun
4	190	96.9	856	ENV_HV1B3	P04624 human immun
5	190	96.9	856	ENV_HV1B4	P03377 human immun
6	190	96.9	856	ENV_HV1B5	P03377 human immun
7	187	95.4	853	ENV_HV1B6	P19551 human immun
8	185	94.4	853	ENV_HV1B7	P19551 human immun
9	184	93.9	856	ENV_HV1B8	P08878 human immun
10	182	92.9	852	ENV_HV1B9	P19549 human immun
11	181	92.3	847	ENV_HV1B10	P19550 human immun
12	181	92.3	856	ENV_HV1B11	P03376 human immun
13	180	91.8	853	ENV_HV1B12	P12487 human immun
14	180	91.8	855	ENV_HV1B13	P04580 human immun
15	177	90.3	867	ENV_HV1B14	P12489 human immun
16	175	89.3	847	ENV_HV1B15	P03378 human immun
17	174	88.8	855	ENV_HV1B16	P03378 human immun
18	174	88.8	855	ENV_HV1B17	P03378 human immun
19	172	87.8	856	ENV_HV1B18	P03378 human immun
20	170	86.7	853	ENV_HV1B19	P04581 human immun
21	170	86.7	855	ENV_HV1B20	P08888 human immun
22	168	85.7	843	ENV_HV1B21	P20888 human immun
23	167	85.2	846	ENV_HV1B22	P18799 human immun
24	167	85.2	848	ENV_HV1B23	P20871 human immun
25	167	85.2	861	ENV_HV1B24	P18191 human immun
26	166	84.7	859	ENV_HV1B25	P04583 human immun
27	165	84.2	852	ENV_HV1B26	P12488 human immun
28	161	82.1	868	ENV_HV1B27	P05879 human immun
29	157	80.1	863	ENV_HV1B28	P05881 human immun
30	149	76.0	854	ENV_HV1B29	P17281 chimpanzee
31	148	75.5	856	ENV_HV1B30	P05881 human immun
32	91	46.4	854	ENV_HV1B31	O02837 simian immu
33	86	43.9	885	ENV_HV1B32	P12492 simian immu

34	85	43.4	860	ENV_HV2BE	P18094 human immun
35	84	42.9	881	ENV_HV2BK	P05884 simian immu
36	84	42.9	882	ENV_HV2BL	P05885 simian immu
37	82	41.8	857	ENV_HV2BR	O74126 human immun
38	82	41.8	859	ENV_HV2BS	P15831 human immun
39	81	41.3	859	ENV_HV2CA	P24105 human immun
40	81	41.3	889	ENV_HV2CB	P19503 simian immu
41	80	40.8	880	ENV_HV2CC	P11267 simian immu
42	79	40.3	858	ENV_HV2CD	P04577 human immun
43	78	39.8	768	ENV_HV2CE	P27757 simian immu
44	78	39.8	851	ENV_HV2CF	P17755 human immun
45	78	39.8	851	ENV_HV2CG	P18040 human immun

## ALIGNMENTS

RESULT 1	ENV_HV1B8	STANDARD:	PRT:	851 AA.
ID	ENV_HV1B8			
AC	P04582:			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentiviridae.			
OX	NCBI_TaxID=11684;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8511123; Pubmed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumanster K., Ivanoff L., Peltway S.R., Pearson M.L., Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;			
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RT	Nature 313:277-284(1985).			
RL				
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CC	EMBL: K02011; AAA4661.1; -			
DR	HIV: K02011; ENV5B8.			
DR	Glycositedb: P04582; -			
DR	InterPro: IPR000328; Env GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120.1.			
DR	Pfam: PF00517; GP41.1.			
KW	AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	851	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	296	331	BY SIMILARITY.
FT	DISULFID	378	440	BY SIMILARITY.
FT	DISULFID	385	413	BY SIMILARITY.
FT	CARBOHYD	88	88	N-LINKED (GLCNAc: . . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAc: . . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAc: . . .) (POTENTIAL).



C:Superfamily: type E retrovirus env polypeptide

Query Match 91.8%; Score 180; DB 2; Length 357;  
Best Local Similarity 91.7%; Pred. No. 4,8e-14;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTSIHRLEESQNOQEKNEOELLELDKASLWNF 36  
DB 139 YTGILYRLIEESQNOQEKNEOELLELDKASLWNF 174

RESULT 12

S54384

envelope polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999

C:Accession: S54384

R:Rheodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

Reference number: S54377

Accession: S54384

status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-853 <THX>

A:Cross-references: EMBL:M2639; NID:g329377; PIDN:AAA45370.1; PID:g329385

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: polypeptide

Query Match 91.8%; Score 180; DB 2; Length 853;  
Best Local Similarity 91.7%; Pred. No. 1.3e-13;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTSIHRLEESQNOQEKNEOELLELDKASLWNF 36  
DB 635 YTGILYRLIEESQNOQEKNEOELLELDKASLWNF 670

RESULT 13

VCLJZR

env polypeptide precursor - human immunodeficiency virus Zr-6

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus Zr-6

C>Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999

C:Accession: D26192

R:Srivivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

Gene 52, 71-82, 1987

A:Title: Molecular characterization of human immunodeficiency virus from zaire: nucleotid

Reference number: A26192; MUID:87248097; PMID:3036660

Accession: D26192

A:Molecule type: DNA

A:Residues: 1-855 <SRI>

A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-85/Product: env polypeptide #status predicted <MAT>

F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>

F:501-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,145,158,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 91.8%; Score 180; DB 1; Length 855;  
Best Local Similarity 91.7%; Pred. No. 1.3e-13;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

env polypeptide M - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

C:Accession: A41621

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence divers

A:Reference number: A41621; MUID:92107924; PMID:1763038

Accession: A41621

A:Molecule type: DNA

A:Residues: 1-445 <BUR>

A:Cross-references: GB:M77228; NID:g328627; PIDN:AA03790.1; PID:g555013

A>Note: this virus was isolated from the mother

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:426-445/Domain: transmembrane #status predicted <TM>

F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding s1

QY 1 YTSIHRLEESQNOQEKNEOELLELDKASLWNF 36  
DB 380 YTSIYRLIEESQNOQEKNEOELLELDKASLWNF 415

RESULT 15

T09448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JREF)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

C:Accession: T09448

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

Accession: T09448

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

Query Match 90.3%; Score 177; DB 2; Length 847;  
Best Local Similarity 91.7%; Pred. No. 2.9e-13;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTSIHRLEESQNOQEKNEOELLELDKASLWNF 36  
DB 629 YTSIYRLIEESQNOQEKNEOELLELDKASLWNF 664

Search completed: May 16, 2003, 11:25:11

Job time: 13.1446 secs



env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03973  
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A93353; MUID:85111123; PMID:2578615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAAA42  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:511/Product: exterior membrane glycoprotein #status predicted <TM>  
F:2-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic  
Query Match 96.9%; Score 190; DB 1; Length 856;  
Best Local Similarity 97.2%; Pred. No. 8.1e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWNMF 36  
Db 638 YTSLIHSLIEESQNOEKNEQELLELDKWSLWNMF 673  
RESULT 4  
VCLJ3W  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allzon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; MUID:85099333; PMID:2981635  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <WAI>  
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB5951.1; PID:g326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-516/Product: exterior membrane glycoprotein #status predicted <TM>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic  
Query Match 96.9%; Score 190; DB 1; Length 861;  
Best Local Similarity 97.2%; Pred. No. 8.2e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWNMF 36  
Db 643 YTSLIHSLIEESQNOEKNEQELLELDKWSLWNMF 678  
RESULT 5  
CA1621  
env polyprotein P - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polyprotein

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: CA1621  
R:Bugter, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi  
A:Reference number: A41621; MUID:92107924; PMID:1763038  
A:Accession: CA1621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015  
A>Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:424-443/Domain: transmembrane #status predicted <TM>  
F:9,23,36,48,76,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:  
Query Match 94.4%; Score 185; DB 2; Length 443;  
Best Local Similarity 94.4%; Pred. No. 1.5e-14;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWNMF 36  
Db 378 YTSLIYNLIEESQNOEKNEQELLELDKWSLWNMF 413  
RESULT 6  
VCLJ3W  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1).  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks,  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-841/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,  
Query Match 94.4%; Score 185; DB 1; Length 856;  
Best Local Similarity 94.4%; Pred. No. 3.2e-14;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLIHRLIEESQNOEKNEQELLELDKWSLWNMF 36  
Db 638 YTSLIYNLIEESQNOEKNEQELLELDKWSLWNMF 673  
RESULT 7  
VCLJ3C  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-538

Perfect score: 196

Sequence: 1 YTSLIHRLIESQNOEKNEOELLELDKWSIWMNF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	96.9	851	2	S33985 env polypeptide -
2	190	96.9	854	2	S13288 env protein - huma
3	190	96.9	856	1	VCLJH3 env polypeptide pr
4	190	96.9	861	1	VCLJH3 env polypeptide pr
5	185	94.4	443	2	CA1621 env polypeptide P
6	185	94.4	856	1	VCLJ3W env polypeptide pr
7	184	93.9	861	1	VCLJ3C env polypeptide pr
8	181	92.3	357	2	S21994 env polypeptide g
9	181	92.3	358	2	S21998 env polypeptide g
10	181	92.3	856	1	VCLJVL env polypeptide pr
11	180	91.8	357	2	S21996 env polypeptide pr
12	180	91.8	853	2	S54384 env polypeptide g
13	180	91.8	855	1	VCLJ2R env polypeptide pr
14	177	90.3	847	2	T09448 env polypeptide M
15	177	90.3	847	2	S13289 env polypeptide g
16	175	89.3	358	2	S22002 env protein - huma
17	175	89.3	358	2	S22000 env polypeptide g
18	175	89.3	358	2	S70417 env polypeptide g
19	175	89.3	358	2	S70417 env polypeptide g
20	174	88.8	855	1	VCLJ2A env polypeptide pr
21	172	87.8	852	2	T12016 env polypeptide pr
22	172	87.8	859	1	VCLJMN env polypeptide pr
23	171	87.2	357	2	S22006 env polypeptide pr
24	171	87.2	357	2	S22004 env polypeptide g
25	168	85.7	357	2	S21992 env polypeptide pr
26	168	85.7	843	1	H44001 env polypeptide pr
27	167	85.2	729	1	VCLJXK env polypeptide pr
28	167	85.2	846	1	VCLJND env polypeptide pr
29	167	85.2	861	1	VCLJKB env polypeptide pr

30	166	84.7	859	2	T01672 env polypeptide
31	165	84.2	454	2	B41621 env polypeptide D
32	165	84.2	852	1	VCLJBR env polypeptide -
33	161	82.1	868	1	VCLJH4 env polypeptide -
34	159	81.1	136	2	JU0266 env polypeptide
35	159	81.1	136	2	JU0954 env polypeptide
36	149	76.0	854	1	VCLJST1 env polypeptide pr
37	148	75.5	856	1	A44963 env polypeptide pr
38	145	74.0	357	2	S21990 env polypeptide g
39	136	69.4	877	2	S49197 env polypeptide p
40	119	60.7	863	2	A53034 env polypeptide -
41	86	43.9	151	2	S30448 env protein - huma
42	86	43.9	151	2	S30452 env protein - huma
43	86	43.9	151	2	S30451 env protein - huma
44	86	43.9	366	2	B41565 env polypeptide -
45	86	43.9	885	2	S04322 env polypeptide -

## ALIGNMENTS

## RESULT 1

S33985 env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F. submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:Z11530; NID:960192; PDB:CAA77628.1; PID:960199

C:Superfamily: type E retrovirus env polypeptide

Query Match 96.9%; Score 190; DB 2; Length 851;

Best Local Similarity 97.2%; Pred. No. 8.1e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIESQNOEKNEOELLELDKWSIWMNF 36

DB 633 YTSLIHRLIESQNOEKNEOELLELDKWSIWMNF 668

RESULT 2

S13288 env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 96.9%; Score 190; DB 2; Length 854;

Best Local Similarity 97.2%; Pred. No. 8.1e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIESQNOEKNEOELLELDKWSIWMNF 36

DB 636 YTSLIHRLIESQNOEKNEOELLELDKWSIWMNF 671

RESULT 3

VCLJH3

AC AAY89136;

XX 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 574.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS WO9959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

PS Disclosure; Page 30; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y9005 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

SQ Sequence 36 AA;

Query Match 96.9%; Score 190; DB 21; Length 36;

Best Local Similarity 97.2%; Pred. No. 1.8e-16;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIHRIEESONQOEKNEOELLELDKMASLWMWF 36

DB 1 YTSIHRIEESONQOEKNEOELLELDKMASLWMWF 36

Search completed: May 16, 2003, 11:12:06  
 Job time : 33.4578 secs

XX Sequence 36 AA:

Query Match 96.9%; Score 190; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESQNOEKNEDELLELDKWSLWNMF 36  
1 YTSLIHSLIEESQNOEKNEDELLELDKWSLWNMF 36

RESULT 13

AA8729 AAY8729 standard; peptide: 36 AA.

AC AAY8729;

XX 23-MAY-2000 (first entry)

DT Core polypeptide fragment T No. 84.

KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KM anti-fusogenic; differentiation factor; interleukin; interferon;  
KM colony stimulating factor; hormone; angiogenic factor.

XX Undefined.

OS WO959615-A1.

XX 25-NOV-1999.

PD 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

PR (TRIM-) TRIMERIS INC.

PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI: 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence -

PS Disclosure; Page 22; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AY88651-190055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.

XX Sequence 36 AA:

Query Match 96.9%; Score 190; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESQNOEKNEDELLELDKWSLWNMF 36

DB 1 YTSLIHSLIEESQNOEKNEDELLELDKWSLWNMF 36

RESULT 14

AA89135 AAY89135 standard; peptide: 36 AA.

AC AAY89135;

XX 23-MAY-2000 (first entry)

DT Core polypeptide fragment T No. 573.

DE Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
XX anti-fusogenic; differentiation factor; interleukin; interferon;  
XX colony stimulating factor; hormone; angiogenic factor.

XX Undefined.

OS WO959615-A1.

XX 25-NOV-1999.

PD 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

PR (TRIM-) TRIMERIS INC.

PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI: 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence -

PS Disclosure; Page 30; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AY88651-190055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.

XX Sequence 36 AA:

Query Match 96.9%; Score 190; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESQNOEKNEDELLELDKWSLWNMF 36

DB 1 YTSLIHSLIEESQNOEKNEDELLELDKWSLWNMF 36

RESULT 15

AA89136 AAY89136 standard; peptide: 36 AA.

XX



XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI: 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX Claim 12; Page 24; 148pp; English.

XX The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
XX helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is  
XX located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
XX critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
XX interacts with members of the formyl peptide receptor (FPR) family and  
XX thereby up-regulates an inflammatory response, and acts as a potent  
XX chemoattractant and activator of human peripheral blood phagocytes  
XX (but not T cells). The present peptide can be used to modulate an  
XX inflammatory response in a subject.

SQ Sequence 36 AA:  
Query Match 96.9%; Score 190; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIRLIEESQNOEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIRLIEESQNOEKNEDELLEDKWASLWNMF 36

RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide; 36 AA.  
AAB52688;  
DT 23-FEB-2001 (first entry)  
DE T20/DP178 peptide fragment #66.  
XX Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX chemoattractant.  
XX Human immunodeficiency virus type 1.  
XX WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI: 2000-656493/63.

XX PT Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
XX PT antagonist is used to modulate inflammation -  
XX Claim 12; Page 25; 148pp; English.

XX The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
XX helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is  
XX located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
XX critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
XX interacts with members of the formyl peptide receptor (FPR) family and  
XX thereby up-regulates an inflammatory response, and acts as a potent  
XX chemoattractant and activator of human peripheral blood phagocytes  
XX (but not T cells). The present peptide can be used to modulate an  
XX inflammatory response in a subject.

SQ Sequence 36 AA:  
Query Match 96.9%; Score 190; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIRLIEESQNOEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIRLIEESQNOEKNEDELLEDKWASLWNMF 36

RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide; 36 AA.  
AAB52818;  
DT 23-FEB-2001 (first entry)  
DE T20/DP178 peptide fragment #97.  
XX Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX chemoattractant.  
XX Human immunodeficiency virus type 1.  
XX WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI: 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX Claim 14; Page 40; 148pp; English.

XX The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
XX helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is  
XX located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
XX critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
XX interacts with members of the formyl peptide receptor (FPR) family and  
XX thereby up-regulates an inflammatory response, and acts as a potent  
XX chemoattractant and activator of human peripheral blood phagocytes  
XX (but not T cells). The present peptide can be used to modulate an  
XX inflammatory response in a subject.



RESULT	6
AAY31955	
ID	AAY31955 standard; Peptide: 36 AA.
XX	
AC	AAY31955;
XX	
DT	21-DEC-1999 (first entry)
XX	
DE	Synthetic peptide T-20 (DP-178).
XX	
KM	T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
OS	Synthetic.
OS	Human immunodeficiency virus type 1.
FT	
FT	Key Location/Qualifiers
FT	Modified-site 1 /note= "N-terminal acetyl"
FT	Modified-site 36 /note= "C-terminal amide"
XX	
PN	W09948513-A1.
PD	
PD	30-SEP-1999.
XX	
PF	22-MAR-1999; 99WO-US06230.
XX	
PR	23-MAR-1998; 98US-0045920.
PR	01-MAY-1998; 98US-0071877.
PA	(TRIM-) TRIMERIS INC.
PI	
PI	Kang M, Bray B, Lichy M, Mader C, Merutka G;
XX	
DR	WPI; 1999-591038/50.
XX	
PT	Methods of peptide synthesis, particularly used to produce T-20 or
PT	T-20 like peptides -
PS	
PS	Claim 1; Page 102; 120pp; English.
XX	
CC	The present sequence represents an N- and C-terminal modified
CC	peptide, designated T-20 (or DP-178), corresponding to amino acids
CC	638-673 of the Transmembrane protein gp41 of HIV-1 LAI isolate.
CC	The invention relates to methods for the synthesis of peptides,
CC	in particular T-20 and T-20-like peptides. The method involves
CC	synthesizing specific side-chain protected peptide fragment
CC	intermediates of T-20 or a T-20-like peptide on a solid support,
CC	coupling the protected fragments in solution to form a protected
CC	T-20 or T-20-like peptide, followed by deprotection of the side
CC	chains to yield the final T-20 or T-20-like peptide. The invention
CC	also relates to individual peptide fragments (see AAY31956-73) which
CC	act as intermediates in the synthesis of peptides of interest (e.g.
CC	T-20), and to particular groups of peptide fragments which act as
CC	intermediates for the synthesis of the peptide of interest. The
CC	method allows for the large scale, economical production of high
CC	purity peptides.
XX	
XX	
SQ	Sequence 36 AA:
OQuery Match	96.9%; Score 190; DB 20; Length 36;
Best Local Similarity	97.2%; Pred No. 1.8e-16;
Matches 35; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 YTSLIHRLIEESQNOEKNEDELLELDKASLMMNF 36 
Db	1 YTSLIHSLIEESQNOEKNEDELLELDKASLMMNF 36

ID	AAV31974	standard; Peptide; 36 AA.
XX		
AC	AAV31974;	
XX		
DT	21-DEC-1999	(first entry)
XX		
DE	HIV-1 LAI gp41 T-20 peptide.	
XX		
KW	T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.	
XX		
OS	Human immunodeficiency virus type 1.	
XX		
PN	W09948513-A1.	
PD	30-SEP-1999.	
XX		
PF	22-MAR-1999; 99WO-US06230.	
XX		
PR	23-MAR-1998; 98US-0045920.	
PR	01-MAY-1998; 98US-0071877.	
XX		
PA	(TRIM-) TRIMERIS INC.	
XX		
PI	Kang M, Bray B, Lichty M, Mader C, Merutka G;	
XX		
DR	WPI; 1999-591038/50.	
XX		
PT	Methods of peptide synthesis, particularly used to produce T-20 or	
PT	T-20 like peptides	
PS	Disclosure; Page 9; 120pp; English.	
XX		
CC	The present sequence represents a peptide, designated T-20 (or	
CC	DP-178), that corresponds to amino acids 638-673 of the	
CC	transmembrane protein gp41 of HIV-1 LAI isolate. The invention	
CC	relates to methods for the synthesis of peptides, in particular	
CC	C- and N-terminal modified T-20 (see AAV31955) and T-20-like peptides.	
CC	The method involves synthesizing specific side-chain protected	
CC	peptide fragment intermediates (see AAV31956-73) of T-20 or a	
CC	T-20-like peptide on a solid support, coupling the protected	
CC	fragments in solution to form a protected T-20 or T20-like peptide,	
CC	followed by deprotection of the side chains to yield the final T-20	
CC	or T-20-like peptide. The invention also relates to individual	
CC	peptide fragments which act as intermediates in the synthesis of	
CC	peptides of interest (e.g. T-20), and to particular groups of	
CC	peptide fragments which act as intermediates in the synthesis of	
CC	the peptide of interest. The method allows for the large scale,	
CC	economical production of high purity peptides.	
SO		
Sequence	36 AA:	
Query Match	96.9%; Score 190; DB 20; Length 36;	
Best Local Similarity	97.2%; Pred. No. 1.8e-16;	
Matches	35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	1 YTSILHRLIEESONQOEKNEQELLELDKWSLIMNF 36	
DB	1 YTSILHSLIEESONQOEKNEQELLELDKWSLIMNF 36	
RESULT 8		
AAAB52655		
ID	AAAB52655 standard; Peptide; 36 AA.	
XX		
AC	AAAB52655;	
XX		
DT	23-FEB-2001 (first entry)	
XX		
DE	T20/DP178 peptide fragment #33.	
XX		
KW	Antiinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;	
KW	formyl peptide receptor family; FPR; inflammatory response up-regulation;	
KW	chemottractant.	

ID	AA	Seq ID	Score	DB	Length	Pred. No.	Mismatches	Indels	Gaps
1	AYY22912	19-AUG-1999 (first entry)	96.9%	190	36	1.8e-16	0	0	0
2	AYY22912	SEQ ID NO. 108 from WO9820036.	96.9%	190	36	1.8e-16	0	0	0
3	AYY22912	HIV; gp41 protein; constrained helical peptide; HIV infection; vaccine; antibody; viral membrane fusion; viral infectivity; ligand affinity purification; protein A replacement; immunoglobulin purification; epitope mimic.	96.9%	190	36	1.8e-16	0	0	0
4	AYY22912	Human immunodeficiency virus.	96.9%	190	36	1.8e-16	0	0	0
5	AYY22912	WO9820036-A1.	96.9%	190	36	1.8e-16	0	0	0
6	AYY22912	14-MAY-1998.	96.9%	190	36	1.8e-16	0	0	0
7	AYY22912	05-NOV-1997; 97WO-US20069.	96.9%	190	36	1.8e-16	0	0	0
8	AYY22912	16-JUN-1997; 97US-0876698.	96.9%	190	36	1.8e-16	0	0	0
9	AYY22912	06-NOV-1996; 96US-0743698.	96.9%	190	36	1.8e-16	0	0	0
10	AYY22912	(GETH ) GENENTECH INC.	96.9%	190	36	1.8e-16	0	0	0
11	AYY22912	Bristed A, Judice JK, McDowell RS, Phelan JC, Starovarsnik MA, Wells JA;	96.9%	190	36	1.8e-16	0	0	0
12	AYY22912	WPI: 1998-286866/25.	96.9%	190	36	1.8e-16	0	0	0
13	AYY22912	Production of constrained helical peptide(s) by linking side chains on termini of octa-peptide - derived from human immunodeficiency virus gp41 protein, useful in vaccines for treatment and prevention of infection	96.9%	190	36	1.8e-16	0	0	0
14	AYY22912	Disclosure; Page 233-234; 279pp; English.	96.9%	190	36	1.8e-16	0	0	0
15	AYY22912	Peptides AYY22805-Y22912 are derived from Human immunodeficiency virus (HIV). Specifically, AYY22810-Y22910 are derived from gp41 proteins of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and AAY22903 represent consensus sequences of various sections of the gp41 protein). Sequences derived from the peptides are used to produce constrained helical peptides of the invention. The constrained helical peptide is produced by synthesizing an octapeptide in which both terminal amino acids have a side-chain that includes a group able to form an amide bond, and cyclizing the octapeptide by reacting the specified side-chain residues with a difunctional linker to produce two amide bonds.	96.9%	190	36	1.8e-16	0	0	0
16	AYY22912	The constrained helical peptides are used to treat or prevent HIV infection, especially as vaccines that generate antibodies that prevent viral membrane fusion or infectivity. Vaccines may contain, constrained helical peptides derived from several different strains of HIV. The antibodies are also useful for diagnosing HIV infection. Other uses for the constrained helical peptides are in affinity purification of ligands (particularly where complete binding protein is not readily available), e.g. replacements for protein A in immunoglobulin purification; as epitope mimics for antibody production; for isolation of synthetic antibody clones from phage display libraries; or as stable forms of "floppy" peptides or proteins.	96.9%	190	36	1.8e-16	0	0	0
17	AYY22912	Sequence 36 AA:	96.9%	190	36	1.8e-16	0	0	0
18	AYY22912	Query Match	96.9%	190	36	1.8e-16	0	0	0
19	AYY22912	Best Local Similarity 97.2%; Pred. No. 1.8e-16;	96.9%	190	36	1.8e-16	0	0	0
20	AYY22912	Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	96.9%	190	36	1.8e-16	0	0	0
21	AYY22912	1 YTSILHRIIEESONOEKNEDELLDKWASLWNNF 36	96.9%	190	36	1.8e-16	0	0	0
22	AYY22912	1 YTSILHRIIEESONOEKNEDELLDKWASLWNNF 36	96.9%	190	36	1.8e-16	0	0	0

Query Match	Best Local Similarity	Score 190;	DB 19;	Length 36;
Matches 35; Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
1 YTSLLHRLIEESQNOOEKNEDELLDLKQKASLMMNF 36	1 YTSLLHRLIEESQNOOEKNEDELLDLKQKASLMMNF 36			
1 YTSLLHRLIEESQNOOEKNEDELLDLKQKASLMMNF 36	1 YTSLLHRLIEESQNOOEKNEDELLDLKQKASLMMNF 36			

PA (UYDU-) UNIV DUKE.  
 XX  
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Petterway SR, Wild CT;  
 XX  
 XX WPI: 1995-036105/05.  
 XX  
 XX Computer search generated synthetic peptides - are inhibitors of  
 PT HIV transmission  
 XX  
 PS Claim 11; Page 132, 182pp; English.  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibit transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.

XX SQ Sequence 36 AA;

Query Match 96.9%; Score 190; DB 16; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEOELLEDKWASLWMPF 36  
 |||||  
 DB 1 YTSLIHSLIEESONOQEKNEOELLEDKWASLWMPF 36

RESULT 2  
 AAR98398

ID AAR98398 standard; peptide; 36 AA.

XX AC AAR98398;

XX DT 17-FEB-1997 (first entry)

XX DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.

XX PR Antifusogenic activity; antiviral capability; coiled-coil peptide;

KW ALLMORT5; 107x178x4; PLZIP search motif; viral transmission; HIV;

KW influenza virus; hepatitis B virus.

XX Human immunodeficiency virus type 1.

PN W09619495-A1.

XX PD 27-JUN-1996.

XX PF 20-DEC-1995; 95WO-US16733.

XX PR 06-JUN-1995; 95US-0470896.

XX PA 20-DEC-1994; 94US-0360107.

XX (TRIM-) TRIMERIS INC.

XX PA (UYDU-) UNIV DUKE.

XX PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;

XX PI Matthews TJ, Petterway SR, Wild CT;

XX DR WPI: 1996-309517/31.

XX PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALLMORT5, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX  
 XX Disclosure: Fig 1; 471pp; English.

CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALLMORT5,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
 CC hepatitis B virus, to a cell.

XX SQ Sequence 36 AA;

Query Match 96.9%; Score 190; DB 17; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEOELLEDKWASLWMPF 36  
 |||||  
 DB 1 YTSLIHSLIEESONOQEKNEOELLEDKWASLWMPF 36

RESULT 3  
 AAW17011

ID AAW17011 standard; peptide; 36 AA.

XX AC AAW17011;

XX DT 30-JUN-1997 (first entry)

XX DE HIV-1 derived peptide useful for treatment of HIV infection.

XX KW HIV; HIV: human; simian immunodeficiency virus; glycoprotein 41;

KW transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;

XX replication; transmission.

XX OS Human immunodeficiency virus type 1 LAI isolate.

XX PN W09640191-A1.

XX PD 19-DEC-1996.

XX PF 06-JUN-1996; 96WO-US09499.

XX PR 07-JUN-1995; 95US-0481957.

XX PA (TRIM-) TRIMERIS INC.

XX PI Johnson RM, Lambert DM;

XX DR WPI: 1997-099886/09.

XX Compns. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.

XX Claim 2; Figure 1; 84pp; English.

CC AAW17011 represents a peptide designated DP-178, a peptide derived  
 CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
 CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
 CC derivatives are used in combination with a therapeutic agent, e.g. a  
 CC reverse transcriptase, viral protease, cyclidine, glycosylation or viral  
 CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
 CC by inhibiting viral replication or inhibiting transmission. They may  
 CC also be used in vaccines for protecting against HIV infection.

XX SQ Sequence 36 AA;

Query Match 96.9%; Score 190; DB 18; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEOELLEDKWASLWMPF 36  
 |||||  
 DB 1 YTSLIHSLIEESONOQEKNEOELLEDKWASLWMPF 36



```

; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 41
; LENGTH: 46
; TYPE: PRF
; ORGANISM: Human immunodeficiency virus type 1
; US-09-779-451-41

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Query Match          97.4%; Score 189; DB 10; Length 46;
Best Local Similarity 97.2%; Pred. No. 8.4e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY      1 YTSLSLIESONQOEKNEQELLELDKWSLWNF 36
      |||||:|||||:|||||:|||||:|||||:|||||
DB      11 YTSLSLIESONQOEKNEQELLELDKWSLWNF 46

```

Search completed: May 16, 2003, 12:10:25  
 Job time : 15.759 secs

J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovashnik  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: DP178  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-854-816-1

Query Match 97.4%; Score 189; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,5e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLIEESONQOEKNEDELLELDKWSLWNMF 36  
1 YTSLSLIEESONQOEKNEDELLELDKWSLWNMF 36

RESULT 13  
US-09-854-816-108  
Sequence 108, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovashnik  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:

US-09-854-816-108

Query Match 97.4%; Score 189; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,5e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLIEESONQOEKNEDELLELDKWSLWNMF 36  
1 YTSLSLIEESONQOEKNEDELLELDKWSLWNMF 36

Db 1 YTSLSLIEESONQOEKNEDELLELDKWSLWNMF 36

RESULT 14  
US-09-848-616-176  
Sequence 176, Application US/09848616  
Publication No. US20030054010A1  
GENERAL INFORMATION:  
APPLICANT: Seibel, Peter  
Dunant, Nicolas  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Lechner, Franziska

TITLE OF INVENTION: Molecular Antigen Array

FILE REFERENCE: 1700.0180002

CURRENT APPLICATION NUMBER: US/09/848,616

CURRENT FILING DATE: 2001-05-05

NUMBER OF SEQ ID NOS: 186

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 176

LENGTH: 37

TYPE: PPT

ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: DPL78c peptide

US-09-848-616-176

Query Match 97.4%; Score 189; DB 9; Length 37;  
Best Local Similarity 97.2%; Pred. No. 6,7e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLIEESONQOEKNEDELLELDKWSLWNMF 36  
1 YTSLSLIEESONQOEKNEDELLELDKWSLWNMF 36

Db 2 YTSLSLIEESONQOEKNEDELLELDKWSLWNMF 37

RESULT 15  
US-09-779-451-41  
Sequence 41, Application US/09779451  
Patent No. US20020094521A1



CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Phd., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-854-816-12  
Query Match 98.5%; Score 191; DB 10; Length 269;  
Best Local Similarity 97.2%; Pred. No. 3,2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYSLIESQNOQEKNEDELLELDKWSLWNF 36  
DB 169 YTSLYSLIESQNOQEKNEDELLELDKWSLWNF 204  
RESULT 5  
US-09-854-816-46  
Sequence 46, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovansik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Phd., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-854-816-46  
Query Match 97.9%; Score 190; DB 10; Length 269;  
Best Local Similarity 97.2%; Pred. No. 4,1e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYSLIESQNOQEKNEDELLELDKWSLWNF 36  
DB 169 YTSLYSLIESQNOQEKNEDELLELDKWSLWNF 204  
RESULT 6  
US-09-874-475-16  
Sequence 16, Application US/09874475  
Publication No. US20020182592A1  
GENERAL INFORMATION:  
APPLICANT: Petropoulos, Christos J.  
APPLICANT: Parkin, Neil T.  
APPLICANT: Whitcomb, Jeanette  
APPLICANT: Huang, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
FILE REFERENCE: 2793/65166  
CURRENT APPLICATION NUMBER: US/09/874,475  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16  
Query Match 97.4%; Score 189; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,5e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYSLIESQNOQEKNEDELLELDKWSLWNF 36  
DB 1 YTSLYSLIESQNOQEKNEDELLELDKWSLWNF 36  
RESULT 7  
US-10-116-797-1  
Sequence 1, Application US/10116797  
Publication No. US20030044411A1  
GENERAL INFORMATION:  
APPLICANT: Oisen, William C.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
FILE REFERENCE: 64672-A  
CURRENT APPLICATION NUMBER: US/10/116,797  
CURRENT FILING DATE: 2002-10-15  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1



LENGTH: 268 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-854-816-13

Query Match 99.0%; Score 192; DB 10; Length 268;  
Best Local Similarity 97.2%; Pred. No. 2.4e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 36  
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Db 168 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 203

RESULT 2  
US-09-854-816-50  
Sequence 50, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
Making Same

NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 233 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-854-816-50

Query Match 98.5%; Score 191; DB 10; Length 233;  
Best Local Similarity 97.2%; Pred. No. 2.7e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 36  
|||||  
Db 168 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 203

RESULT 3

US-09-854-816-9  
Sequence 9, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
Making Same

NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-854-816-9

Query Match 98.5%; Score 191; DB 10; Length 268;  
Best Local Similarity 97.2%; Pred. No. 3.1e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 36  
|||||  
Db 168 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 203

RESULT 4  
US-09-854-816-12

Sequence 12, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
Making Same

NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(Without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-537  
Perfect score: 194  
Sequence: 1 YTSILYSLIESSONQOEKNEDELDKWSLWNVF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*  
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10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	191	98.5	233	10	US-09-854-816-50
3	191	98.5	268	10	US-09-854-816-9
4	191	98.5	269	10	US-09-854-816-12
5	190	97.9	269	10	US-09-854-816-46
6	189	97.4	36	9	US-09-874-475-16
7	189	97.4	36	9	US-10-116-797-1
8	189	97.4	36	9	US-09-493-346-1
9	189	97.4	36	10	US-09-796-202-10
10	189	97.4	36	10	US-09-779-451-5
11	189	97.4	36	10	US-09-834-628-1
12	189	97.4	36	10	US-09-854-816-1
13	189	97.4	36	10	US-09-854-816-108
14	189	97.4	37	9	US-09-848-616-176
15	189	97.4	46	10	US-09-779-451-41
16	189	97.4	56	10	US-09-779-451-4
17	189	97.4	177	9	US-10-040-349B-2
18	189	97.4	221	9	US-10-059-271-84
19	189	97.4	232	9	US-10-059-271-81

20	189	97.4	254	9	US-10-059-271-82	Sequence 82, Appl
21	189	97.4	256	9	US-10-059-271-97	Sequence 97, Appl
22	189	97.4	268	10	US-09-854-816-16	Sequence 16, Appl
23	189	97.4	268	10	US-09-854-816-17	Sequence 17, Appl
24	189	97.4	268	10	US-09-854-816-18	Sequence 18, Appl
25	189	97.4	269	10	US-09-854-816-28	Sequence 28, Appl
26	189	97.4	344	9	US-10-040-349B-1	Sequence 1, Appl1
27	189	97.4	345	9	US-10-026-741-49	Sequence 8, Appl1
28	189	97.4	345	10	US-09-779-451-8	Sequence 93, Appl1
29	189	97.4	391	9	US-10-059-271-93	Sequence 8, Appl1
30	189	97.4	519	10	US-09-756-551A-8	Sequence 8, Appl1
31	189	97.4	853	9	US-10-003-035-33	Sequence 33, Appl1
32	189	97.4	856	10	US-09-476-242-1	Sequence 1, Appl1
33	189	97.4	861	9	US-10-026-741-103	Sequence 103, App
34	189	97.4	1101	9	US-10-003-035-53	Sequence 53, Appl
35	189	97.4	1186	9	US-10-003-035-55	Sequence 55, Appl
36	188	96.9	268	10	US-09-854-816-26	Sequence 26, Appl
37	188	96.9	619	10	US-09-881-609-4	Sequence 4, Appl1
38	188	96.9	646	10	US-09-891-609-2	Sequence 2, Appl1
39	188	96.9	847	10	US-09-476-242-2	Sequence 2, Appl1
40	187	96.4	46	10	US-09-854-816-109	Sequence 109, App
41	187	96.4	267	10	US-09-854-816-38	Sequence 38, Appl
42	187	96.4	268	10	US-09-854-816-41	Sequence 41, Appl
43	187	96.4	269	10	US-09-854-816-6	Sequence 6, Appl1
44	187	96.4	269	10	US-09-854-816-42	Sequence 42, Appl1
45	187	96.4	269	10	US-09-854-816-43	Sequence 43, Appl

## ALIGNMENTS

RESULT 1  
US-09-854-816-13  
Sequence 13, Application US/09854816  
Patent No. US20020151473A1

GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovassnik  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatlin (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-6674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:

APPLICANT: J. Kevin Judice  
 APPLICANT: Robert S. McDowell  
 APPLICANT: J. Christopher Phelan  
 APPLICANT: Melissa A. Starovasnik  
 APPLICANT: James A. Wells  
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
 TITLE OF INVENTION: Making Same  
 NUMBER OF SEQUENCES: 113  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/965,056  
 FILING DATE: 05-No. 6271198-1997  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Torchia, Phd., Timothy E.  
 REGISTRATION NUMBER: 36,700  
 REFERENCE/DOCKET NUMBER: PI00582  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 269 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

Query Match 98.5%; Score 191; DB 4; Length 269;  
Best Local Similarity 97.2%; Pred. No. 2,7e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

OY 1 YTSLIYSLIEESQNOOEKNEOELLELDKWASIMNMF 36  
|||||:|||||:|||||:|||||:|||||:  
DB 169 YTSLIYTLIEESQNOOEKNEOELLELDKWASIMNMF 204

RESULT 15  
Sequence 14, Application US/07956483  
Patent No. 626179

GENERAL INFORMATION:  
APPLICANT: KIENY, Marie-Paule.  
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED  
TITLE OF INVENTION: 9P160 VARIANT  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/956483  
FILING DATE: 31-DEC-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

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1 APPLICATION NUMBER: WO 92/19742
2 FILING DATE: 12-NOV-1992
3
4 PRIOR APPLICATION DATA:
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6 APPLICATION NUMBER: FR 91 05392
7 FILING DATE: 02-MAY-1991
8 ATTORNEY/AGENT INFORMATION:
9 NAME: Crane-Ferguson, Sharon E
10 REGISTRATION NUMBER: 36,113
11 REFERENCE/DOCKET NUMBER: 017753-005
12
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (703) 836-6620
15 TELEFAX: (703) 836-6620
16 INFORMATION FOR SEQ ID NO: 14:
17
18 SEQUENCE CHARACTERISTICS:
19
20 LENGTH: 855 amino acids
21
22 TYPE: amino acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25
26 MOLECULE TYPE: DNA (genomic)
27
28 OS-07-956-483-14

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Query Match	98.5%	Score 191	DB 4	Length 855
Best Local Similarity	97.2%	Pred. No.	9.5e-16	
Matches	35	Conservative	1	Mismatches 0
				Indels 0
				Gaps 0
Qy	1	YTSLLYSLIEESQNOOEKNEDELLDKKASLWNNF	36	-
Db	638	YTSLLYSLIEESQNOOEKNEDELLDKKASLWNNF	673	

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Job time : 10.1928 secs



RESULT 8  
US-08-388-809-6  
Sequence 6, Application US/08388809  
Patent No. 5576000  
GENERAL INFORMATION:  
APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,  
APPLICANT: GENOVEFFA, MARKHAM, PHILIP D. GALLO, ROBERT  
APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND  
APPLICANT: GARTNER, SUZANNE  
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK, 3.5"  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,809  
FILING DATE: 15-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/022,835  
FILING DATE: 25-FEB-1993  
APPLICATION NUMBER: US 07/599,491  
FILING DATE: 17-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: LESLIE A. SERUNIAN  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 2026-4092US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 855 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-388-809-6  
Query Match 99.0%; Score 192; DB 1; Length 855;  
Best Local Similarity 97.2%; Pred. No. 7.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 636 YTSIYSLIEESONQOEKNEOELLELDKASLNNWF 671  
YQ 1 YTSIYSLIEESONQOEKNEOELLELDKASLNNWF 36  
DB 636 YTSIYSLIEESONQOEKNEOELLELDKASLNNWF 671  
RESULT 9  
US-08-647-714-6  
Sequence 6, Application US/08647714  
Patent No. 5869313  
GENERAL INFORMATION:  
APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,  
APPLICANT: GENOVEFFA, MARKHAM, PHILIP D. GALLO, ROBERT  
APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND  
APPLICANT: GARTNER, SUZANNE  
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK

STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK, 3.5"  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/647,714  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,809  
FILING DATE: 15-FEB-1995  
APPLICATION NUMBER: US 08/022,835  
FILING DATE: 25-FEB-1993  
APPLICATION NUMBER: US 07/599,491  
FILING DATE: 17-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: LESLIE A. SERUNIAN  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 2026-4092US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 855 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-647-714-6  
Query Match 99.0%; Score 192; DB 2; Length 855;  
Best Local Similarity 97.2%; Pred. No. 7.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
YQ 1 YTSIYSLIEESONQOEKNEOELLELDKASLNNWF 36  
DB 636 YTSIYSLIEESONQOEKNEOELLELDKASLNNWF 671  
RESULT 10  
US-09-570-921-12  
Sequence 12, Application US/09570921  
Patent No. 6455265  
GENERAL INFORMATION:  
APPLICANT: SERRES, PIERRE-FRANCOIS  
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE  
FILE REFERENCE: 106213  
CURRENT APPLICATION NUMBER: US/09/570,921  
CURRENT FILING DATE: 2000-05-15  
PRIOR APPLICATION NUMBER: PCT/FR98/02447  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: FR/97/14387  
PRIOR FILING DATE: 1997-11-17  
NUMBER OF SEQ. ID NOS: 144  
SOFTWARE: PatentIn Ver. 2.1  
SEQ. ID NO 12  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Human  
US-09-570-921-12  
Query Match 98.5%; Score 191; DB 4; Length 138;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
YQ 1 YTSIYSLIEESONQOEKNEOELLELDKASLNNWF 36  
DB 99 YTSIYSLIEESONQOEKNEOELLELDKASLNNWF 134

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SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,739
FILING DATE: 27-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/134,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
REFERENCE/DOCKET NUMBER: 14918-704
TELEPHONE: 415-393-2000
TELEFAX: 415-393-2286
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 850 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-492-739-28

Query Match          100.0%; Score 194; DB 4; Length 850;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 36
DB 632 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 667

RESULT 6
US-08-965-056-13
Sequence 13, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Pheasant
APPLICANT: Melissa A. Starovasinik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

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LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-965-056-13

Query Match          99.0%; Score 192; DB 4; Length 268;
Best Local Similarity 97.2%; Pred. No. 2e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 36
DB 168 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 203

RESULT 7
US-08-022-835-6
Sequence 6, Application US/08022835
Patent No. 5420030
GENERAL INFORMATION:
APPLICANT: Reitz Jr., Marvin S.
APPLICANT: Franchini, Genevieve
APPLICANT: Markham, Phillip D.
APPLICANT: Gallo, Robert C.
APPLICANT: Lori, Franco C.
APPLICANT: Popovic, Mikulas
APPLICANT: Gartner, Suzanne
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,835
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-022-835-6

Query Match          99.0%; Score 192; DB 1; Length 855;
Best Local Similarity 97.2%; Pred. No. 7.2e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 36
DB 636 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 671

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PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 642  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-642

Query Match 100.0%; Score 194; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLIEESONOEKNEOELELDKWSLWNMF 36  
DB 1 YTSLYSLIEESONOEKNEOELELDKWSLWNMF 36

LT 3  
US-448-603A-28

Sequence 28, Application US/08448603A  
Patent No. 5864027

GENERAL INFORMATION:  
APPLICANT: Berman, Phillip W.  
TITLE OF INVENTION: HIV Envelope Polypeptides  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
STREET: 3 Embarcadero Center  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448, 603A  
FILING DATE: 07-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/072,833  
FILING DATE: 07-JUN-93

ATTORNEY/AGENT INFORMATION:  
NAME: Haliday, Emily  
REGISTRATION NUMBER: 38903  
REFERENCE/DOCKET NUMBER: 14918-704  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-393-2000  
TELEFAX: 415-393-2286  
TELEX:

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 850 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-448-603A-28

Query Match 100.0%; Score 194; DB 2; Length 850;  
Best Local Similarity 100.0%; Pred. No. 4e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLIEESONOEKNEOELELDKWSLWNMF 36  
DB 632 YTSLYSLIEESONOEKNEOELELDKWSLWNMF 667

RESULT 4  
US-09-134-075-28

Sequence 28, Application US/09134075  
Patent No. 6042836

GENERAL INFORMATION:  
APPLICANT: Berman, Phillip W.  
TITLE OF INVENTION: HIV Envelope Polypeptides  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
STREET: 3 Embarcadero Center  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,075  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/448, 603  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Haliday, Emily  
REGISTRATION NUMBER: 38903  
REFERENCE/DOCKET NUMBER: 14918-704  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-393-2000  
TELEFAX: 415-393-2286  
TELEX:

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 850 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-134-075-28

Query Match 100.0%; Score 194; DB 3; Length 850;  
Best Local Similarity 100.0%; Pred. No. 4e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLIEESONOEKNEOELELDKWSLWNMF 36  
DB 632 YTSLYSLIEESONOEKNEOELELDKWSLWNMF 667

RESULT 5  
US-09-492-739-28

Sequence 28, Application US/09492739  
Patent No. 6331404

GENERAL INFORMATION:  
APPLICANT: Berman, Phillip W.  
TITLE OF INVENTION: HIV Envelope Polypeptides  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP  
STREET: 3 Embarcadero Center  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533a-537  
Perfect score: 194  
Sequence: 1 YTSLSLIESONQOEKNEDELLEDKWASLWMPF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2.6/ptodata/1/1aa/PCUTS.COMB.pep.\*  
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194	100.0	36	4	US-09-082-279B-642
2	194	100.0	36	4	US-09-315-304B-642
3	194	100.0	850	2	US-08-448-603A-28
4	194	100.0	850	3	US-09-134-075-28
5	194	100.0	850	4	US-09-492-739-28
6	192	99.0	268	4	US-08-965-056-13
7	192	99.0	855	1	US-08-022-835-6
8	192	99.0	855	1	US-08-388-809-6
9	192	99.0	855	2	US-08-647-714-6
10	191	98.5	138	4	US-09-570-921-12
11	191	98.5	138	4	US-09-570-921-27
12	191	98.5	233	4	US-08-965-056-50
13	191	98.5	268	4	US-08-965-056-9
14	191	98.5	269	4	US-08-965-056-12
15	191	98.5	855	4	US-07-956-483-14
16	191	98.5	867	4	US-08-472-240A-5
17	190	97.9	269	4	US-08-965-056-46
18	189	97.4	36	1	US-08-073-028-1
19	189	97.4	36	1	US-08-486-099-1
20	189	97.4	36	3	US-09-071-877-1
21	189	97.4	36	3	US-08-360-107A-1
22	189	97.4	36	3	US-08-484-223B-1
23	189	97.4	36	3	US-08-919-597-1
24	189	97.4	36	3	US-08-475-668A-1
25	189	97.4	36	3	US-08-485-551A-1
26	189	97.4	36	3	US-08-471-913A-1
27	189	97.4	36	4	US-08-554-616-1

28	189	97.4	36	4	US-08-485-264A-1	Sequence 1, Appli
29	189	97.4	36	4	US-09-082-279B-15	Sequence 15, Appl
30	189	97.4	36	4	US-09-082-279B-497	Sequence 497, App
31	189	97.4	36	4	US-09-082-279B-498	Sequence 498, App
32	189	97.4	36	4	US-09-082-279B-603	Sequence 603, App
33	189	97.4	36	4	US-09-082-279B-630	Sequence 630, App
34	189	97.4	36	4	US-09-082-279B-631	Sequence 631, App
35	189	97.4	36	4	US-09-082-279B-705	Sequence 705, App
36	189	97.4	36	4	US-09-082-279B-834	Sequence 834, App
37	189	97.4	36	4	US-09-082-279B-1076	Sequence 1076, App
38	189	97.4	36	4	US-09-082-279B-1121	Sequence 1121, Ap
39	189	97.4	36	4	US-09-082-279B-1161	Sequence 1161, Ap
40	189	97.4	36	4	US-08-965-056-1	Sequence 1, Appli
41	189	97.4	36	4	US-08-965-056-108	Sequence 108, App
42	189	97.4	36	4	US-09-045-920-1	Sequence 1, Appli
43	189	97.4	36	4	US-08-474-349A-1	Sequence 399, App
44	189	97.4	36	4	US-08-474-349A-399	Sequence 413, App
45	189	97.4	36	4	US-08-474-349A-413	

## ALIGNMENTS

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RESULT 1
US-09-082-279B-642
; Sequence 642, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Merutka, Moimed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: PHARMACOKINETIC PROPERTIES
; CURRENT APPLICATION NUMBER: US/09/082, 279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 642
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-642

Query Match          100.0%; Score 194; DB 4; Length 36;
Best local similarity 100.0%; Pred. No. 1.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIESONQOEKNEDELLEDKWASLWMPF 36
DB 1 YTSLSLIESONQOEKNEDELLEDKWASLWMPF 36

RESULT 2
US-09-315-304B-642
; Sequence 642, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: PROPERTIES
; CURRENT APPLICATION NUMBER: US/09/315, 304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082, 279

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C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
R:Gnorgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-
Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
K:Keywords: capsid protein; coat protein; glycoprotein; polypotein; transmembrane p
F.1-29/domain: signal sequence #status predicted <SIG>
F.30-861/Product: env polypotein #status predicted <EPP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,
Query Match 96.9%; Score 190; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 5,6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTSLIHTLIESQNOQEKNEDELLELDKWSASLWNNF 36
|||||
DB 643 YTSLIYTLIESQNOQEKNEDELLELDKWSASLWNNF 678

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C; Species: human immunodeficiency virus type 1, HIV-1

CDate: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
CAccession: S21994, S70421  
RSteuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as detected by polymerase chain reaction  
A:Reference number: S21990  
A:Accession: S21994

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

A:Accession: F70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cervical tissues from heterosexuals  
 A:Reference number: F70417; MUID:92144209; PMID:1736940  
 A:Accession: F70421  
 A:Status: preliminary  
 A:Molecule type: DNA

QY	1	YTSLHTLTLEESQNOOEKNEDELLELDKWKASLWNNF	36	
		:		
Db	139	YTTLTITLTLEESQNOOEKNEDELLELDKWKASLWNNF	174	

C/Species: human immunodeficiency virus type 1, HIV-1

A:valley: isolate 20  
C:date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21998; S70425  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as detected

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A:Reference number: S21990
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <STE1>
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70425
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222, 'X', 224-358 <STE2>
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
C:Superfamily: type E retrovirus env polypotein

Query Match
Best Local Similarity 94.4%; Score 187; DB 2; Length 358;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 YTSLIHTLIEESONQOEKNEDELLELDKNASLWNMF 36
|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 YTSLIHTLIEESONQOEKNEDELLELDKNASLWNMF 175

RESULT 8
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129
A:Experimental source: patient 27L
A>Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypotein

Query Match
Best Local Similarity 94.9%; Score 186; DB 2; Length 357;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 YTSLIHTLIEESONQOEKNEDELLELDKNASLWNMF 36
|||||:|||||:|||||:|||||:|||||:|||||
Db 139 YTGILTYLIEESONQOEKNEDELLELDKNASLWNMF 174

RESULT 9
C41621
env polypotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polypotein
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:g328631; PIDN:AA803792.1; PID:g555015
A>Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env

```

```

C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
E:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
E:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
E:424-443/Domain: transmembrane #status predicted <TM>
E:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match
Best Local Similarity 94.4%; Score 185; DB 2; Length 443;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESONQOEKNEDELLELDKNASLWNMF 36
|||||:|||||:|||||:|||||:|||||:|||||
Db 378 YTSLIHTLIEESONQOEKNEDELLELDKNASLWNMF 413

RESULT 10
VCLJ3W
env polypotein precursor - human immunodeficiency virus type 1 (isolate WM01)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C:Accession: A24774
R:Starck, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks,
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the
A:Reference number: A24774; MUID:86218077; PMID:2423250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: coat protein; glycoprotein; polypotein; transmembrane protein
E:1-25/Domain: signal sequence #status predicted <SIG>
E:30-501/Product: coat protein gp120 #status predicted <GP1>
E:502-847/Product: coat protein gp41 #status predicted <GP2>
E:7,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,
Query Match
Best Local Similarity 94.4%; Score 185; DB 1; Length 856;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESONQOEKNEDELLELDKNASLWNMF 36
|||||:|||||:|||||:|||||:|||||:|||||
Db 638 YTSLIHTLIEESONQOEKNEDELLELDKNASLWNMF 673

RESULT 11
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRF1)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C:Accession: T09448
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: EMBL:663632; NID:g1465777; PID:g1465781
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein

Query Match
Best Local Similarity 93.4%; Score 183; DB 2; Length 847;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESONQOEKNEDELLELDKNASLWNMF 36
|||||:|||||:|||||:|||||:|||||:|||||

```

Db 629 YTSLEYTLIEESQNOQEKNEQDLELDKWSLWNF 664

## RESULT 12

env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13289  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-847 <ORF>  
C:Superfamily: type E retrovirus env polypotein

Query Match 93.4%; Score 183; DB 2; Length 847;

Best Local Similarity 94.4%; Pred. No. 3.8e-14;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHTLIEESQNOQEKNEQDLELDKWSLWNF 36  
||||:|||||  
Db 629 YTSLEYTLIEESQNOQEKNEQDLELDKWSLWNF 664

RESULT 13  
VCLJVL  
env polypotein precursor - human immunodeficiency virus type 1 (isolate LV)

N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03974  
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov

A:Reference number: A93355; MUID:85111157; PMID:2982104  
A:Accession: A03974  
A:Molecule type: DNA  
A:Residues: 1-856 <MUE>  
A:Cross-references: GB:K02083; NID:9555008; PIDN:AA59873.1; PID:9328559  
C:Genetics:

A:Gene: env  
C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
C:Domain: signal sequence #status predicted <STC>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88.136.141.156.160.197.230.234.241.262.276.289.295.301.332.339.356.386.392.397.406  
F:611.616.625.637.674.750.816/Binding site: carbohydrate (asn) (covalent) #status predic

Query Match 93.4%; Score 183; DB 1; Length 856;

Best Local Similarity 94.3%; Pred. No. 3.9e-14;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLHTLIEESQNOQEKNEQDLELDKWSLWNF 35  
||||:|||||  
Db 638 YTSLHTLIEESQNOQEKNEQDLELDKWSLWNF 672

## RESULT 14

S22002

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 3L  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22002; S70418

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi

A:Reference number: S21990

A:Accession: S22002

A:Molecule type: DNA

A:Residues: 1-358 <STEL>

A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70418

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333, 'X', 335-358 <STEL>

A:Cross-references: EMBL:X61352; NID:960186

C:Superfamily: type E retrovirus env polypotein

Query Match 92.3%; Score 181; DB 2; Length 358;

Best Local Similarity 91.7%; Pred. No. 2.5e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHTLIEESQNOQEKNEQDLELDKWSLWNF 36  
||||:|||||  
Db 140 YTSLEYTLIEESQNOQEKNEQDLELDKWSLWNF 175

## RESULT 15

S22000

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995

C:Accession: S22000

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22000

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STEL>

A:Cross-references: EMBL:X61351

C:Superfamily: type E retrovirus env polypotein

Query Match 92.3%; Score 181; DB 2; Length 358;

Best Local Similarity 91.7%; Pred. No. 2.5e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHTLIEESQNOQEKNEQDLELDKWSLWNF 36  
||||:|||||  
Db 140 YTSLEYTLIEESQNOQEKNEQDLELDKWSLWNF 175

Search completed: May 16, 2003, 11:25:11  
Job time: 12.146 secs



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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

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Query Match 98.0% Score 192; DB 1; Length 851;
Best Local Similarity 97.2% Pred. No. 4.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSLIHTLIEESQNOOEKNEDELLDKWASLWMP 36
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DB 633 YTSLIHTLIEESQNOOEKNEDELLDKWASLWMP 668

```

```

RESULT 2
ENV_HV1B1 STANDARD: PRT; 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BHD isolate) (HIV-1).
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumanister K., Ivanoff U., Peteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Ghayee J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
Chinese hamster ovary cells.";
RT J. Biol. Chem. 265:10373-10382(1990).
CC -----
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CC EMBL: M15654; AAA44205.1;
CC FIC: A03973; VCLJH3.
CC HIV: M15654; EVNSBH102.
CC Interpro: IPR000328; Env_GP41.
CC Interpro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Glycoprotein; Polypeptide; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 512 856
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
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FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
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FT CARBOHYD 463 463
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FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFB1A18931BB27 CRC64;

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EXTERIOR MEMBRANE GLYCOPROTEIN.  
TRANSMEMBRANE GLYCOPROTEIN.

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Query Match 98.0% Score 192; DB 1; Length 856;
Best Local Similarity 97.2% Pred. No. 4.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTSLIHTLIEESQNOOEKNEDELLDKWASLWMP 36
    |||||:|||||:|||||:|||||:|||||:
DB 638 YTSLIHTLIEESQNOOEKNEDELLDKWASLWMP 673

```

```

RESULT 3
ENV_HV1H2 STANDARD: PRT; 856 AA.
ID ENV_HV1H2
AC P04578; 009779;

```

FT	CARBOHYD	397	397	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	406	406 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	448	448 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	463	463 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	611	611 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	616	616 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	624	624 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	637	637 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	674	674 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	750	750 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	816	816 <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
SO	SEQUENCE	856 AA;	97212 MW;	65A16A185107FE0	CRC64;	

  

Query Match	Best Local Similarity	98.0%;	Score 192;	DB 1;	Length 856;
Matches 35;	Conservative %	1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	YTSLIHTLIESQNOEKNEBELLELDKWSALMWF	36		
Db	638	YTSLIHTLIESQNOEKNEBELLELDKWSALMWF	673		

  

RESULT 4	ENV_HY1H3	STANDARD;	PRT;	856 AA.
AC	P04624;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).			
OC	Viruses; Retrovid viruses; Retroviridae; Lentivirales.			
OX	NCBI_TaxID=11707;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85228248; Pubmed=2988795;			
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;			
RT	"HIV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";			
RL	Cell 41:979-986(1985).			
CC	-----			
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CC	-----			
CC	EMBL: M14100; AAA44679.1; -			
DR	HIV; M14100; ENVSHXB3.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.			
KW	Signal.			
FT	CHAIN	1	30	
FT	CHAIN	31	511	
FT	CHAIN	512	856	
FT	DISULFID	119	205	
FT	DISULFID	126	196	
FT	DISULFID	131	157	
FT	DISULFID	218	247	
FT	DISULFID	228	239	
FT	DISULFID	296	331	
FT	DISULFID	378	445	
FT	DISULFID	385	418	
FT	CARBOHYD	88	88	
FT	CARBOHYD	136	136	

  

FT <th>CARBOHYD</th> <th>397</th> <th>397</th> <th>N-LINKED</th> <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	CARBOHYD	397	397	N-LINKED	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>406</td> <td>406</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	406	406	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>448</td> <td>448</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	448	448	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>463</td> <td>463</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	463	463	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>611</td> <td>611</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	611	611	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>616</td> <td>616</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	616	616	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>624</td> <td>624</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	624	624	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>637</td> <td>637</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	637	637	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>674</td> <td>674</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	674	674	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>750</td> <td>750</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	750	750	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>816</td> <td>816</td> <td>N-LINKED<th>(GLCNAC. . .)</th><th>(POTENTIAL)</th></td>	816	816	N-LINKED <th>(GLCNAC. . .)</th> <th>(POTENTIAL)</th>	(GLCNAC. . .)	(POTENTIAL)
SO	SEQUENCE <td>856 AA;</td> <td>97212 MW;</td> <td>65A16A185107FE0</td> <td>CRC64;</td> <td></td>	856 AA;	97212 MW;	65A16A185107FE0	CRC64;	

  

Query Match	Best Local Similarity	98.0%;	Score 192;	DB 1;	Length 856;
Matches 35;	Conservative %	1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	YTSLIHTLIESQNOEKNEBELLELDKWSALMWF	36		
Db	638	YTSLIHTLIESQNOEKNEBELLELDKWSALMWF	673		

  

RESULT 4	ENV_HY1H3	STANDARD;	PRT;	856 AA.
AC	P04624;			
DT	13-AUG-1987 (Rel. 05, Created)			

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 220 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 33736688B84C1AFC CRC64;

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Query Match          98.0%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 4.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTSLHTLIEESONOQKNEOELLELDKWSLWNMF 36
DB 638 YTSLSHLSLIEESONOQKNEOELLELDKWSLWNMF 673

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RESULT 5
ENV_HVILW STANDARD; PRT; 856 AA.
AC 070626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
US Human immunodeficiency virus type 1 (IW12.3 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
Shaw G.M., Kong L.T., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, U12055; AAA76690.1;
CC DR GLCOSUITEB; 070626;
CC DR InterPro; IPR000328; Env_GP41.

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DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

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Query Match          98.0%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 4.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTSLHTLIEESONOQKNEOELLELDKWSLWNMF 36
DB 638 YTSLSHLSLIEESONOQKNEOELLELDKWSLWNMF 673

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```

RESULT 6
ENV_HVILW STANDARD; PRT; 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein-GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
US Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;
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Query Match 96.9%; Score 190; DB 1; Length 856;  
Best Local Similarity 97.2%; Pred. No. 7.6e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 YTSLIHTLIESQNOQEKNEQELLELDKWSLWME 36
Db 638 YTSLIHTLIESQNOQEKNEQELLELDKWSLWME 673
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RESULT 8  
ENV\_HV1MF STANDARD; PRT: 853 AA.

```
AC P19551:
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
```

```
OX NCBI_TaxID=11704;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
RA Wasilak A.; Cloning and characterization of human immunodeficiency virus type 1
RA "variants diminished in the ability to induce syncytium-independent
cytolysis."
RL J. Virol. 64:3792-3803(1990).
```

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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

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CC EMBL: M33943; AAA44850.1; .
CC DR HIV: M33943; ENVSMFA.
CC DR InterPro: IPR000328; Env_GP41.
CC DR InterPro: IPR000777; GP120.
CC DR Pfam: PF00516; GP120.1.
CC DR Pfam: PF00517; GP41.1.
CC KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
CC Signal.
CC FT SIGNAL 1 30
CC FT CHAIN 1 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
CC FT CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.
CC FT DISULFID 54 74 BY SIMILARITY.
CC FT DISULFID 119 203 BY SIMILARITY.
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FT DISULFID 126 194 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 329 BY SIMILARITY.
FT DISULFID 376 443 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 337B93B6F22ABA CRC64;
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Query Match 96.4%; Score 189; DB 1; Length 853;  
Best Local Similarity 94.4%; Pred. No. 1e-15;  
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 YTSLIHTLIESQNOQEKNEQELLELDKWSLWME 36
Db 636 YTSLIHTLIESQNOQEKNEQELLELDKWSLWME 671
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RESULT 9  
ENV\_HV1S3 STANDARD; PRT: 852 AA.

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AC P19549:
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
```

```
OX NCBI_TaxID=11690;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RA "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome."
RL J. Virol. 64:4016-4020(1990).
```

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FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 856 AA: 97339 MW: 5FCDBIDC3C1209B3 CRC64;

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Query Match  
Best Local Similarity 93.4%; Score 183; DB 1; Length 856;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTSLHTLIEESONOQKNEOELLELDKNASLNMW 35
Db 638 YTSLHTLIEESONOQKNEOELLELDKNASLNMW 672

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RESULT 13
ENV_HV1J3 STANDARD: PRT: 867 AA.
AC P12489:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RP MEDLINE=89352108; PubMed=2669897;
   Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
   "Nucleotide sequences of gag and env genes of a Japanese isolate of
   HIV-1 and their expression in bacteria.";
   AIDS Res. Hum. Retroviruses 5:411-419(1989).
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CC -----
CC EMBL, M21138; AA03526.1; -
CC DR HIV; M21138; ENV5JH3.
CC DR InterPro: IPR000328; Env_GP41.
CC DR InterPro: IPR000777; GP120.
CC DR Pfam: PF00516; GP120.1.
CC DR Pfam: PF00517; GP41.1.
CC DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
CC Signal.
CC KW SIGNAL.
CC FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
CC FT CHAIN 517 516 TRANSMEMBRANE GLYCOPROTEIN.
CC FT CHAIN 867 867 BY SIMILARITY.
CC FT DISULFID 53 73

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FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 368 457 BY SIMILARITY.
FT DISULFID 395 430 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 867 AA: 98399 MW: 5F23101468E8680 CRC64;

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Query Match  
Best Local Similarity 93.4%; Score 183; DB 1; Length 867;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTSLHTLIEESONOQKNEOELLELDKNASLNMW 36
Db 649 YTSLHTLIEESONOQKNEOELLELDKNASLNMW 684

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RESULT 14
ENV_HV1A2 STANDARD: PRT: 855 AA.
AC P03378:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP MEDLINE=85090453; PubMed=2578227;
   Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
   Rasmussen M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
   Levy J.A., Dina D., Lucif P.A.;
   "Nucleotide sequence and expression of an AIDS-associated retrovirus
   (ARV-2).";
   Science 227:484-492(1985).
CC -----
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FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 847 AA: 96466 MW: CDIE33D73AA5BCAE CRC64;

Query Match 90.3%; Score 177; DB 1; Length 847;  
 Best Local Similarity 88.9%; Pred. No. 3e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHTLIESONQOEKNEQELLELDKQASLWMP 36  
 |||:::||||||| |||||||||||||  
 Db 629 YTSIISLIESONQOEKNEQELLELDKQASLWMP 664

Search completed: May 16, 2003, 11:13:37  
 Job time : 6.07229 secs

**IS PAGE BLANK (USPTO)**



GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-540  
Perfect score: 196  
Sequence: 1 YTSLIHTLIEESONQOEKNEOELLELDKWSIWMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	98.0	645	15	Q993A6 human immun
2	192	98.0	747	15	Q70607 human immun
3	192	98.0	748	15	Q70606 human immun
4	192	98.0	752	15	Q70604 human immun
5	192	98.0	752	15	Q70605 human immun
6	192	98.0	752	15	Q70608 human immun
7	192	98.0	851	15	Q78243 human immun
8	192	98.0	852	15	Q89797 human immun
9	192	98.0	854	15	Q85582 human immun
10	192	98.0	854	15	Q72502 human immun
11	192	98.0	856	15	Q92877 simian-huma
12	192	98.0	856	15	Q74599 human immun
13	192	98.0	856	15	Q74090 human immun
14	190	96.9	442	15	Q69910 human immun
15	190	96.9	841	15	Q41556 human immun
16	190	96.9	849	15	Q77368 human immun

17	190	96.9	849	15	Q80851 human immun
18	190	96.9	851	15	Q56110 human immun
19	190	96.9	851	15	Q80852 human immun
20	190	96.9	856	15	Q72993 human immun
21	190	96.9	856	15	Q41539 human immun
22	190	96.9	857	15	Q80170 human immun
23	190	96.9	859	15	Q80185 human immun
24	190	96.9	859	15	Q80180 human immun
25	190	96.9	859	15	Q80179 human immun
26	190	96.9	859	15	Q80177 human immun
27	190	96.9	859	15	Q80173 human immun
28	190	96.9	859	15	Q80850 human immun
29	190	96.9	862	15	Q80184 human immun
30	190	96.9	862	15	Q80183 human immun
31	190	96.9	862	15	Q80182 human immun
32	190	96.9	862	15	Q80178 human immun
33	190	96.9	862	15	Q80174 human immun
34	190	96.9	868	15	Q80186 human immun
35	188	95.9	123	15	Q9YXR3 human immun
36	188	95.9	854	15	Q90178 human immun
37	188	95.9	854	15	Q78705 human immun
38	188	95.9	855	15	Q9E1R7 human immun
39	188	95.9	858	15	Q80867 human immun
40	188	95.9	858	15	Q80865 human immun
41	188	95.9	864	15	Q9E610 simian-huma
42	187	95.4	117	15	Q9Q0N5 human immun
43	187	95.4	122	15	Q9YXN9 human immun
44	187	95.4	122	15	Q9E6A9 human immun
45	187	95.4	358	15	Q78120 human immun

## ALIGNMENTS

## RESULT 1

Q993A6 PRELIMINARY; PRT; 645 AA.  
ID Q993A6;  
AC Q993A6;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP .SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurtwitz J.L.;  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
DR EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;  
KW Transmembrane.  
FT NON\_TER 1 1  
SQ SEQUENCE 645 AA; 72485 MW; B076514BB93362EC CRC64;

Query Match 98.0%; Score 192; DB 15; Length 645;  
Best Local Similarity 97.2%; Pred. No. 2.1e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESONQOEKNEOELLELDKWSIWMWF 36  
DB 607 YTSLIHTLIEESONQOEKNEOELLELDKWSIWMWF 642

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RESULT 2
070607 PRELIMINARY: PRT: 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RX MEDLINE-95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12034; AAA76669.1; -
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A5224514 CRC64;

Query Match 98.0%; Score 192; DB 15; Length 747;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESONOQEKNEDELLELDKWSLWNMF 36
DB 633 YTSLIHTLIEESONOQEKNEDELLELDKWSLWNMF 668

RESULT 3
070606 PRELIMINARY: PRT: 748 AA.
AC 070606;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RX MEDLINE-95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12034; AAA76669.1; -
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AEB94013B45A CRC64;

Query Match 98.0%; Score 192; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESONOQEKNEDELLELDKWSLWNMF 36
DB 633 YTSLIHTLIEESONOQEKNEDELLELDKWSLWNMF 673

RESULT 5
070605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748 748
SQ SEQUENCE 748 AA; 84224 MW; 56BBD186C67694B CRC64;

Query Match 98.0%; Score 192; DB 15; Length 748;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESONOQEKNEDELLELDKWSLWNMF 36
DB 634 YTSLIHTLIEESONOQEKNEDELLELDKWSLWNMF 669

RESULT 4
070604 PRELIMINARY: PRT: 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RX MEDLINE-95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12030; AAA76669.1; -
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AEB94013B45A CRC64;

Query Match 98.0%; Score 192; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESONOQEKNEDELLELDKWSLWNMF 36
DB 638 YTSLIHTLIEESONOQEKNEDELLELDKWSLWNMF 673

RESULT 5
070605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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DB	638	YTSLIHSLIESQNOEKNEQELLELDKRWASLWMPF	673
RESULT 7			
ID	078243	PRELIMINARY:	PRT: 851 AA.
AC	078243		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	Env polyprotein.		
GN	ENV.		
OS	Human immunodeficiency virus type 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11676;		
RN	11		
RP	SEQUENCE FROM N.A.		
RA	Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai O.,		
RA	Verani P., Rossi G.B.;		
RT	"Sequence analysis of HIV-1 proviral DNA from a non producer		
RT	chronically infected HUT-78 cellular clone.";		
RL	J. Viral Diseases 1:40-55(1992).		
RN	12		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89352106; PubMed=2765297;		
RA	Federico M., Tilti F., Butto S., Orecchia A., Carlini F., Taddeo B.,		
RA	Macchi B., Mangiano N., Verani P., Rossi G.;		
RT	"Biological and molecular characterization of producer and non		
RT	producer clones from HUT-78 infected with a patient HIV isolate.";		
RL	AIDS Res. Hum. Retroviruses 5:385-396(1989).		
RN	13		
RP	SEQUENCE FROM N.A.		
RA	Tilti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,		
RA	Borsetti A., Saggio I., Verani P., Rossi G.;		
RT	"Variability of HIV-1 virus: characteristics of an infected but not		
RT	productive clone.";		
RL	Int. J. Immunopharmacol. 3:17-23(1990).		
DR	EMBL; Z11530; CAAT7628.1;		
DR	InterPro: IPR000328; Env_GP41.		
DR	InterPro: IPR000777; GP120.		
DR	Pfam: PF00516; GP120:1.		
DR	Pfam: PF00517; GP41:1.		
KW	AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.		
SO	SEQUENCE 851 AA; 96630 MW; 1A3767B95E98027 CRC64;		
Query Match	98.0%; Score 192; DB 15; Length 851;		
Best Local Similarity	97.2%; Pred. NO. 2.8e-15;		
Matches	35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
QY	1	YTSLIHSLIESQNOEKNEQELLELDKRWASLWMPF	36
DB	633	YTSLIHSLIESQNOEKNEQELLELDKRWASLWMPF	668
RESULT 8			
ID	Q89797	PRELIMINARY:	PRT: 852 AA.
AC	Q89797		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-OCT-2001	(TREMBLrel. 18, Last annotation update)	
DE	Envelope glycoprotein.		
GN	ENV.		
OS	Human immunodeficiency virus type 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11676;		
RN	11		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=LM90-2;		
RX	MEDLINE=95127297; PubMed=7826699;		
RA	Reitz M., Hall E., Robert-Guroff M., Lautenberger J., Hahn B.,		
RA	Shaw G., Kong L., Weiss S., Walters D., Gallo R., Blattner W.;		
RT	"Viral variability and serum antibody response in a laboratory worker		

Matches	35: Conservative	1: Mismatches	0: Indels	0: Gaps
QY	1 YTSLIHTLIEESQNOQEKNEQELLELDKWSLWNMF 36	:		
Db	636 YTSLIHTLIEESQNOQEKNEQELLELDKWSLWNMF 671			
RESULT 10				
ID	072502	PRELIMINARY;	PRT;	854 AA.
AC	072502:			
DT	01-NOV-1996 (TREMBlrel. 01, Created)			
DT	01-NOV-1996 (TREMBlrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	ENV polypeptin.			
GN	ENV.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-NL4-3:			
RX	MEDLINE=86281827; PubMed=3016298;			
RA	Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,			
RA	Martin M.A.;			
RT	"Production of acquired immunodeficiency syndrome-associated			
RT	retrovirus in human and nonhuman cells transfected with an infectious			
RL	molecular clone.";			
RN	J. Virol. 59:284-291(1986).			
RP	EMBL; U26942; AAB60578.1;			
RC	InterPro: IPR000328; Env-GP1.			
RX	InterPro: IPR000777; GP120.			
RA	Pfam: PF00516; GP120. 1.			
RT	Pfam: PF00517; GP1. 1.			
KW	AIDS; Coat protein; glycoprotein; Polypeptin; Transmembrane.			
FT	CONFLICT 214 H -> L (IN REF. 2).			
FT	CONFLICT 530 A -> S (IN REF. 2).			
FT	CONFLICT 739 G -> D (IN REF. 2).			
SO	SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;			
Query Match	98.0%;	Score 192;	DB 15;	Length 854;
Best Local Similarity	97.2%;	Pred. No. 2.8e-15;		
Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0
QY	1 YTSLIHTLIEESQNOQEKNEQELLELDKWSLWNMF 36	:		
Db	636 YTSLIHTLIEESQNOQEKNEQELLELDKWSLWNMF 671			
RESULT 11				
ID	092877	PRELIMINARY;	PRT;	856 AA.
AC	092877:			
DT	01-NOV-1998 (TREMBlrel. 08, Created)			
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	Envelope glycoprotein.			
GN	ENV.			
OS	Simian-human immunodeficiency virus.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=57667;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99098984; PubMed=9882298;			

RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,  
 Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodiroski J.G.;  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 responsible for the pathogenicity of a multiply passaged simian-human  
 immunodeficiency virus (SHIV-HXBc2).";  
 RT J. Virol. 73:976-984(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodiroski J.G.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041850, AAD12142.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97151 MW; C50BE038FB73659 CRC64;

Query Match 98.0%; Score 192; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIESQNOEKNEDELLELDKWSLWNF 36  
 Db 638 YTSLIHTLIESQNOEKNEDELLELDKWSLWNF 673

RESULT 12  
 ID 074599 PRELIMINARY; PRT; 856 AA.  
 AC 074599;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 RT Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86068; BAA12895.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97287 MW; 238042A234C56688 CRC64;

Query Match 98.0%; Score 192; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIESQNOEKNEDELLELDKWSLWNF 36  
 Db 638 YTSLIHTLIESQNOEKNEDELLELDKWSLWNF 673

RESULT 13  
 074090

ID 074090 PRELIMINARY; PRT; 856 AA.  
 AC 074090;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 RT Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 98.0%; Score 192; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIESQNOEKNEDELLELDKWSLWNF 36  
 Db 638 YTSLIHTLIESQNOEKNEDELLELDKWSLWNF 673

RESULT 14  
 ID 069910 PRELIMINARY; PRT; 42 AA.  
 AC 069910;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Gp41 (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94211861; PubMed=7512731;  
 RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,  
 RA Keller P.M., Shaw A.R., Emini E.A.;  
 RT "Neutralization of divergent human immunodeficiency virus type 1  
 variants and primary isolates by IAM-41-2F5, an anti-gp41 human  
 monoclonal antibody.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).  
 DR EMBL: U06740; AAA19153.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 FT 42  
 SO SEQUENCE 42 AA; 5248 MW; 613E1B2DBB31A722 CRC64;

Query Match 96.9%; Score 190; DB 15; Length 42;  
 Best Local Similarity 97.2%; Pred. No. 2.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHHTLIESQNOEKNEQELLELDKWSLWNMF 36  
 ||||:|||||  
 Db 7 YTSIHHTLIESQNOEKNEQELLELDKWSLWNMF 42

## RESULT 15

ID 041556 PRELIMINARY; PRT: 841 AA.  
 AC 041556;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C17;  
 RT MEDLINE=98105804; Pubmed=9445059;  
 RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,  
 Walker B.D., Neumann A.U., Vermund S.H., Westsky J., Jackson S.,  
 Penamere E., Cao Y., Gao F., Kalams S., Kunstman K.J., McDonald D.,  
 McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;  
 "Immunodeficiency and virological analyses of persons infected by human  
 recombinant gp120 subunit vaccines.";  
 RT J. Virol. 72:1552-1576(1998).  
 RL J. EMBL: U84814; AAC58844.1; -;  
 DR EMBL: U84814; AAC58844.1; -;  
 DR InterPro: IPR000328; Env-GP41.  
 DR InterPro: IPR00777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 FT NON\_TER  
 SO SEQUENCE 841 AA; 95802 MW; AAFc104893D91667 CRC64;

## Query Match

96.9%; SCORE 190; DB 15; Length 841;

Best Local Similarity 97.2%; Pred. No. 4.9e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHHTLIESQNOEKNEQELLELDKWSLWNMF 36  
 ||||:|||||  
 Db 623 YTSIHHTLIESQNOEKNEQELLELDKWSLWNMF 658

Search completed: May 16, 2003, 11:19:49  
 time : 26.3124 secs



DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWMNF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 98.0%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 9.6e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWMNF 36

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWMNF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichly, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Merutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWMNF 36

CURRENT APPLICATION NUMBER: US/09/071,877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 1

LENGTH: 36

TYPE: PPT

ORGANISM: Human immunodeficiency virus

US-09-071-877-1

Query Match 98.0%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 9.6e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWMNF 36

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWMNF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 98.0%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 9.6e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWMNF 36



```

|||||:|||||
Db 1 YTSLHSLIEESQNOQEKNEQELLELDKWSIWNWF 36

```

RESULT 5  
US-08-484-223B-1

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:

```

1  COMPUTER READABLE FORM:
2
3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6
7  SOFTWARE: PatentIn Release #1.0, Version #1.3C
8
9  CURRENT APPLICATION DATA:
10
11  APPLICATION NUMBER: US/08/484,223B
12
13  FILING DATE: 07-JUN-1995
14
15  CLASSIFICATION: 435

```

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-022  
TELECOMMUNICATION INFORMATION:

```

: INFORMATION FOR SEQ ID NO: 1
: SEQUENCE CHARACTERISTICS:
: LENGTH: 36 amino acids
: TYPE: amino acid
: STRANDEDNESS:

```

MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match	98.0%	Score 193	DB 3	length 36
Best Local Similarity	97.2%	Pred. No. 9.6e-18		
Matches 35; Conservative	1	Mismatches 0	Indels 0	Gaps 0

QY 1 YTSLIHTLIEESQNOQEKNEQELLELDKQASLWNWF 366  
|||||:|||||  
Db 1 YTSLIHSLIEESQNOQEKNEQELLELDKQASLWNWF 366

RESULT 6  
US-08-919-597-1.  
; Sequence 1, Application US/08919597

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: PatentIn Release #1.0, Version #1.3
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/919,597
8  FILING DATE:

```

1  
 2 PRIORITY APPLICATION DATA:  
 3 APPLICATION NUMBER: US 08/470,899  
 4 FILING DATE: 06-JUN-1995  
 5  
 6 ATTORNEY/AGENT INFORMATION:  
 7 NAME: Coruzzi, Laura A.  
 8 REGISTRATION NUMBER: 30,742  
 9 REFERENCE/DOCKET NUMBER: 7872-022  
 10 TELECOMMUNICATION INFORMATION:  
 11 TELEPHONE: 313-760-0000  
 12

```

; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 36 amino acids
;     TYPE: amino acid
;     COMPLETENESS:

```

```

;      TOPOLOGY:  unknown
;      MOLECULE TYPE:  peptide
US-08-919-597-1

```

Query Match	98.0%;	Score 192;	DB 3;	Length 36;
Best Local Similarity	97.2%;	Pred. No. 9.6e-18;		
Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0

```

QY      1 YTSLIHTLIEESQÑQÖKEKNEÖELLELDKMASLWNWF 36
        |||||:|||||
Db      1 YTSLIHSLIEESQÑQÖKEKNEÖELLELDKMASLWNWF 36

```

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A

GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

```
Oy      1 YTSLIHTLIEESQNOQEKNEDELLDLDKWA$LMWNF    36  
        ||||| : ||||| : ||||| : ||||| : ||||| :  
Db      1 YTSLIHSLIEESQNOQEKNEDELLDLDKWA$LMWNF    36
```

```

; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-485-551A-1

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```
QY 1 YTSLIHTLIEESQNOQEKNEQELLELDKWSASLNNVF 36
      |||||:|||||:|||||:|||||:|||||:|||||:
Db 1 YTSLIHSLIEESQNOQEKNEQELLELDKWSASLNNVF 36
```

RESULT 9  
US-08-471-913A-1  
; Sequence 1, Application US/08471913A  
; Patent No. 6093794

1 APPLICANT: Bolognesi, Dani P.  
 2 APPLICANT: Matthews, Thomas J.  
 3 APPLICANT: Wild, Carl T.  
 4 APPLICANT: Barney, Shawn O.  
 5 APPLICANT: Lambert, Dennis M.  
 6 APPLICANT: Petleway, Stephen R.  
 7 APPLICANT: Langlois, Alphonse J.  
 8 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
 9 TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
 10 TITLE OF INVENTION: TRANSMISSION  
 11 NUMBER OF SEQUENCES: 214  
 12 CORRESPONDENCE ADDRESS:  
 13

ADDRESS: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match	98.08;	Score 192;	DB 3;	Length 36;
Best Local Similarity	97.28;	Pred. No. 9.6e-18;		
Matches 35; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

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OY 1 YTSLIHTLIESQNOQEKNEQELLELDKWSLWNWF 36
    |||||:|||||
Db 1 YTSLIHSLIESQNOQEKNEQELLELDKWSLWNWF 36

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RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1

Query Match 98.0%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,6e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pelletway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1

Query Match 98.0%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,6e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRP  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15

Query Match 98.0%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,6e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

Db 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

## RESULT 13

US-09-082-279B-497

Sequence 497, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 497

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

## Query Match

Best Local Similarity 97.2%; Score 192; DB 4; Length 36;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

## RESULT 14

US-09-082-279B-498

Sequence 498, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 498

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

## Query Match

Best Local Similarity 97.2%; Score 192; DB 4; Length 36;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

## RESULT 15

US-09-082-279B-603

Sequence 603, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 603

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

## Query Match

Best Local Similarity 97.2%; Score 192; DB 4; Length 36;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:22:14  
Job time: 11.1928 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-540

Perfect score: 196  
Sequence: 1 YTSLIHTLIESONOEKNEOELLELDKWSLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published\_Applications\_AA.\*  
1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	98.0	36	9 US-09-874-475-16	Sequence 16, Appl
2	192	98.0	36	9 US-10-116-797-1	Sequence 1, Appl
3	192	98.0	36	9 US-09-493-346-1	Sequence 10, Appl
4	192	98.0	36	10 US-09-779-451-5	Sequence 5, Appl
5	192	98.0	36	10 US-09-834-628-1	Sequence 1, Appl
6	192	98.0	36	10 US-09-854-816-1	Sequence 108, App
7	192	98.0	36	10 US-09-854-816-108	Sequence 176, App
8	192	98.0	36	10 US-09-848-616-176	Sequence 41, Appl
9	192	98.0	46	10 US-09-779-451-41	Sequence 2, Appl
10	192	98.0	56	10 US-10-040-349B-2	Sequence 84, Appl
11	192	98.0	177	9 US-10-059-271-84	Sequence 81, Appl
12	192	98.0	221	9 US-10-059-271-81	Sequence 97, Appl
13	192	98.0	232	9 US-10-059-271-82	Sequence 16, Appl
14	192	98.0	254	9 US-10-059-271-97	Sequence 17, Appl
15	192	98.0	256	10 US-09-854-816-16	Sequence 18, Appl
16	192	98.0	268	10 US-09-854-816-17	
17	192	98.0	268	10 US-09-854-816-17	
18	192	98.0	268	10 US-09-854-816-17	
19	192	98.0	268	10 US-09-854-816-17	

20	192	98.0	344	9 US-10-040-349B-1	Sequence 1, Appl
21	192	98.0	345	9 US-10-026-741-49	Sequence 49, Appl
22	192	98.0	345	10 US-09-779-451-8	Sequence 8, Appl
23	192	98.0	391	9 US-10-059-271-93	Sequence 93, Appl
24	192	98.0	519	10 US-09-756-551A-8	Sequence 8, Appl
25	192	98.0	853	9 US-10-003-035-33	Sequence 33, Appl
26	192	98.0	856	10 US-09-476-242-1	Sequence 103, App
27	192	98.0	861	9 US-10-026-741-103	Sequence 53, Appl
28	192	98.0	1101	9 US-10-003-035-53	Sequence 55, Appl
29	192	98.0	1186	9 US-10-003-035-55	Sequence 9, Appl
30	190	96.9	268	10 US-09-854-816-9	Sequence 12, Appl
31	190	96.9	269	10 US-09-854-816-12	Sequence 1, Appl
32	189	96.4	36	10 US-09-912-824-1	Sequence 19, Appl
33	189	96.4	268	10 US-09-854-816-19	Sequence 26, Appl
34	188	95.9	268	10 US-09-854-816-28	Sequence 2, Appl
35	187	95.4	268	10 US-09-854-816-26	Sequence 109, App
36	187	95.4	619	10 US-09-891-609-4	Sequence 38, Appl
37	187	95.4	646	10 US-09-891-609-2	Sequence 41, Appl
38	187	95.4	847	10 US-09-476-242-2	Sequence 6, Appl
39	186	94.9	46	10 US-09-854-816-109	Sequence 42, Appl
40	186	94.9	267	10 US-09-854-816-38	Sequence 94, Appl
41	186	94.9	268	10 US-09-854-816-41	Sequence 50, Appl
42	186	94.9	269	10 US-09-854-816-6	
43	186	94.9	269	10 US-09-854-816-42	
44	186	94.9	1231	9 US-10-059-271-94	
45	185	94.4	233	10 US-09-854-816-50	

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
Sequence 16, Application US/09874475  
Publication No. US20020182592A1  
GENERAL INFORMATION:  
APPLICANT: Petropoulos, Christos J.  
APPLICANT: Parkin, Neil T.  
APPLICANT: Whitcomb, Jeanette  
APPLICANT: Huang, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS  
FILE REFERENCE: 2793/65166  
CURRENT APPLICATION NUMBER: US/09/874,475  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16  
Query Match 98.0%; Score 192; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLIHTLIESONOEKNEOELLELDKWSLWNMF 36  
DB 1 YTSLIHTLIESONOEKNEOELLELDKWSLWNMF 36  
RESULT 2  
US-10-116-797-1  
Sequence 1, Application US/10116797  
Publication No. US2003004441A1  
GENERAL INFORMATION:  
APPLICANT: Olsen, William C.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
FILE REFERENCE: 64672-A  
CURRENT APPLICATION NUMBER: US/10/116,797  
CURRENT FILING DATE: 2002-10-15

**Q7** 1 YTSLIHTLIEESQNQEKNEDLELDKASIMNMF 36  
||||| : ||||| : ||||| : ||||| :  
**D8** 1 YTSLIHSILIEESQNQEKNEDLELDKASIMNMF 36



Db 2 YTSLSHSLIEESQNOQEKNEOELLELDKWSLWNMF 37

RESULT 10

US-09-779-451-41

; Sequence 41, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT APPLICATION NUMBER: US/09/779,451

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 41

; LENGTH: 46

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match 98.0%; Score 192; DB 10; Length 46;

Best Local Similarity 97.2%; Pred. No. 1,7e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOQEKNEOELLELDKWSLWNMF 36

Db 11 YTSLSHSLIEESQNOQEKNEOELLELDKWSLWNMF 46

RESULT 11

US-09-779-451-4

; Sequence 4, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT APPLICATION NUMBER: US/09/779,451

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 56

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match 98.0%; Score 192; DB 10; Length 56;

Best Local Similarity 97.2%; Pred. No. 2,1e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOQEKNEOELLELDKWSLWNMF 36

Db 16 YTSLSHSLIEESQNOQEKNEOELLELDKWSLWNMF 51

RESULT 12

US-10-040-349B-2

; Sequence 2, Application US/10040349B

; Publication No. US20030082521A1

; GENERAL INFORMATION:

; APPLICANT: Brasseur, Robert

; APPLICANT: Charlotaux, Benoit

; APPLICANT: Chevallier, Michel

; APPLICANT: El Habib, Raphaelle

; APPLICANT: Krell, Tino

; TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

; FILE REFERENCE: 01-078-A

; CURRENT APPLICATION NUMBER: US/10/040,349B

; CURRENT FILING DATE: 2002-07-09

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 177

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: (1)..(177)

; OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match 98.0%; Score 192; DB 9; Length 177;

Best Local Similarity 97.2%; Pred. No. 7,2e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOQEKNEOELLELDKWSLWNMF 36

Db 104 YTSLSHSLIEESQNOQEKNEOELLELDKWSLWNMF 139

RESULT 13

US-10-059-271-84

; Sequence 84, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPKE, HEINRICH

; APPLICANT: BUDDÉ, ECKHARD

; APPLICANT: NICOLAUS, STERAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

; FILE REFERENCE: ALBRE-22

; CURRENT APPLICATION NUMBER: US/10/059,271

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: DE 101 06 295

; PRIOR FILING DATE: 2001-02-02

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 84

; LENGTH: 221

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-059-271-84

Query Match 98.0%; Score 192; DB 9; Length 221;

Best Local Similarity 97.2%; Pred. No. 9,2e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOQEKNEOELLELDKWSLWNMF 36

Db 131 YTSLSHSLIEESQNOQEKNEOELLELDKWSLWNMF 166

RESULT 14

US-10-059-271-81

; Sequence 81, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPKE, HEINRICH

; APPLICANT: BUDDÉ, ECKHARD

; APPLICANT: NICOLAUS, STERAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND



```

; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 81
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-81

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```

Query Match          98.0%; Score 192; DB 9; Length 232;
Best Local Similarity 97.2%; Pred. No. 9,7e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

1 YTSLIHTLIEESQNOQEKNEQELLELDKNASLNMWF 36
|||||:|||||:|||||:|||||:|||||:|||||:
DB 144 YTSLIHTLIEESQNOQEKNEQELLELDKNASLNMWF 179

```

```

RESULT 15
US-10-059-271-82
; Sequence 82, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKKE, HEINRICH
; APPLICANT: BUDEDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

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Query Match          98.0%; Score 192; DB 9; Length 254;
Best Local Similarity 97.2%; Pred. No. 1.1e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSLIHTLIEESQNOQEKNEQELLELDKNASLNMWF 36
|||||:|||||:|||||:|||||:|||||:|||||
DB 166 YTSLIHTLIEESQNOQEKNEQELLELDKNASLNMWF 201

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Search completed: May 16, 2003, 12:10:25  
Job time : 15.759 secs

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RESULT 4  
AAV22912  
ID AAV22912 standard; Peptide: 36 AA.  
XX  
XX AAV22912:  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 108 from W09820036.  
XX  
XX HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
XX W09820036-A1.  
XX  
XX 14-MAY-1998.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
XX  
XX 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Braisted A, Judice JK, McDowell RS, Phehan JC, Starovasnik MA;  
PI Wells JA;  
XX  
DR WPI: 1998-286866/25.  
XX  
XX Production of constrained helical peptide(s) by linking side chains  
PT on terminal of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
XX  
PS Disclosure: Page 233-234; 279pp; English.  
XX  
XX Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
XX  
SQ Sequence 36 AA:  
XX  
XX  
Query Match 99.0%; Score 193; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
AAV22805  
ID AAV22805 standard; Peptide: 36 AA.  
XX  
XX AAV22805:  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 1 from W09820036.  
XX  
XX HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
XX W09820036-A1.  
XX  
XX 14-MAY-1998.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
XX  
XX 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Braisted A, Judice JK, McDowell RS, Phehan JC, Starovasnik MA;  
PI Wells JA;  
XX  
DR WPI: 1998-286866/25.  
XX  
XX Production of constrained helical peptide(s) by linking side chains  
PT on terminal of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
XX  
PS Disclosure: Page 143-144; 279pp; English.  
XX  
XX Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
XX  
SQ Sequence 36 AA:  
XX  
XX  
Query Match 99.0%; Score 193; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 AAY31955  
 ID AAY31955 standard; Peptide: 36 AA.  
 AC AAY31955;  
 DT 21-DEC-1999 (first entry)  
 DE Synthetic peptide T-20 (DP-178).  
 KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Modified-site /note= "N-terminal acetyl"  
 PM Modified-site 36  
 PM Modified-site /note= "C-terminal amide"  
 XX W09948513-A1.  
 PN 30-SEP-1999.  
 PD 22-MAR-1999; 99WO-US06230.  
 PF 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX (TRIM-) TRIMERIS INC.  
 PI Kang M, Bray B, Lichty M, Mader C, Merutka G;  
 DR WPI: 1999-591038/50.  
 PT Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides  
 XX Claim 1; Page 102; 120pp; English.  
 PS The present sequence represents an N- and C-terminal modified  
 CC peptide, designated T-20 (or DP-178), corresponding to amino acids  
 CC 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.  
 CC The invention relates to methods for the synthesis of peptides,  
 CC in particular T-20 and T-20-like peptides. The method involves  
 CC synthesizing specific side-chain protected peptide fragment  
 CC intermediates of T-20 or a T-20-like peptide on a solid support,  
 CC coupling the protected fragments in solution to form a protected  
 CC T-20 or T-20-like peptide, followed by deprotection of the side  
 CC chains to yield the final T-20 or T-20-like peptide. The invention  
 CC also relates to individual peptide fragments (see AAY31956-73) which  
 CC act as intermediates in the synthesis of peptides of interest (e.g.  
 CC T-20), and to particular groups of peptide fragments which act as  
 CC intermediates in the synthesis of the peptide of interest. The  
 CC method allows for the large scale, economical production of high  
 CC purity peptides.  
 CC  
 SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSIWNMF 36  
 DB 1 YTSLSHLSIESQNOQEKNEQELLELDKWSIWNMF 36  
 RESULT 7  
 AAY31974

ID AAY31974 standard; Peptide: 36 AA.  
 AC AAY31974;  
 DT 21-DEC-1999 (first entry)  
 DE HIV-1 LAI gp41 T-20 peptide.  
 KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 OS Human immunodeficiency virus type 1.  
 PN W09948513-A1.  
 PD 30-SEP-1999.  
 PF 22-MAR-1999; 99WO-US06230.  
 PR 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX (TRIM-) TRIMERIS INC.  
 PI Kang M, Bray B, Lichty M, Mader C, Merutka G;  
 DR WPI: 1999-591038/50.  
 PT Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides  
 XX Disclosure; Page 9; 120pp; English.  
 PS The present sequence represents a peptide, designated T-20 (or  
 CC DP-178), that corresponds to amino acids 638-673 of the  
 CC transmembrane protein gp41 of HIV-1 LAI isolate. The invention  
 CC relates to methods for the synthesis of peptides, in particular  
 CC C- and N-terminal modified T-20 (see AAY31955) and T-20-like peptides.  
 CC The method involves synthesizing specific side-chain protected  
 CC peptide fragment intermediates (see AAY31956-73) of T-20 or a  
 CC T-20-like peptide on a solid support, coupling the protected  
 CC fragments in solution to form a protected T-20 or T-20-like peptide,  
 CC followed by deprotection of the side chains to yield the final T-20  
 CC or T-20-like peptide. The invention also relates to individual  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC peptides of interest (e.g. T-20), and to particular groups of  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC the peptide of interest. The method allows for the large scale,  
 CC economical production of high purity peptides.  
 CC  
 SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSIWNMF 36  
 DB 1 YTSLSHLSIESQNOQEKNEQELLELDKWSIWNMF 36  
 RESULT 8  
 AAB52655  
 ID AAB52655 standard; Peptide: 36 AA.  
 AC AAB52655;  
 DT 23-FEB-2001 (first entry)  
 DE T20/DP178 peptide fragment #33.  
 KW Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemottractant.

XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX RA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI; 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
XX Claim 12; Page 24; 148pp; English.  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
XX Sequence 36 AA:  
SQ  
XX  
XX Query Match 99.0%; Score 193; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
XX Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLSHLSLEESQNOQEKNEDELLELDKMASLWNMF 36  
DB 1 YTSLSHLSLEESQNOQEKNEDELLELDKMASLWNMF 36  
RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide; 36 AA.  
XX  
XX AAB52688;  
DT 23-FEB-2001 (first entry)  
XX  
XX T20/Dp178 peptide fragment #66.  
DE  
XX  
XX Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; Inflammatory response up-regulation;  
XX chemoattractant.  
XX  
XX Human immunodeficiency virus type 1.  
XX OS  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX RA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI; 2000-656493/63.

XX  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
XX Claim 12; Page 25; 148pp; English.  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
XX Sequence 36 AA:  
SQ  
XX  
XX Query Match 99.0%; Score 193; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
XX Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLSHLSLEESQNOQEKNEDELLELDKMASLWNMF 36  
DB 1 YTSLSHLSLEESQNOQEKNEDELLELDKMASLWNMF 36  
RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide; 36 AA.  
XX  
XX AAB52818;  
DT 23-FEB-2001 (first entry)  
XX  
XX T20/Dp178 peptide fragment #97.  
DE  
XX  
XX Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; Inflammatory response up-regulation;  
XX chemoattractant.  
XX  
XX Human immunodeficiency virus type 1.  
XX OS  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX RA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI; 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
XX Claim 14; Page 40; 148pp; English.  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.

[illegible]

	HIV strains and isolates. The peptide compositions may be administered as a prophylactic or therapeutic vaccine to generate antibodies which reduce or inhibit the ability of HIV to infect uninfected cells.	A
	composition comprising polyclonal or monoclonal antibodies can be administered to reduce HIV infection of uninfected cells. Antibodies raised against entry-relevant gp41 structures may also be used therapeutically and as tools to further elucidate the mechanism of HIV cell entry.	X
SQ	Sequence      36 AA:	
OY	Query Match                  99.0%; Score 193; DB 21;	
Dd	Best Local Similarity        97.2%; Pred. No. 7.6e-17; Matches     35; Conservative    1; Mismatches    0; Indels     0; Gaps     0;	
	1 YTSLIHSLSIESONOEKNEOELLELDKASIMNMF    36      :       :       :       : 1 YTSLIHSLSIESONOEKNEOELLELDKWSLWMPF    36	
	RESULT 12 AAV88665 ID AAV88665 standard; peptide; 36 AA.  AC AAV88665; XX DT 23-MAY-2000 (first entry) DE Core polypeptide fragment T NO. 20.  XX Retrovirus: hybrid polypeptide: enhancer: gp41; envelope protein: HIV-1; KM HIV-2; SIV; pharmacokinetic: half-life; growth factor: cytokine; viral; KN anti-fusogenic; differentiation factor; interleukin; interferon; XX colony stimulating factor; hormone; angiogenic factor. OS Unidentified. XX PN WO9959615-A1. XX PD 25-NOV-1999. XX PF 20-MAY-1999; 99WO-US11219. PR 20-MAY-1998; 98US-0082279. PA (TRIM-) TRIMERIS INC. PI Barney S., Guthrie KI, Merutka G, Anwer MK, Lambert DM; PT WPI: 2000-136792/I2. PS A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence - XX Disclosure; Page 21; 124pp; English. XX CC The invention relates to hybrid polypeptides comprising enhancer peptide sequences linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacologically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a group consisting of: cytokines, differentiation factors, interleukins, interferons, colony stimulating factors, hormones or angiogenic factors. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-tumorigenic treatments. Sequences AAV88651-Y9005 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides.	CX



XX Sequence 36 AA:  
SQ Query Match 99.0%; Score 193; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7, 6e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 36

RESULT 13  
ID AAY88729 standard; peptide; 36 AA.  
AC AAY88729;  
XX 23-MAY-2000 (first entry)  
DT Core polypeptide fragment T No. 84.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX Unidentified.  
OS  
XX WO9595615-A1.  
PN 25-NOV-1999.  
XX 20-MAY-1999; 99WO-US11219.  
PF 20-MAY-1998; 98US-0082279.  
PR (TRIM-) TRIMERIS INC.  
PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI: 2000-136792/12.  
XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence -  
XX Disclosure; Page 22; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
PS sequence linked to core polypeptides. The enhancer polypeptides are  
derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.

XX Sequence 36 AA:  
SQ Query Match 99.0%; Score 193; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7, 6e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 36

DB 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 36

RESULT 14  
ID AAY89135 standard; peptide; 36 AA.  
AC AAY89135;  
XX 23-MAY-2000 (first entry)  
DT Core polypeptide fragment T No. 573.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX Unidentified.  
OS  
XX WO9595615-A1.  
PN 25-NOV-1999.  
XX 20-MAY-1999; 99WO-US11219.  
PF 20-MAY-1998; 98US-0082279.  
PR (TRIM-) TRIMERIS INC.  
PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI: 2000-136792/12.  
XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence -  
XX Disclosure; Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
PS sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.

XX Sequence 36 AA:  
SQ Query Match 99.0%; Score 193; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7, 6e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 36

RESULT 15  
ID AAY89136 standard; peptide; 36 AA.  
XX

AC AAY89136;

XX 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 574.

DE Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS WO959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI: 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties

XX comprises enhancer sequence -

XX Disclosure: Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX Sequence 36 AA;

XX Query Match 99.0%; Score 193; DB 21; Length 36;

XX Best local Similarity 97.2%; Pred. No. 7.6e-17;

XX Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 YTSLSHLEESONQOEKNEQELLELDKNAASLNMF 36

XX DB 1 YTSLSHLEESONQOEKNEQELLELDKNAASLNMF 36

Search completed: May 16, 2003, 11:12:06

Job time : 32.4578 secs

GenCore version 5.1.4-p5\_4578  
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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-541  
Perfect score: 195  
Sequence: 1 YTSLSLHSLLESQNOQEKNEQELLEDKWSLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
A number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	99.0	851	2 S33985	env polyprotein -
2	193	99.0	854	2 S13288	env protein - huma
3	193	99.0	856	1 VCLJH3	env polyprotein pr
4	193	99.0	861	1 VCLJLV	env polyprotein pr
5	184	94.4	443	2 C41621	env polyprotein p
6	184	94.4	856	1 VCLJVL	env polyprotein pr
7	184	94.4	856	1 VCLJ3W	env polyprotein pr
8	184	94.4	861	1 VCLJSC	env polyprotein pr
9	181	92.8	357	2 S21994	env polyprotein pr
10	181	92.8	358	2 S21998	env polyprotein g
11	180	92.3	357	2 S21996	env polyprotein g
12	179	91.8	859	1 VCLJMN	env polyprotein pr
13	178	91.3	855	1 VCLJAZ	env polyprotein pr
14	177	90.8	847	2 T09448	env polyprotein g
15	177	90.8	847	2 S13289	env protein - huma
16	176	90.3	445	2 A41621	env polyprotein M
17	175	89.7	358	2 S22002	env polyprotein g
18	175	89.7	358	2 S22000	env polyprotein g
19	175	89.7	358	2 S70417	env polyprotein g
20	175	89.7	852	2 T12016	env polyprotein g
21	174	89.2	357	2 S22004	env polyprotein g
22	172	88.2	357	2 S21992	env polyprotein g
23	172	88.2	853	2 S54384	env polyprotein g
24	172	88.2	855	1 VCLJZR	env polyprotein pr
25	171	87.7	843	2 S22006	env polyprotein pr
26	171	87.7	843	1 H44001	env polyprotein pr
27	170	86.2	846	1 VCLJND	env polyprotein pr
28	168	86.2	852	1 VCLJBR	env polyprotein pr
29	166	85.1	729	1 VCLJXK	env polyprotein pr

30	166	85.1	861	1 VCLJKB	env polyprotein pr
31	165	84.6	859	2 T01672	env polyprotein pr
32	162	83.1	454	2 B41621	env polyprotein D
33	161	82.6	868	1 VCLJH4	env polyprotein -
34	158	81.0	136	2 JU0266	env polyprotein -
35	158	81.0	136	2 JU0266	env polyprotein -
36	153	78.5	854	1 VCLJ51	env polyprotein pr
37	147	75.4	856	1 A44963	env polyprotein pr
38	145	74.4	357	2 S21990	env polyprotein g
39	134	68.7	877	2 S49197	env polyprotein g
40	117	60.0	863	2 A53034	env polyprotein p
41	88	45.1	881	1 VCLJG3	env polyprotein -
42	88	45.1	881	2 S03068	env protein - huma
43	88	45.1	889	1 VCLJG5	env polyprotein -
44	87	44.6	151	2 S30448	env protein - huma
45	87	44.6	151	2 S30452	env protein - huma

## ALIGNMENTS

RESULT 1  
S33985  
env polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlisi, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-references: EMBL:Z11530; NID:960192; PIDN:CAAT7628.1; PID:960199  
C:Superfamily: type E retrovirus env polyprotein

Query Match  
Best Local Similarity 99.0%; Score 193; DB 2; Length 851;  
Matches 35; Conservative 1; Mismatches 0; Indels 0;

QY 1 YTSLSLHSLLESQNOQEKNEQELLEDKWSLWNF 36  
Db 633 YTSLSLHSLLESQNOQEKNEQELLEDKWSLWNF 668

## RESULT 2

S13288  
env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, N.  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polyprotein

Query Match  
Best Local Similarity 99.0%; Score 193; DB 2; Length 854;  
Matches 35; Conservative 1; Mismatches 0; Indels 0;

QY 1 YTSLSLHSLLESQNOQEKNEQELLEDKWSLWNF 36  
Db 636 YTSLSLHSLLESQNOQEKNEQELLEDKWSLWNF 671

## RESULT 3

VCLJH3

```

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Accession: A03973
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberger, J.A.; Papas, T.S.; Garyaga, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <TMN>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 4,1e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 4

```

VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Accession: A03975
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAI>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 99.0%; Score 193; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 4,1e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 5

```

VCLJ3M
env polyprotein precursor - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Accession: A03973
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberger, J.A.; Papas, T.S.; Garyaga, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <TMN>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 4,1e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 6

```

VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Accession: A03974
R:Messing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MGF>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polytyp
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 94.4%; Score 184; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 4,9e-14;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 7

```

VCLJ3M
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversit
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polytyp
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match 94.4%; Score 184; DB 2; Length 443;
Best Local Similarity 91.7%; Pred. No. 2,3e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 8

```

VCLJ3M
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversit
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polytyp
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match 94.4%; Score 184; DB 2; Length 443;
Best Local Similarity 91.7%; Pred. No. 2,3e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
Cell 45, 637-648, 1986  
A>Title: Identification and characterization of conserved and variable regions in the en  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <STG>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
E:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match            94.4%; Score 184; DB 1; Length 856;  
Rest Local Similarity   91.7%; Pred. No. 4,9e-14;  
Matches     33; Conservative     3; Mismatches       0; Indels       0; Gaps       0;

Oy      1 YTSLSILSEESONOOEKNEOELELDKWASTLMNFE 36  
        |||||:::|||||||||||  
Db      638 YTSLSYLNIEESONOEEKNEOELELDKWASTLMNFE 673

```

Query Match Similarity    94.4%; Score 184; DB 1; Length 856;
Best Local Similarity    91.7%; Pred. No. 4.9e-14;
Matches      33; Conservative      3; Mismatches     0; Indels       0; Gaps        0;

QY          1 YTSLIHSLEESONQOEKNEDELLDLKWSLWNMF 36
|||||:::|||||||
DB         638 YTSLIYNLTIEESQNQEKNQELLELDKWSLWNMF 673

RESULT 8
VCLJSC
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
R:Gutgog, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal, P.; Weiss, R.A.; Johnson, V.A.; et al., 1988
P:Virology 164, 531-536, 1988
A>Title: Envelope sequences of two new United States HIV-1 isolates.
I:Reference number: A28922; MIDB:88219542; PMID:3369091
A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polypotein; transmembrane prote
F:1-29/Domains: signal sequence #status predicted <SIG>
F:80-861/Product: env polyprotein #status predicted <EPP>
S:129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match              94.4%; Score 184; DB 1; Length 861;
Best Local Similarity    91.7%; Pred. No. 4.9e-14;
Matches      33; Conservative      3; Mismatches     0; Indels       0; Gaps        0;

QY          1 YTSLIHSLEESONQOEKNEDELLDLKWSLWNMF 36
|||||:::|||||||
DB         643 YTSLIYTIEESQNQEKNQELLELDKWSLWNMF 678

RESULT 9
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Waldemar, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STFI>
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A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAAA3622.1; PTD:960180  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
Aids Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:9214209; PMID:1736940  
A:Accession: S70421  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
A:Cross-references: EMBL:X61355; NID:960179  
C:Superfamily: type E retrovirus env polypeptide

Query Match            92.8%; Score 181; DB 2; Length 357;  
Best Local Similarity   88.9%; Pred. No. 4,le-14;  
Matches     32; Conservative   4; Mismatches     0; Indels     0; Gaps     0;

OY        1   YTSLIHSLEESONOEKNROELLELDKMAIWMWF   36  
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db      139   YTTLYTLESNOOEKNROELLELDKMAIWMWF   174

```

RESULT 10
S21998
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 28
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21998; S70425
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as deter
A:Reference number: S21990
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <STE1>
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70425
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222; X, 224-358 <STE2>
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
C:Superfamily: type E retrovirus env polyprotein

Query Match          92.8%; Score 181; DB 2; Length 358;
Match Local Similarity 88.9%; Pred. No. 4, 2e-14;
Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSILHSILLESQNOQEKNEDELLELDKMASLWMWF 36
        |||||::||:|||||:|||||:|||||:|||||
Db      140 YTSILYTLIBQSQNOQEKNEDELLELDKMASLWMWF 175

RESULT 11
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STE2>
A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129
A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library July 1991

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Page 4



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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

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Query Match 99.0%; Score 193; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 7.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTSLSHLSLEESONOEKNEDELLELDKNASLWNMF 36
DB 633 YTSLSHLSLEESONOEKNEDELLELDKNASLWNMF 668

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RESULT 2
ENV_HV1B1 STANDARD; PRT: 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
GN glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
NCBI_TaxID=11678;

```

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RA MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Dorn E.R., Ratslki S.A., Whitehorn E.A.,
RA Baumesister K., Ivanoff L., Peteway J.S. Jr., Pearson M.L.,
RA Laubenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RA Nature 313:277-284(1985).

```

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RA DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RA MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
RT potential glycosylation sites of the type I recombinant human
RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells."
RA J. Biol. Chem. 265:10373-10382(1990).

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CC

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```

CC -----
CC DR EMBL; M15654; AAA4205.1;
CC DR PIR; A03973; VCLPH3.
CC DR HIV; M15654; ENVSBH102.
CC DR InterPro; IPR000328; Env_GP41.
CC DR InterPro; IPR00777; GP120.
CC DR Pfam; PF00516; GP120.1.
CC DR Aids; Coat protein; Glycoprotein; Transmembrane;
CC Signal.

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KW SIGNAL.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 31 511 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 256 331
FT DISULFID 378 445
FT DISULFID 385 418
FT DISULFID 88 88

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FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .)
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FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97224 MW; 0BFB1A18931BB27 CRC64;

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Query Match 99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 7.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

OY 1 YTSLSHLSLEESONOEKNEDELLELDKNASLWNMF 36
DB 638 YTSLSHLSLEESONOEKNEDELLELDKNASLWNMF 673

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RESULT 3
ENV_HV1H2 STANDARD; PRT: 856 AA.
ID ENV_HV1H2
AC P04578; 009779;

```





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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;

```

```

Query Match          99.0% Score 193; DB 1; Length 856;
Best Local Similarity 97.2% Pred. No. 7, 3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTSLSHLSLEESONOEKNEOELLELDKMSLWNMF 36
    |||||:|||||:|||||:|||||:|||||:|||||
DB 638 YTSLSHLSLEESONOEKNEOELLELDKMSLWNMF 673

```

```

RESULT 5
ENV_HVILW STANDARD; PRT: 856 AA.
ID ENV_HVILW
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;

```

```

RN [1]
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U12055; AAA76690.1; -
CC DR GlycosultedB: 070626; -
CC DR InterPro: IPR000328; Env_GP41.

```

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane;
Signal.
FT SIGNAL 1 30
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CE7E687 CRC64;

```

```

Query Match          99.0% Score 193; DB 1; Length 856;
Best Local Similarity 97.2% Pred. No. 7, 3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTSLSHLSLEESONOEKNEOELLELDKMSLWNMF 36
    |||||:|||||:|||||:|||||:|||||:|||||
DB 638 YTSLSHLSLEESONOEKNEOELLELDKMSLWNMF 673

```

```

RESULT 6
ENV_HVILW STANDARD; PRT: 861 AA.
ID ENV_HVILW
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

```





[illegible]











FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 855 AA: 97438 MW: A3BC20573AAC41A2 CRC64;

Query Match 91.3%; Score 178; DB 1; Length 855;  
Best Local Similarity 88.9%; Pred. No. 4.8e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YNLIHSLEESONOEKNEOELELDKMASLWNP 36  
DB 637 YNLIHSLEESONOEKNEOELELDKMASLWNP 672

Job completed: May 16, 2003, 11:13:38  
Job time : 7.07229 secs

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GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-541

Perfect score: 195

Sequence: 1 YTSLSHLSIESONQOEKNEQLLELDKWSLWNF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	99.0	645	15	0993A6 human immun
2	193	99.0	747	15	070607 human immun
3	193	99.0	748	15	070606 human immun
4	193	99.0	752	15	070604 human immun
5	193	99.0	752	15	070605 human immun
6	193	99.0	752	15	070608 human immun
7	193	99.0	851	15	078243 human immun
8	193	99.0	852	15	089797 human immun
9	193	99.0	854	15	085582 human immun
10	193	99.0	854	15	072502 human immun
11	193	99.0	856	15	092877 simian-huma
12	193	99.0	856	15	074599 human immun
13	193	99.0	856	15	074090 human immun
14	189	96.9	854	15	090178 human immun
15	189	96.9	854	15	078705 human immun
16	188	96.4	856	15	0905M7 human immun

17	187	95.9	616	15	0993B0 human immun
18	187	95.9	618	15	0993B2 human immun
19	187	95.9	757	15	090722 human immun
20	187	95.9	848	15	069990 human immun
21	186	95.4	855	15	09E1R7 human immun
22	186	95.4	858	15	080867 human immun
23	186	95.4	858	15	080865 human immun
24	186	95.4	864	15	09E610 human immun
25	185	94.9	122	15	09YXR6 human immun
26	185	94.9	838	15	003806 human immun
27	185	94.9	854	15	078225 human immun
28	185	94.9	855	15	003805 human immun
29	184	94.4	42	15	069910 human immun
30	184	94.4	443	15	080023 human immun
31	184	94.4	841	15	041556 human immun
32	184	94.4	849	15	077368 human immun
33	184	94.4	849	15	080851 human immun
34	184	94.4	851	15	056110 human immun
35	184	94.4	851	15	080852 human immun
36	184	94.4	856	15	072993 human immun
37	184	94.4	856	15	041539 human immun
38	184	94.4	857	15	080170 human immun
39	184	94.4	858	15	080190 human immun
40	184	94.4	858	15	080188 human immun
41	184	94.4	859	15	080185 human immun
42	184	94.4	859	15	080180 human immun
43	184	94.4	859	15	080179 human immun
44	184	94.4	859	15	080177 human immun
45	184	94.4	859	15	080173 human immun

## ALIGNMENTS

## RESULT 1

ID 0993A6 PRELIMINARY; PRT; 645 AA.  
AC 0993A6;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update).  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RA MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
DR EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;  
KW Transmembrane.  
FT NON\_TER 1 1  
SO SEQUENCE 645 AA; 72485 MW; B07651ABE9336ZEC CRC64;

## Query Match

99.0%; Score 193; DB 15; Length 645;

## Best Local Similarity

97.2%; Pred. No. 2.4e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQLLELDKWSLWNF 36  
DB 607 YTSLSHLSIESONQOEKNEQLLELDKWSLWNF 642

## RESULT 2

070607 PRELIMINARY: PRT: 747 AA.  
AC 070607: 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LM87-1;  
RX MEDLINE=95127297; PubMed=7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
"Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HTLV type IIIB)."  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RM [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=LM87-1;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
DR EMBL: U12034; AAA76669.1; -  
DR InterPro: IPR000328; ENV\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120.1.  
DR KMW AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
FT NON\_TER 747  
SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245F14 CRC64:

Query Match 99.0%; Score 193; DB 15; Length 747;  
Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSLEESONOEKNEQELLELDKWSLWNMF 36  
DB 633 YTSLSLSLEESONOEKNEQELLELDKWSLWNMF 668

## RESULT 3

070606 PRELIMINARY: PRT: 748 AA.  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LM881;  
RX MEDLINE=95127297; PubMed=7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
"Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HTLV type IIIB)."  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RM [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=LM881;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
DR EMBL: U12032; AAA76668.1; -

DR InterPro: IPR000328; ENV\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120.1.  
DR KMW AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
FT NON\_TER 748  
SQ SEQUENCE 748 AA: 84254 MW: 56BEDF186C67694B CRC64:

Query Match 99.0%; Score 193; DB 15; Length 748;  
Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSLEESONOEKNEQELLELDKWSLWNMF 36  
DB 634 YTSLSLSLEESONOEKNEQELLELDKWSLWNMF 669

## RESULT 4

070604 PRELIMINARY: PRT: 752 AA.  
AC 070604: 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LM851;  
RX MEDLINE=95127297; PubMed=7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
"Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HTLV type IIIB)."  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RM [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=LM851;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
DR EMBL: U12030; AAA76666.1; -  
DR InterPro: IPR000328; ENV\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120.1.  
DR KMW AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
FT NON\_TER 752  
SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013845A CRC64:

Query Match 99.0%; Score 193; DB 15; Length 752;  
Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSLEESONOEKNEQELLELDKWSLWNMF 36  
DB 638 YTSLSLSLEESONOEKNEQELLELDKWSLWNMF 673

## RESULT 5

070605 PRELIMINARY: PRT: 752 AA.  
AC 070605: 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM852;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12031; AAA76667.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752 752  
 SO SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 99.0%; Score 193; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 638 YTSLSHLSLEESONOEKNEDELLELDKWSLWMP 673

RESULT 6  
 O70608 PRELIMINARY; PRT; 752 AA.  
 AC O70608;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM87-2;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752 752  
 SO SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 638 YTSLSHLSLEESONOEKNEDELLELDKWSLWMP 673

DB 638 YTSLSHLSLEESONOEKNEDELLELDKWSLWMP 673

RESULT 7  
 O78243 PRELIMINARY; PRT; 851 AA.  
 AC O78243;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env polypotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federico M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
 Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 RT chronically infected HUT-78 cellular clone."  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Macchi B., Mangano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 RT producer clones from HUT-78 infected with a patient HIV isolate."  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Borsetti A., Saglio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 RT productive clone."  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL: Z11530; CAA77628.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 KW SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 633 YTSLSHLSLEESONOEKNEDELLELDKWSLWMP 668

RESULT 8  
 O89797 PRELIMINARY; PRT; 852 AA.  
 AC O89797;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker

RT Infected with HIV type 1 (HTLV type IIIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LW90-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12053; AAA76685.1; -;  
DR EMBL: U12036; AAA76671.1; -;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
KW Transmembrane.  
SQ SEQUENCE 852 AA; 96347 MW; 4E865229DAEB33CF CRC64;  
  
Query Match 99.0%; Score 193; DB 15; Length 852;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
1 YTSLSHLSLEESONOQKNEQLELDKWSLWNMF 36  
634 YTSLSHLSLEESONOQKNEQLELDKWSLWNMF 669  
  
RESULT 9  
085582 PRELIMINARY: PRT: 854 AA.  
AC 085582;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
RT Envelope polyprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone.";  
RT J. Virol. 59:284-291(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RL Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
RT Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RL Buckler C.E.;  
RT Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92219406; PubMed=1373204;  
RA Dai L.C., Litcua R., Takahashi K., Ennis F.A.;  
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T  
lymphocytes.";  
RT J. Virol. 66:3151-3154(1992).  
DR EMBL: M19921; AAA4992.1; -;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
KW SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;  
  
Query Match 99.0%; Score 193; DB 15; Length 854;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 YTSLSHLSLEESONOQKNEQLELDKWSLWNMF 36  
DB 636 YTSLSHLSLEESONOQKNEQLELDKWSLWNMF 671  
  
RESULT 10  
072502 PRELIMINARY: PRT: 854 AA.  
AC 072502;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
RT Env polyprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96036482; PubMed=7483282;  
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
from primary virus cultures using the polymerase chain reaction.";  
RT Virology 213:80-86(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-NLA-3;  
RX MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone.";  
RT J. Virol. 59:284-291(1986).  
DR EMBL: U26942; AAB60578.1; -;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT CONFLICT 214 H -> L (IN REF. 2).  
FT CONFLICT 530 A -> S (IN REF. 2).  
FT CONFLICT 739 G -> D (IN REF. 2).  
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;  
  
Query Match 99.0%; Score 193; DB 15; Length 854;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 YTSLSHLSLEESONOQKNEQLELDKWSLWNMF 36  
DB 636 YTSLSHLSLEESONOQKNEQLELDKWSLWNMF 671  
  
RESULT 11  
092877 PRELIMINARY: PRT: 856 AA.  
AC 092877;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
RT Envelope glycoprotein.  
GN ENV.  
OS Simian-Human immunodeficiency virus.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=57667;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9098984; PubMed=9882298;

RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
RA Steenbeke T., Halloran M., Fanton J.W., Axelhelm M.K., Letvin N.L.,  
RA Sodroski J.G.;  
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
RT responsible for the pathogenicity of a multiply passaged simian-human  
RT immunodeficiency virus (SHIV-HXBc2).";  
RL J. Virol. 73:976-984(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
RA Halloran M., Axelhelm M.W., Letvin N.L., Sodroski J.G.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF041850; AAD12142.1; -  
DR InterPro: IPR000328; Env-GP41.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
DB 638 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 673

RESULT 12  
O74599 PRELIMINARY; PRT; 856 AA.  
AC Q74599;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.;  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates.";  
RL Virology 174:103-116(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RA Iwatani Y.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: D86068; BAA1295.1; -  
DR InterPro: IPR000328; Env-GP41.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
DB 638 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 673

RESULT 13  
O74090

ID 074090 PRELIMINARY; PRT; 856 AA.  
AC 074090;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
RA Halloran M., Axelhelm M.W., Letvin N.L., Sodroski J.G.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: D86069; BAA13003.1; -  
DR InterPro: IPR000328; Env-GP41.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 99.0%; Score 193; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
DB 638 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 673

RESULT 14  
O90178 PRELIMINARY; PRT; 854 AA.  
AC O90178;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RX MEDLINE=95074930; PubMed=7983770;  
RA Fang H., Pincus S.H.;  
RT "Unique insertion sequence and pattern of CD4 expression in variants  
RT selected with immunotoxins from human immunodeficiency virus type 1-  
RT infected T cells.";  
RL J. Virol. 69:75-81(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Fang H., Pincus S.H.;  
RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
RT immunotoxin-resistant variant T cell line";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF070521; AAC28452.1; -  
DR InterPro: IPR000328; Env-GP41.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;







Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486.099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichy, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Merutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

US-09-071-877-1

CURRENT APPLICATION NUMBER: US/09/071,877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 36

TYPE: PPT

ORGANISM: Human immunodeficiency virus

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESONOEKNEOEELLEDKWSLWMP 36

RESULT 5  
US-08-484-223B-1  
Sequence 1, Application US/08484223B  
Patent No. 6020459

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONOEKNEOEELLEDKWSLWMP 36  
Db 1 YTSLSHLSIESONOEKNEOEELLEDKWSLWMP 36

RESULT 6  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONOEKNEOEELLEDKWSLWMP 36  
Db 1 YTSLSHLSIESONOEKNEOEELLEDKWSLWMP 36

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6060065

GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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      LENGTH: 36 amino acids
      TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-485-551A-1

Query Match          99.0%; Score 193; DB 3; Length 36;
Best Local Similarity 97.2%; Pred. No. 2,3e-17;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSLIHSILLESQNQQEKNEGELLELDKWSLWNMF 36
        |||||:|||||:|||||:|||||:|||||:|||||:
Db       1 YTSLIHSILLESQNQQEKNEGELLELDKWSLWNMF 36

RESULT 9
US-08-471-913A-1
Sequence 1, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognai, Danl P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Peteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-471-913A-1

Query Match          99.0%; Score 193; DB 3; Length 36;
Best Local Similarity 97.2%; Pred. No. 2,3e-17;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSLIHSILLESQNQQEKNEGELLELDKWSLWNMF 36
        |||||:|||||:|||||:|||||:|||||:|||||:
Db       1 YTSLIHSILLESQNQQEKNEGELLELDKWSLWNMF 36

```

RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Danl P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1  
Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 YTSLSHLSLEESONQOEKNEOELLELDKWSLWNMF 36  
1 YTSLSHLSLEESONQOEKNEOELLELDKWSLWNMF 36

RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Danl P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Lamberty, Dennis M.  
APPLICANT: Langlois, Alphonse R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1  
Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 YTSLSHLSLEESONQOEKNEOELLELDKWSLWNMF 36  
1 YTSLSHLSLEESONQOEKNEOELLELDKWSLWNMF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Amer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15  
Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 YTSLSHLSLEESONQOEKNEOELLELDKWSLWNMF 36  
1 YTSLSHLSLEESONQOEKNEOELLELDKWSLWNMF 36

Db 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 13

US-09-082-279B-497

Sequence 497, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 497

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match 99.0%; Score 193; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 14

US-09-082-279B-498

Sequence 498, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 498

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

Query Match 99.0%; Score 193; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 15

US-09-082-279B-603

Sequence 603, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 603

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 99.0%; Score 193; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:22:14  
Job time : 10.1928 secs

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-541  
Perfect score: 195  
Sequence: 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLWVNF 36

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCR\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
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- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.0	36	9 US-09-874-475-16	Sequence 16, Appl
2	193	99.0	36	9 US-10-116-797-1	Sequence 1, Appl
3	193	99.0	36	9 US-09-493-346-1	Sequence 1, Appl
4	193	99.0	36	10 US-09-779-202-10	Sequence 10, Appl
5	193	99.0	36	10 US-09-779-451-5	Sequence 5, Appl
6	193	99.0	36	10 US-09-834-828-1	Sequence 1, Appl
7	193	99.0	36	10 US-09-854-816-1	Sequence 1, Appl
8	193	99.0	36	10 US-09-854-816-108	Sequence 108, App
9	193	99.0	37	9 US-09-848-616-176	Sequence 176, App
10	193	99.0	46	10 US-09-779-451-41	Sequence 41, Appl
11	193	99.0	56	10 US-09-779-451-4	Sequence 4, Appl
12	193	99.0	177	9 US-10-040-349B-2	Sequence 2, Appl
13	193	99.0	221	9 US-10-059-271-84	Sequence 84, Appl
14	193	99.0	232	9 US-10-059-271-81	Sequence 81, Appl
15	193	99.0	254	9 US-10-059-271-82	Sequence 82, Appl
16	193	99.0	256	9 US-10-059-271-97	Sequence 97, Appl
17	193	99.0	268	10 US-09-854-816-16	Sequence 16, Appl
18	193	99.0	268	10 US-09-854-816-17	Sequence 17, Appl
19	193	99.0	268	10 US-09-854-816-15	Sequence 18, Appl

20	193	99.0	344	9 US-10-040-349B-1	Sequence 1, Appl
21	193	99.0	345	9 US-10-026-741-49	Sequence 49, Appl
22	193	99.0	345	9 US-09-779-451-8	Sequence 8, Appl
23	193	99.0	391	9 US-10-059-271-93	Sequence 93, Appl
24	193	99.0	519	10 US-09-756-551A-8	Sequence 8, Appl
25	193	99.0	853	9 US-10-003-035-33	Sequence 33, Appl
26	193	99.0	856	10 US-09-476-242-1	Sequence 1, Appl
27	193	99.0	861	9 US-10-026-741-103	Sequence 103, Appl
28	193	99.0	1101	9 US-10-003-035-53	Sequence 53, Appl
29	193	99.0	1186	9 US-10-003-035-55	Sequence 55, Appl
30	190	97.4	36	10 US-09-912-624-1	Sequence 1, Appl
31	190	97.4	268	10 US-09-854-816-19	Sequence 19, Appl
32	187	95.9	1231	9 US-10-059-271-94	Sequence 94, Appl
33	186	95.4	269	10 US-09-854-816-28	Sequence 28, Appl
34	185	94.9	268	10 US-09-854-816-13	Sequence 13, Appl
35	184	94.4	233	10 US-09-854-816-50	Sequence 50, Appl
36	184	94.4	268	10 US-09-854-816-9	Sequence 9, Appl
37	184	94.4	269	10 US-09-854-816-12	Sequence 12, Appl
38	183	93.8	269	10 US-09-854-816-46	Sequence 46, Appl
39	181	92.8	268	10 US-09-854-816-26	Sequence 26, Appl
40	181	92.8	619	10 US-09-891-609-4	Sequence 4, Appl
41	181	92.8	646	10 US-09-891-609-2	Sequence 2, Appl
42	181	92.8	847	10 US-09-476-242-2	Sequence 2, Appl
43	180	92.3	46	10 US-09-854-816-109	Sequence 109, App
44	180	92.3	267	10 US-09-854-816-38	Sequence 38, Appl
45	180	92.3	268	10 US-09-854-816-41	Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
; Sequence 16, Application US/09874475  
; Publication No. US20020182592A1  
; GENERAL INFORMATION:  
; APPLICANT: Petropoulos, Christos J.  
; APPLICANT: Parkin, Neil T.  
; APPLICANT: Whitcomb, Jeanette  
; APPLICANT: Huang, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
; TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS  
; FILE REFERENCE: 2793/65166  
; CURRENT APPLICATION NUMBER: US/09/874,475  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. NO. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLWVNF 36  
DB 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLWVNF 36

RESULT 2  
US-10-116-797-1  
; Sequence 1, Application US/10116797  
; Publication No. US2003004411A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen, William C.  
; APPLICANT: Maddon, Paul J.  
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
; FILE REFERENCE: 64672-A  
; CURRENT APPLICATION NUMBER: US/10/116,797  
; CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Patent No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Madison, William C  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE: NAME/KEY: PEPTIDE  
LOCATION: (1)-(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:

APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36

US-09-834-628-1  
Sequence 1, Application US/09834628

Patent No. US2002011922A1  
GENERAL INFORMATION:  
APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: Dp178  
US-09-834-628-1

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNMF 36





Db 2 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 37

RESULT 10

US-09-779-451-41

Sequence 41, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 46

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match

Best Local Similarity 99.0%; Score 193; DB 10; Length 46;

Best Local Similarity 97.2%; Pred. No. 1,3e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 11 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 46

RESULT 11

US-09-779-451-4

Sequence 4, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match

Best Local Similarity 99.0%; Score 193; DB 10; Length 56;

Best Local Similarity 97.2%; Pred. No. 1,6e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 16 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 51

RESULT 12

US-10-040-349B-2

Sequence 2, Application US/10040349B

Publication No. US20030082521A1

GENERAL INFORMATION:

APPLICANT: Brasseur, Robert

APPLICANT: Charlotieux, Benoit

APPLICANT: Chevalier, Michel

APPLICANT: El Habib, Raphaelle

APPLICANT: Krell, Tino

TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

FILE REFERENCE: 01-078-A

CURRENT FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)..(177)

OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match

Best Local Similarity 99.0%; Score 193; DB 9; Length 177;

Best Local Similarity 97.2%; Pred. No. 5,3e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 104 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 139

RESULT 13

US-10-059-271-84

Sequence 84, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

TITLE OF INVENTION: BEING IMMOBILIZED

FILE REFERENCE: ALBRE-22

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: DE 101 06 295

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide

US-10-059-271-84

Query Match

Best Local Similarity 99.0%; Score 193; DB 9; Length 221;

Best Local Similarity 97.2%; Pred. No. 6,7e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 131 YTSLSHLSIESONQOEKNEQELLELDKWSLWNMF 166

RESULT 14

US-10-059-271-81

Sequence 81, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

```

; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-81

```

```

Query Match          99.0%; Score 193; DB 9; Length 232;
Best Local Similarity 97.2%; Pred. No. 7,1e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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1 YTSLIHSLIESQNOEKNEQELLELDKWSLWNMF 36
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Db 144 YTSLIHSLIESQNOEKNEQELLELDKWSLWNMF 179

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RESULT 15
US-10-059-271-82
; Sequence 82, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDDÉ, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

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Query Match          99.0%; Score 193; DB 9; Length 254;
Best Local Similarity 97.2%; Pred. No. 7,8e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSLIHSLIESQNOEKNEQELLELDKWSLWNMF 36
|||||:|||||:|||||:|||||:|||||
Db 166 YTSLIHSLIESQNOEKNEQELLELDKWSLWNMF 201

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Search completed: May 16, 2003, 12:10:26  
Job time : 16.759 secs

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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-1  
Perfect score: 195  
Sequence: 1 YTSLSHSLIESQNOEKNEQELLDKWSLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 segs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PC1\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	36	9	US-09-874-475-16
2	195	100.0	36	9	US-10-116-797-1
3	195	100.0	36	9	US-09-493-346-1
4	195	100.0	36	10	US-09-796-202-10
5	195	100.0	36	10	US-09-779-451-5
6	195	100.0	36	10	US-09-834-628-1
7	195	100.0	36	10	US-09-854-816-1
8	195	100.0	36	10	US-09-854-816-108
9	195	100.0	37	9	US-09-848-616-176
10	195	100.0	46	10	US-09-779-451-41
11	195	100.0	56	10	US-09-779-451-4
12	195	100.0	177	9	US-10-040-349B-2
13	195	100.0	221	9	US-10-059-271-84
14	195	100.0	232	9	US-10-059-271-81
15	195	100.0	254	9	US-10-059-271-82
16	195	100.0	256	9	US-10-059-271-97
17	195	100.0	268	10	US-09-854-816-16
18	195	100.0	268	10	US-09-854-816-17
19	195	100.0	268	10	US-09-854-816-18

20	195	100.0	344	9	US-10-040-349B-1	Sequence 1, Appl1
21	195	100.0	345	9	US-10-026-741-49	Sequence 49, Appl1
22	195	100.0	345	9	US-09-779-451-8	Sequence 8, Appl1
23	195	100.0	391	9	US-10-059-271-93	Sequence 93, Appl1
24	195	100.0	519	10	US-09-756-551A-8	Sequence 8, Appl1
25	195	100.0	853	9	US-10-003-035-33	Sequence 33, Appl1
26	195	100.0	856	10	US-09-476-242-1	Sequence 1, Appl1
27	195	100.0	861	9	US-10-026-741-103	Sequence 103, App
28	195	100.0	1101	9	US-10-003-035-53	Sequence 53, Appl1
29	195	100.0	1186	9	US-10-003-035-55	Sequence 55, Appl1
30	192	98.5	36	10	US-09-912-824-1	Sequence 1, Appl1
31	192	98.5	268	10	US-09-854-816-19	Sequence 19, Appl1
32	189	96.9	1231	9	US-10-059-271-94	Sequence 94, Appl1
33	187	95.9	268	10	US-09-854-816-13	Sequence 13, Appl1
34	186	95.4	233	10	US-09-854-816-50	Sequence 50, Appl1
35	186	95.4	268	10	US-09-854-816-9	Sequence 9, Appl1
36	186	95.4	269	10	US-09-854-816-12	Sequence 12, Appl1
37	185	94.9	269	10	US-09-854-816-46	Sequence 46, Appl1
38	184	94.4	269	10	US-09-854-816-28	Sequence 28, Appl1
39	183	93.8	268	10	US-09-854-816-26	Sequence 26, Appl1
40	183	93.8	619	10	US-09-891-609-4	Sequence 4, Appl1
41	183	93.8	646	10	US-09-891-609-2	Sequence 2, Appl1
42	183	93.8	847	10	US-09-476-242-2	Sequence 2, Appl1
43	182	93.3	46	10	US-09-854-816-109	Sequence 109, App
44	182	93.3	267	10	US-09-854-816-38	Sequence 38, Appl1
45	182	93.3	268	10	US-09-854-816-41	Sequence 41, Appl1

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
Sequence 16, Application US/09874475  
Publication No. US20020182592A1  
GENERAL INFORMATION:  
APPLICANT: Petropoulos, Christos J.  
APPLICANT: Parkin, Neil T.  
APPLICANT: Whitcomb, Jeanette  
APPLICANT: Huang, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
FILE REFERENCE: 2793/5516  
CURRENT APPLICATION NUMBER: US/09/874,475  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16

Query Match 100.0%; Score 195; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOEKNEQELLDKWSLWNF 36  
DB 1 YTSLSHSLIESQNOEKNEQELLDKWSLWNF 36

RESULT 2  
US-10-116-797-1  
Sequence 1, Application US/10116797  
Publication No. US20030044411A1  
GENERAL INFORMATION:  
APPLICANT: Olsen, William C.  
APPLICANT: Madon, Paul J.  
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
FILE REFERENCE: 64672-A  
CURRENT APPLICATION NUMBER: US/10/116,797  
CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 100.0%; Score 195; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 3

US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Maddon, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 100.0%; Score 195; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 4

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US2002006813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JEP/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 5

US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human Immunodeficiency virus type 1  
US-09-779-451-5

Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 6

US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US20020119922A1  
GENERAL INFORMATION:

APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 7  
US-09-854-816-1  
Sequence 1, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
MOLECULE TYPE: DP178  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
p-854-816-1  
Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
Db 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 8  
US-09-854-816-108  
Sequence 108, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
MOLECULE TYPE: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108  
Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0;  
OY 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
Db 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 9  
US-09-848-616-176  
Sequence 176, Application US/09848616  
Publication No. US20030054010A1  
GENERAL INFORMATION:  
APPLICANT: Sebbel, Peter  
APPLICANT: Dunant, Nicolas  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Lechner, Franziska  
TITLE OF INVENTION: Molecular Antigen Array  
FILE REFERENCE: 1700.0180002  
CURRENT APPLICATION NUMBER: US/09/848,616  
CURRENT FILING DATE: 2001-05-05  
NUMBER OF SEQ ID NOS: 186  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 176  
LENGTH: 37  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DP178c peptide  
US-09-848-616-176  
Query Match 100.0%; Score 195; DB 9; Length 37;  
Best Local Similarity 100.0%; Pred. No. 8e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36

Db 2 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 37

RESULT 10

US-09-779-451-41

Sequence 41, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900 0300003

CURRENT APPLICATION NUMBER: US/09/779,451

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 46

TYPE: PRT

ORGANISM: Human Immunodeficiency virus type 1

US-09-779-451-41

Query Match

Best Local Similarity 100.0%; Score 195; DB 10; Length 46;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 36

Db 11 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 46

RESULT 11

US-09-779-451-4

Sequence 4, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900 0300003

CURRENT APPLICATION NUMBER: US/09/779,451

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match

Best Local Similarity 100.0%; Score 195; DB 10; Length 56;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 36

Db 16 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 51

RESULT 12

US-10-040-349B-2

Sequence 2, Application US/10040349B

Publication No. US20030082521A1

GENERAL INFORMATION:

APPLICANT: Brasseur, Robert

APPLICANT: Charlotteaux, Benoit

APPLICANT: Chevalier, Michel

APPLICANT: El Habib, Raphaelle

APPLICANT: Krell, Tino

TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

FILE REFERENCE: 01-078-A

CURRENT APPLICATION NUMBER: US/10/040,349B

CURRENT FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

ORGANISM: Human Immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)...(177)

OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match

Best Local Similarity 100.0%; Score 195; DB 9; Length 177;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 36

Db 104 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 139

RESULT 13

US-10-059-271-84

Sequence 84, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDDÉ, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

FILE REFERENCE: ALBRE-22

CURRENT APPLICATION NUMBER: US/10/059,271

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: DE 101 06 295

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide

US-10-059-271-84

Query Match

Best Local Similarity 100.0%; Score 195; DB 9; Length 221;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 36

Db 131 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 166

RESULT 14

US-10-059-271-81

Sequence 81, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDDÉ, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND



;; TITLE OF INVENTION: BEING IMMOBILIZED  
;; FILE REFERENCE: ALBRE-22  
;; CURRENT APPLICATION NUMBER: US/10/059,271  
;; CURRENT FILING DATE: 2002-01-31  
;; PRIOR APPLICATION NUMBER: DE 101 06 295  
;; PRIOR FILING DATE: 2001-02-02  
;; NUMBER OF SEQ ID NOS: 97  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 81  
;; LENGTH: 232  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
US-10-059-271-81

Query Match 100.0%; Score 195; DB 9; Length 232;  
Best Local Similarity 100.0%; Pred. No. 5.5e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSHSLIEESQNOEKNEQELLELDKVASLWNMF 36  
|||||  
Db 144 YTSLSHSLIEESQNOEKNEQELLELDKVASLWNMF 179

RESULT 15  
US-10-059-271-82  
;; Sequence 82, Application US/10059271  
;; Publication No. US20030082208A1  
;; GENERAL INFORMATION:  
;; APPLICANT: REPKE, HEINRICH  
;; APPLICANT: BUDE, ECKHARD  
;; APPLICANT: NICOLAUS, STEFAN  
;; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
;; TITLE OF INVENTION: BEING IMMOBILIZED  
;; FILE REFERENCE: ALBRE-22  
;; CURRENT APPLICATION NUMBER: US/10/059,271  
;; CURRENT FILING DATE: 2002-01-31  
;; PRIOR APPLICATION NUMBER: DE 101 06 295  
;; PRIOR FILING DATE: 2001-02-02  
;; NUMBER OF SEQ ID NOS: 97  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 82  
;; LENGTH: 254  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
US-10-059-271-82

Query Match 100.0%; Score 195; DB 9; Length 254;  
Best Local Similarity 100.0%; Pred. No. 6.1e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHSLIEESQNOEKNEQELLELDKVASLWNMF 36  
|||||  
Db 166 YTSLSHSLIEESQNOEKNEQELLELDKVASLWNMF 201

Search completed: May 16, 2003, 12:10:21  
Job time : 16.759 secs

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GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533A-3  
Perfect score: 198  
Sequence: 1 YTNVLYTLLESQNDQEKNEQDLLELDKXASLWVWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A.Geneseq\_101002:\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
24: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	36	AA19837	Core polypeptide f
2	198	100.0	36	AAU70180	HIV viral envelope
3	198	100.0	36	ABB01244	Viral DP178/107-11
4	198	100.0	36	ABB01245	Viral DP178/107-11
5	198	100.0	36	ABB02830	Viral core polypep
6	198	100.0	36	AAU13790	DP178-1like/DP107-1
7	198	100.0	36	AAU13791	DP178-1like/DP107-1
8	198	100.0	36	AA192245	Virus related pept
9	198	100.0	36	AA192237	Core polypeptide T
10	198	100.0	36	AA192238	Core polypeptide T

11	198	100.0	36	AA192286	HIV antiviral acti
12	198	100.0	269	AA1922834	SEQ ID NO. 30 from
13	198	100.0	269	AA1922835	SEQ ID NO. 31 from
14	198	100.0	269	ABG68305	Envelope protein g
15	198	100.0	269	ABG68306	Envelope protein g
16	198	100.0	275	AAW33615	SOD/env-5b protein
17	198	100.0	275	AAW33615	HIV-1 env5b/human
18	198	100.0	700	AAW05795	HIV-1 env mutcin 1
19	198	100.0	855	AAW53112	ENV protein contai
20	198	100.0	855	AAW77298	HIV-1 (ATCC CRL 85
21	198	100.0	855	AAW77302	HIV-1 (ATCC CRL 85
22	198	100.0	860	AAW31284	HIV-SF2 virus gp12
23	198	100.0	863	AAW31284	Sequence of ARV-2
24	198	100.0	863	AAW31284	env gene decoded f
25	193	97.5	36	AAW67698	DP-178 homologue d
26	193	97.5	36	AAW67698	DP185 corresponds
27	193	97.5	36	AAW17012	DP-178-like peptid
28	193	97.5	36	AAW89836	Core polypeptide f
29	193	97.5	36	AAW67040	HIV-1 gp41 peptide
30	193	97.5	36	AAU14012	DP178 homologue, p
31	193	97.5	854	AAW43070	HIV-1 gp120 protei
32	190	96.0	268	AAW22830	SEQ ID NO. 26 from
33	190	96.0	268	ABG68301	Envelope protein g
34	190	96.0	619	AAU75156	N-terminal mutant
35	190	96.0	646	AAU75155	Modified full-leng
36	190	96.0	847	AAU97073	Variant HIV-1 SF16
37	187	94.4	36	AAW89665	Core polypeptide f
38	187	94.4	36	ABB01073	Viral DP178/107-11
39	187	94.4	36	ABB02524	Viral core polypep
40	187	94.4	36	AAU13619	DP178-1like/DP107-1
41	187	94.4	36	AAW78066	Core polypeptide T
42	187	94.4	268	AAW22811	SEQ ID NO. 7 from
43	187	94.4	268	ABG68282	Envelope protein g
44	187	94.4	269	AAW22832	SEQ ID NO. 28 from
45	187	94.4	269	ABG68303	Envelope protein g

## ALIGNMENTS

RESULT 1  
AA19837  
ID AAY9837 standard; peptide: 36 AA.  
XX  
AC AAY9837;  
XX  
ID 23-MAY-2000 (first entry)  
XX  
DE Core polypeptide fragment T No. 1406.  
XX  
DE  
XX  
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KW HIV-2; HIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX  
OS Unidentified.  
XX  
PN W09959615-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US11219.  
XX  
PR 20-MAY-1998; 98US-0082279.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KL, Merutka G, Anwer MK, Lambert DM;  
XX WPI; 2000-136792/12.  
XX  
PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
comprises enhancer sequence -

XX Disclosure: Page 45; 124pp; English.  
 PS  
 XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fibrogenic treatments. Sequences AA98651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

CC Sequence 36 AA:

Query Match 100.0%; Score 198; DB 21; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTITITLLEESONOEKNEDELLEDKWASLWMPF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YNTITITLLEESONOEKNEDELLEDKWASLWMPF 36

RESULT 2  
 AAU70180

ID AAU70180 standard; Peptide: 36 AA.

AC AAU70180;

DT 14-FEB-2002 (first entry)

DE HIV viral envelope protein stabilising peptide #2.

XX Human, HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;  
 KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;  
 KM alpha-helical region; ectodomain.  
 XX  
 OS Homo sapiens.

WO200170262-A2.

PD 27-SEP-2001.

PF 15-MAR-2001; 2001WO-US08108.

PR 17-MAR-2000; 2000US-189981P.

PA (PANA-) PANACOS PHARM INC.

PI Wild CT, Allaway GP;

DR WPI; 2001-626098/72.

XX Immunogenic composition for inhibiting HIV infection, comprises viral  
 PT envelope protein or its fragment exterior to viral membrane, a  
 PT stabilising peptide, and optionally, viral cell surface receptor or  
 PT its fragment

XX Claim 6; Page 45; 84pp; English.

XX The invention relates to methods of generating immunogens that elicit  
 CC neutralising antibodies which target regions of viral envelope proteins  
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of  
 CC HIV-1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and

CC AAU70677-AAU70743 represent stabilising peptides modelling the  
 CC alpha-helical regions of the ectodomain of the HIV-1 transmembrane  
 CC protein to stabilise fusion-active intermediate structures, which can be  
 CC used as vaccine immunogens. Immunogenic compositions comprise a viral  
 CC envelope protein or its fragment exterior to the viral membrane, a  
 CC stabilising peptide to disrupt formation of structural intermediates  
 CC necessary for viral fusion and entry, and optionally, a viral cell  
 CC surface receptor or its fragment. The stabilising peptide is capable of  
 CC associating with the envelope protein or its fragment to form a  
 CC stabilised, fusion active structure. Antibody binding assays are used to  
 CC determine the ability of immunogen vaccines to generate an immune  
 CC response to various forms of envelope. Virus neutralisation assays can be  
 CC used to characterise the antibody response raised against HIV-1 gp41  
 CC domains. The sequences and methods are useful for inhibiting HIV  
 CC infection, for inducing an immune response in an animal and for raising  
 CC antibodies.

SQ Sequence 36 AA:

Query Match 100.0%; Score 198; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTITITLLEESONOEKNEDELLEDKWASLWMPF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YNTITITLLEESONOEKNEDELLEDKWASLWMPF 36

RESULT 3  
 ABB01244

ID ABB01244 standard; Peptide: 36 AA.

AC ABB01244;

DT 03-JAN-2002 (first entry)

DE Viral DP178/107-like region peptide T1405.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KM infection.  
 XX

OS Viridiae.

XX Key Location/Qualifiers

FT Modified-site 1 /note="N-terminal is substituted by Ac"

FT Modified-site 36 /note="C-terminal amide"

FT WO200164013-A2.

PD 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US03988.

PR 29-FEB-2000; 2000US-0515965.

PA (TRIM-) TRIMERIS INC.

PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

DR WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection

XX Disclosure: Page 58; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region

CC HRI1 respectively, of HIV-1LAI transmembrane protein gp41. The HRI  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX Sequence 36 AA:

Query Match 100.0%; Score 198; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTNTYTLLEESQNOEKNEQELLELDKWSIWMNF 36  
 DB 1 YNTNTYTLLEESQNOEKNEQELLELDKWSIWMNF 36

LT 4  
 ID 1245

ABB01245 standard; Peptide: 36 AA.

AC ABB01245;

DT 03-JAN-2002 (first entry)

DE Viral DP178/107-like region peptide T1406.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;

KW virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;

XX infection.

OS Viridiae.

PN W0200164013-A2.

XX 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US03988.

XX 29-FEB-2000; 2000US-0515965.

PA (TRIM-) TRIMERIS INC.

PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI: 2001-514829/56.

PT Heptad repeat region peptide analogs useful for inhibiting virus/cells

PS infection, useful for treating HIV and Respiratory Syncytial Virus

XX Disclosure; Page 58; 587pp; English.

CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HRI  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX Sequence 36 AA:

Query Match 100.0%; Score 198; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTNTYTLLEESQNOEKNEQELLELDKWSIWMNF 36  
 DB 1 YNTNTYTLLEESQNOEKNEQELLELDKWSIWMNF 36

RESULT 5

ABB02830

XX ABB02830 standard; Peptide: 36 AA.

AC ABB02830;

DT 03-JAN-2002 (first entry)

DE Viral core polypeptide, SEQ ID NO: 1357.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;

KW virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;

XX infection.

OS Viridiae.

PN W0200164013-A2.

XX 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US03988.

XX 29-FEB-2000; 2000US-0515965.

PA (TRIM-) TRIMERIS INC.

PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI: 2001-514829/56.

PT Heptad repeat region peptide analogs useful for inhibiting virus/cells

PS infection, useful for treating HIV and Respiratory Syncytial Virus

XX Disclosure; Page 524; 587pp; English.

CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HRI  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX Sequence 36 AA:

Query Match 100.0%; Score 198; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTNTYTLLEESQNOEKNEQELLELDKWSIWMNF 36  
 DB 1 YNTNTYTLLEESQNOEKNEQELLELDKWSIWMNF 36

RESULT 6

AAU13790

XX AAU13790 standard; Peptide: 36 AA.

DT 21-NOV-2001 (first entry)

[illegible]

XX	Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
KW	antifusogenic; antiviral; HIV transmission; mutant; mutain.
XX	
OS	Human immunodeficiency virus 1 isolate LAI.
XX	Synthetic.
PN	WO200151673-A2.
XX	
PD	19-JUL-2001.
XX	
PF	05-JUL-2000; 2000WO-US35727.
XX	
PR	09-JUL-1999; 99US-0350841.
XX	
PA	(TRIM-) TRIMERIS INC.
XX	
PI	Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
DR	WPI; 2001-442157/47.
XX	
PT	Identifying a compound that inhibits the formation of or disrupts a
PT	DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT	or intracellular modulatory activity, by detecting the formation of a
PT	DP107/DP178 complex -
XX	
PS	Disclosure; Page 77; 259pp; English.
XX	
CC	The present invention relates to peptides which exhibit anti-retroviral
CC	activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC	DP178-like and DP107-like peptides. The DP178 peptide corresponds
CC	to amino acids 639-673 of the transmembrane protein gp41 from human
CC	immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC	corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC	also relates to a method of identifying compounds that inhibit the
CC	formation of or disrupts a DP107/DP178 complex. The method comprises
CC	detecting the formation of a DP107/DP178 complex, both in the presence
CC	or absence of a test compound, in a reaction mixture containing DP107
CC	and DP178 peptides. The method is useful for identifying compounds,
CC	including small molecule compounds, which may themselves exhibit
CC	antifusogenic, antiviral or intracellular modulatory activity. The
CC	DP178-like/DP107-like peptides are useful to inhibit human and non-human
CC	retroviral, particularly HIV, transmission to uninfected cells. The
CC	present sequence represents one of the DP178-like/DP107-like peptides
CC	of the invention.
XX	
XX	Sequence 36 AA:
XX	
XX	Query Match. 100.0%; Score 198; DB 22; Length 36;
XX	Best Local Similarity 100.0%; Pred. No. 1,4e-17;
XX	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 YNTNTYTLLEESQNOQEKNEDELELDKWKASLWNNF 36
XX	
XX	1 YNTNTYTLLEESQNOQEKNEDELELDKWKASLWNNF 36
ID	AA892245
XX	AA892245 standard; Peptide: 36 AA.
XX	
XX	AA892245:
XX	
XX	22-JUN-2001 (first entry)
XX	
DE	Virus related peptide SEQ ID NO:1421.
XX	
XX	Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW	blood component; modification; succinimidyl; maleimido group; amino;
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX	
XX	Homo sapiens
OS	Synthetic.

WO2000069900-A2.  
 23-NOV-2000.  
 17-MAY-2000; 2000WO-US13576.  
 17-MAY-1999; 99US-0134406.  
 10-SEP-1999; 99US-0153406.  
 15-OCT-1999; 99US-0159783.  
 (CONJ-) CONJUCHEM INC.  
 Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 WPT: 2001-112059/12.  
 Modifying and attaching therapeutic peptides to albumin prevents  
 peptidase degradation, useful for increasing length of in vivo activity  
 Disclosure: Page 662; 733pp; English.  
 The present invention describes a modified therapeutic peptide (I)  
 comprising a therapeutically active amino acid region (II) and a  
 reactive group (II) (e.g. succinimidy and maleimido groups) attached to  
 a less therapeutically active amino acid region (IV), which covalently  
 bonds with amino/hydroxyl/thiol groups on blood components to form a  
 peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 factors and neurotransmitters, to protect them from peptidase activity  
 in vivo for the treatment of various disorders. Endogenous therapeutic  
 peptides are not suitable as drug candidates as they require frequent  
 administration due to rapid degradation by peptidases in the body.  
 Modifying and attaching therapeutic peptides to albumin prevents or  
 reduces the action of peptidases to increase length of activity (half  
 life) and specificity as bonding to large molecules decreases  
 intracellular uptake and interference with physiological processes.  
 AAB90829 to AAB92441 represent peptides which can be used in the  
 exemplification of the present invention.  
 Sequence 36 AA:  
 Query Match 100.0%; Score 198; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 YTNITYTLLEESQNOEKNEOELLELDKRWASIMNMF 36  
 1 YTNITYTLLEESQNOEKNEOELLELDKRWASIMNMF 36  
 RESULT 9  
 AAB78237  
 AAB78237 standard; Peptide: 36 AA.  
 AAB78237;  
 19-APR-2001 (first entry)  
 Core polypeptide T1405.  
 Core polypeptide; enhancer; anti-viral; anti-HIV;  
 vitucide; hepatotropic; antiinflammatory; hybrid polypeptide;  
 coiled-coil peptide interaction; fusion-related disorder;  
 bacterial infection; viral infection.  
 Unidentified.  
 WO200103723-A1.  
 18-JAN-2001.

PE 10-JUL-2000; 2000OWO-US18772.  
XX  
PR 09-JUL-1999; 99US-0350641.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S., Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI: 2001-147136/15.  
DR  
PT New hybrid polypeptide, useful for preventing, treating and diagnosing  
PT e.g. viral infections, comprises an enhancer peptide linked to a core  
PT polypeptide -  
PS Disclosure; Page 58; 151pp; English.

The present sequence is a core polypeptide which may be linked to  
CC an enhancer peptide to form a novel hybrid polypeptide. The hybrid  
CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
CC those exhibited by the core polypeptide when introduced into a living  
CC system. It is used to increase the in vitro or ex vivo half-life of  
CC the core polypeptide. The hybrid and core polypeptides can be used for  
CC modulating isogenic events and intracellular processes involving  
CC coiled-coil peptide interactions. Other uses include preventing,  
CC treating and/or diagnosing disorders involving fusion events (e.g.  
CC modulation of neurotransmitter exchange and sperm-egg fusion),  
CC intracellular processes involving coiled-coil peptides (e.g. bacterial  
CC infections) and viral infections that involve cell-cell and/or  
CC virus-cell fusion (e.g. viral infections caused by human  
CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr  
CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
CC The enhancer peptide sequence increases the half-life and reduces the  
CC clearance rate of therapeutic peptides, which increases their efficacy  
CC and minimises the incidence and severity of adverse side effects.  
CC In addition, this increases the sensitivity of the diagnostic procedure  
CC in which they are used.

Sequence 36 AA:  
XX

Query Match 100.0%; Score 198; DB 22; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1, 4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNITYTLLESNQEKNEDELLELDKWSLWKF 36  
|||  
DB 1 YTNITYTLLESNQEKNEDELLELDKWSLWKF 36

RESULT 10  
AAB78238  
ID AAB78238 standard; Peptide: 36 AA.  
XX  
AC AAB78238;  
XX  
JT 19-Apr-2001 (first entry)  
XX  
DE Core polypeptide T1406.  
XX  
KM Core polypeptide; enhancer; antiviral; anti-HIV;  
KM vitucide; hepatotropic; antiinflammatory; hybrid polypeptide;  
KW coiled-coil peptide interaction; fusion-related disorder;  
KM bacterial infection; viral infection.  
XX  
OS Unidentified.  
XX  
PN WO200103723-A1;  
XX  
PD 18-JAN-2001.  
XX  
PE 10-JUL-2000; 2000OWO-US18772.  
XX  
PR 09-JUL-1999; 99US-0350641.  
XX





DR WPI: 1998-286866/25.  
 XX Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa-peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 XX  
 PS Claim 11: Page 171-172; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 CC  
 SQ Sequence 269 AA;  
 XX  
 Query Match 100.0%; Score 198; DB 19; Length 269;  
 Best Local Similarity 100.0%; Pred. NO. 1.3e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTNNTYTLLESQNOEKNEQELLEDKWSLMMNF 36  
 |||||||  
 DB 169 YTNNTYTLLESQNOEKNEQELLEDKWSLMMNF 204  
 |||||||  
 RESULT 13  
 AAY22835  
 ID AAY22835 standard; Protein: 269 AA.  
 XX  
 AC AAY22835;  
 XX  
 XX 19-AUG-1999 (first entry)  
 DE SEQ ID NO. 31 from W09820036.  
 XX  
 XX HIV; gp41 protein; constrained helical peptide; HIV infection;  
 KW vaccine; antibody; viral membrane fusion; viral infectivity;  
 KW ligand affinity purification; protein A replacement;  
 KW immunoglobulin purification; epitope mimic.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 OS W09820036-A1.  
 XX  
 PN 14-MAY-1998.  
 PD  
 XX  
 PD 05-NOV-1997; 97WO-US20069.  
 PF  
 XX 16-JUN-1997; 97US-0876698.  
 PR 06-NOV-1996; 96US-0743698.  
 PR 16-NOV-1996; 96US-0743698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 XX

DR WPI: 1998-286866/25.  
 XX Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa-peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 XX  
 PS Claim 11: Page 172-173; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 CC  
 SQ Sequence 269 AA;  
 XX  
 Query Match 100.0%; Score 198; DB 19; Length 269;  
 Best Local Similarity 100.0%; Pred. NO. 1.3e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTNNTYTLLESQNOEKNEQELLEDKWSLMMNF 36  
 |||||||  
 DB 169 YTNNTYTLLESQNOEKNEQELLEDKWSLMMNF 204  
 |||||||  
 RESULT 14  
 ABG68305  
 ID ABG68305 standard; Protein: 269 AA.  
 XX  
 AC ABG68305;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Envelope protein gp41 from HIV clade B strain #24.  
 XX  
 KW HIV; glycoprotein; gp41; antigen; helical conformation;  
 KW virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;  
 KW viral envelope protein; vaccine; virucide; anti-HIV.  
 XX  
 OS Human immunodeficiency virus type 1 clade B.  
 XX  
 OS US6271198-B1.  
 XX  
 PN 07-AUG-2001.  
 PD  
 XX  
 PD 05-NOV-1997; 97US-0965056.  
 PF  
 XX 16-JUN-1997; 97US-049787P.  
 PR 06-NOV-1996; 96US-0743698.  
 PR 16-JUN-1997; 97US-0876698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 XX

DR WPI; 2002-487624/52.  
 XX New cyclic peptides from human immune deficiency virus gp41, useful for  
 PT treatment or prevention of HIV infection, are constrained to have  
 PT alpha-helical conformation -  
 XX  
 XX Disclosure: Column 175-176; 175pp; English.  
 XX  
 XX The invention relates to cyclic peptides (A) with a constrained helical  
 CC conformation, derived from gp41 (glycoprotein 41, a viral envelope  
 CC protein) of human immunodeficiency virus (HIV). The cyclic  
 CC peptides have formulas given in the specification part of which are  
 CC derived from a consensus sequence of gp41 derived from HIV clades A, B,  
 CC C, D, E or O. The peptides are used to cause induction of a specific  
 CC immune response, resulting in antibodies that prevent virus-induced  
 CC membrane fusion. The peptides are used to treat subjects with, or at risk  
 CC of, HIV infection, either as antifusion/anti-infection agents or,  
 CC preferably where associated with a carrier, as an immunogen (including as  
 CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or  
 CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency  
 CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in  
 CC cases of health care accidents. The peptides can be based on specific HIV  
 CC strains, e.g. breakthrough isolates of HIV that have developed during  
 CC vaccine trials, so a combination of them should cover a wide range of  
 CC protection. The present sequence is gp41 protein from a particular  
 CC HIV clade used to derive a consensus sequence of gp41.  
 CC  
 SQ Sequence 269 AA:  
 Query Match 100.0%; Score 198; DB 23; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 36  
 Db 169 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 204  
 RESULT 15  
 ID ABG68306 standard; Protein; 269 AA.  
 XX  
 AC ABG68306;  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Envelope protein gp41 from HIV clade B strain #25.  
 XX  
 KW HIV; glycoprotein; gp41; antigen; helical conformation;  
 XX virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;  
 OS viral envelope protein; vaccine; virucide; anti-HIV.  
 XX  
 OS Human immunodeficiency virus type 1 clade B.  
 XX  
 XX US6271198-B1.  
 XX  
 PD 07-AUG-2001.  
 XX  
 PF 05-NOV-1997; 97US-0965056.  
 XX  
 XX 16-JUN-1997; 97US-049787P.  
 PR 06-NOV-1996; 96US-0743696.  
 PR 16-JUN-1997; 97US-0876698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 XX  
 DR WPI; 2002-487624/52.  
 PT New cyclic peptides from human immune deficiency virus gp41, useful for  
 PT treatment or prevention of HIV infection, are constrained to have

PT alpha-helical conformation -  
 XX  
 XX Disclosure: Column 177-178; 175pp; English.  
 XX  
 XX The invention relates to cyclic peptides (A) with a constrained helical  
 CC conformation, derived from gp41 (glycoprotein 41, a viral envelope  
 CC protein) of human immunodeficiency virus (HIV). The cyclic  
 CC peptides have formulas given in the specification part of which are  
 CC derived from a consensus sequence of gp41 derived from HIV clades A, B,  
 CC C, D, E or O. The peptides are used to cause induction of a specific  
 CC immune response, resulting in antibodies that prevent virus-induced  
 CC membrane fusion. The peptides are used to treat subjects with, or at risk  
 CC of, HIV infection, either as antifusion/anti-infection agents or,  
 CC preferably where associated with a carrier, as an immunogen (including as  
 CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or  
 CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency  
 CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in  
 CC cases of health care accidents. The peptides can be based on specific HIV  
 CC strains, e.g. breakthrough isolates of HIV that have developed during  
 CC vaccine trials, so a combination of them should cover a wide range of  
 CC protection. The present sequence is gp41 protein from a particular  
 CC HIV clade used to derive a consensus sequence of gp41.  
 CC  
 SQ Sequence 269 AA:  
 Query Match 100.0%; Score 198; DB 23; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 36  
 Db 169 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 204

Search completed: May 16, 2003, 11:12:01  
 Job time : 33.4578 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-1  
Perfect score: 195  
Sequence: 1 YTSLIHSILIESONQOEKNEQELLELDKWSLMMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mnc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	645	15	Q993A6 human immun
2	195	100.0	747	15	Q70607 human immun
3	195	100.0	748	15	Q70606 human immun
4	195	100.0	752	15	Q70604 human immun
5	195	100.0	752	15	Q70605 human immun
6	195	100.0	752	15	Q70608 human immun
7	195	100.0	851	15	Q78243 human immun
8	195	100.0	852	15	Q89797 human immun
9	195	100.0	854	15	Q85582 human immun
10	195	100.0	854	15	Q72502 human immun
11	195	100.0	856	15	Q92877 simian-huma
12	195	100.0	856	15	Q74599 human immun
13	195	100.0	856	15	Q74090 human immun
14	191	97.9	854	15	Q90178 human immun
15	191	97.9	854	15	Q78705 human immun
16	190	97.4	856	15	Q90SM7 human immun

17	189	96.9	616	15	Q993B0 human immun
18	189	96.9	618	15	Q993B2 human immun
19	189	96.9	757	15	Q9Q722 human immun
20	189	96.9	848	15	Q69990 human immun
21	187	95.9	838	15	Q03806 human immun
22	187	95.9	854	15	Q78225 human immun
23	187	95.9	855	15	Q03805 human immun
24	186	95.4	442	15	Q69910 human immun
25	186	95.4	443	15	Q80023 human immun
26	186	95.4	841	15	Q41556 human immun
27	186	95.4	849	15	Q77368 human immun
28	186	95.4	849	15	Q8Q851 human immun
29	186	95.4	851	15	Q56110 human immun
30	186	95.4	851	15	Q8Q852 human immun
31	186	95.4	856	15	Q72993 human immun
32	186	95.4	856	15	Q41539 human immun
33	186	95.4	857	15	Q8U170 human immun
34	186	95.4	858	15	Q8U190 human immun
35	186	95.4	858	15	Q8U188 human immun
36	186	95.4	859	15	Q8U185 human immun
37	186	95.4	859	15	Q8U180 human immun
38	186	95.4	859	15	Q8U179 human immun
39	186	95.4	859	15	Q8U177 human immun
40	186	95.4	859	15	Q8U173 human immun
41	186	95.4	859	15	Q8Q850 human immun
42	186	95.4	862	15	Q8U184 human immun
43	186	95.4	862	15	Q8U183 human immun
44	186	95.4	862	15	Q8U182 human immun
45	186	95.4	862	15	Q8U178 human immun

## ALIGNMENTS

RESULT 1  
Q993A6 PRELIMINARY: PRT: 645 AA.  
AC Q993A6: STRAIN=1007;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M., White S.W., Boherly P.C., Hurwitz J.L.;  
RT "Localization of CD4 T cell epitope hotspots to exposed strands of HIV envelope glycoprotein suggests structural influences on antigen processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
RL EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein; Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 645 AA: 72485 MW: B076514BE93362EC CRC64;

Query Match 100.0%; Score 195; DB 15; Length 645;  
Best Local Similarity 100.0%; Pred. No. 1,7e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIHSILIESONQOEKNEQELLELDKWSLMMWF 36  
Db 607 YTSLIHSILIESONQOEKNEQELLELDKWSLMMWF 642

## RESULT 2

070607 PRELIMINARY: PRT: 747 AA.

AC 070607; 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 ENV Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retrovirdae: Retroviridae: Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-LM87-1;  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-LM87-1;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12034; AAA76669.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 747 747  
 SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245F14 CRC64;

Query Match 100.0%; Score 195; DB 15; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 2e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 Db 633 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 668

## RESULT 3

070606 PRELIMINARY: PRT: 748 AA.

AC 070606; 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 ENV Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retrovirdae: Retroviridae: Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-LM881;  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-LM881;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12032; AAA76668.1;

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120.1.

DR Pfam: PF00517; GP41.1.

KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON\_TER 748 748

SQ SEQUENCE 748 AA: 84224 MW: 56BEDF186C67694B CRC64;

QY 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 Db 634 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 669

## RESULT 4

070604 PRELIMINARY: PRT: 752 AA.

AC 070604; 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 ENV Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retrovirdae: Retroviridae: Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-LM851;  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-LM851;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12030; AAA76666.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 752 752  
 SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 195; DB 15; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 2e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 Db 638 YTSLSHSLIEESONQOEKNEQELLELDKWSLWNMF 673

## RESULT 5

070605 PRELIMINARY: PRT: 752 AA.

AC 070605; 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DE 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 ENV Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retrovirdae: Retroviridae: Lentivirus.  
 OX NCBI\_Taxid=11676;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12031; AAA76667.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
NON_TER 752
SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 195; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESONQOEKNEQELLELDKWSIWMNF 36
Db 638 YTSLSHSLIESONQOEKNEQELLELDKWSIWMNF 673

RESULT 6
ID 070608 PRELIMINARY; PRT; 752 AA.
AC 070608;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCB1_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12035; AAA76670.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
NON_TER 752
SEQUENCE 752 AA; 84780 MW; 708672A2DC0EB8E8 CRC64;

Query Match 100.0%; Score 195; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESONQOEKNEQELLELDKWSIWMNF 36
Db 638 YTSLSHSLIESONQOEKNEQELLELDKWSIWMNF 673
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Db 638 YTSLSHSLIESONQOEKNEQELLELDKWSIWMNF 673

RESULT 7
ID 078243 PRELIMINARY; PRT; 851 AA.
AC 078243;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Env polypotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCB1_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,
RA Verani P., Rossi G.B.;
RT "Sequence analysis of HIV-1 proviral DNA from a non producer
  chronically infected HUT-78 cellular clone.";
RL J. Viral Diseases 1:40-55(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352106; PubMed=2765297;
RA Federic M., Tilti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Macchi B., Mangiano N., Verani P., Rossi G.;
RT "Biological and molecular characterization of producer and non
  producer clones from HUT-78 infected with a patient HIV isolate.";
RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tilti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Borsetti A., Saggio I., Verani P., Rossi G.;
RT "Variability of HIV-1 virus: characteristics of an infected but not
  productive clone.";
RL Int. J. Immunopharmacol. 3:17-23(1990).
DR EMBL: Z11530; CAA77628.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
NON_TER 851
SEQUENCE 851 AA; 96630 MW; 1A3767B987E98027 CRC64;

Query Match 100.0%; Score 195; DB 15; Length 851;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESONQOEKNEQELLELDKWSIWMNF 36
Db 633 YTSLSHSLIESONQOEKNEQELLELDKWSIWMNF 668

RESULT 8
ID 089797 PRELIMINARY; PRT; 852 AA.
AC 089797;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCB1_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM90-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
```

RT Infected with HIV type 1 (HTLV type IIIB).  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [12]  
 RC SEQUENCE FROM N.A.  
 RA STRAIN-LW90-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U12053; AAA76685.1;  
 DR EMBL; U12036; AAA76671.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SO SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF CRC64;  
 Query Match 100.0%; Score 195; DB 15; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 YTSLSHSLIEESQNOEKNEQELLEDKWSLWNNF 36  
 |||||||||||||||||||||||||||||||||||  
 DB 634 YTSLSHSLIEESQNOEKNEQELLEDKWSLWNNF 669  
 RESULT 9  
 ID 085582 PRELIMINARY; PRT; 854 AA.  
 AC 085582;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope polyprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86281827; PubMed=3016298;  
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
 Martin M.A.;  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone."  
 RT J. Virol. 59:284-291(1986).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92219406; PubMed=1373204;  
 RT Dai L.C., Litaue R., Takahashi K., Ennis F.A.;  
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
 RT gp1 results in loss of killing by CD8+ A24-restricted cytotoxic T  
 RT lymphocytes."  
 RL J. Virol. 66:3151-3154(1992).  
 DR EMBL; M19921; AAA4492.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;  
 Query Match 100.0%; Score 195; DB 15; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-15;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLSHSLIEESQNOEKNEQELLEDKWSLWNNF 36  
 |||||||||||||||||||||||||||||||||||  
 DB 636 YTSLSHSLIEESQNOEKNEQELLEDKWSLWNNF 671  
 RESULT 10  
 ID 072502 PRELIMINARY; PRT; 854 AA.  
 AC 072502;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE ENV polyprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-NL4-3;  
 RX MEDLINE=96036482; PubMed=7483282;  
 RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
 Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
 RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
 RT from primary virus cultures using the polymerase chain reaction."  
 RT Virology 213:80-86(1995).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RP STRAIN-NL4-3;  
 RX MEDLINE=86281827; PubMed=3016298;  
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
 Martin M.A.;  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone."  
 RL J. Virol. 59:284-291(1986).  
 DR EMBL; U26942; AAB60578.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT CONFLICT 214 214 H -> L (IN REF. 2).  
 FT CONFLICT 530 530 A -> S (IN REF. 2).  
 FT CONFLICT 739 739 G -> D (IN REF. 2).  
 SO SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;  
 Query Match 100.0%; Score 195; DB 15; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLSHSLIEESQNOEKNEQELLEDKWSLWNNF 36  
 |||||||||||||||||||||||||||||||||||  
 DB 636 YTSLSHSLIEESQNOEKNEQELLEDKWSLWNNF 671  
 RESULT 11  
 ID 092877 PRELIMINARY; PRT; 856 AA.  
 AC 092877;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Simian-Human immunodeficiency virus.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=57667;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99098984; PubMed=9882298;

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RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
RA Steenbeke T., Halloran M., Fenton J.W., Axthelm M.K., Letvin N.L.,
RA Sodroski J.G.;
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
RT responsible for the pathogenicity of a multiply passaged simian-human
RT immunodeficiency virus (SHIV-HXBc2).";
RL J. Virol. 73:976-984(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF041850; AADI2142.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 856 AA; 97151 MW; C50BF038FB73659 CRC64;

Query Match 100.0%; Score 195; DB 15; Length 856;
Best Local Similarity 100.0%; Pred. No. 2,3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 36
Db 638 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 673

RESULT 12
QY 074599 PRELIMINARY; PRT; 856 AA.
AC 074599;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Env.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCK1;
RX MEDLINE=90101366; PubMed=1688473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
RT (HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MCK1;
RA Iwata Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86068; BAI12995.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;

Query Match 100.0%; Score 195; DB 15; Length 856;
Best Local Similarity 100.0%; Pred. No. 2,3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 36
Db 638 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 673

RESULT 13
QY 074090 PRELIMINARY; PRT; 856 AA.
AC 074090;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Env.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM213;
RX MEDLINE=90101366; PubMed=1688473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
RT (HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PM213;
RA Iwata Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86069; BAI13003.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 100.0%; Score 195; DB 15; Length 856;
Best Local Similarity 100.0%; Pred. No. 2,3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 36
Db 638 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 673

RESULT 14
QY 090178 PRELIMINARY; PRT; 854 AA.
AC 090178;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCK1;
RX MEDLINE=95074930; PubMed=7983770;
RA Fang H., Pincus S.H.;
RT "Unique insertion sequence and pattern of CD4 expression in variants
RT selected with immunotoxins from human immunodeficiency virus type 1-
RT infected T cells.";
RL J. Virol. 69:75-81(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MCK1;
RA Fang H., Pincus S.H.;
RT "Spontaneous activation of human immunodeficiency virus type 1 in an
RT immunotoxin-resistant variant T cell line.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF070521; AAC28452.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

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Query Match 97.9%; Score 191; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 6.9e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESQNOOEKNEQELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 Db 636 YTSLSHSLIEESQNOOEKNEQELLELDKWSLWNMF 671

## RESULT 15

078705 PRELIMINARY; PRT; 854 AA.  
 ID 078705  
 AC 078705;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE Envelope glycoprotein gp120.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 VR Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RX MEDLINE=96013815; PubMed=7474132;  
 RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 RT resistant cell lines chronically infected with human immunodeficiency  
 RT virus type 1."  
 RL J. Virol. 69:7122-7131(1995).  
 DR EMBL; LA2371; AA696326.1;  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 854 AA; 97199 MW; 5B9512216533E256 CRC64;

Query Match 97.9%; Score 191; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 6.9e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESQNOOEKNEQELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 Db 636 YTSLSHSLIEESQNOOEKNEQELLELDKWSLWNMF 671

Search completed: May 16, 2003, 11:19:42  
 Time : 28.3124 secs



GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-1  
Sequence: 1 YTSLSHSLIESQNOEKNEDELLEDKWASLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCrus.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	195	100.0	36 1	US-08-073-028-1
2	195	100.0	36 3	US-08-486-099-1
3	195	100.0	36 3	US-09-071-877-1
4	195	100.0	36 3	US-08-360-107A-1
5	195	100.0	36 3	US-08-484-223B-1
6	195	100.0	36 3	US-08-919-597-1
7	195	100.0	36 3	US-08-475-668A-1
8	195	100.0	36 3	US-08-485-551A-1
9	195	100.0	36 3	US-08-471-913A-1
10	195	100.0	36 4	US-08-554-616-1
11	195	100.0	36 4	US-08-485-264A-1
12	195	100.0	36 4	US-09-082-279B-15
13	195	100.0	36 4	US-09-082-279B-497
14	195	100.0	36 4	US-09-082-279B-498
15	195	100.0	36 4	US-09-082-279B-603
16	195	100.0	36 4	US-09-082-279B-630
17	195	100.0	36 4	US-09-082-279B-631
18	195	100.0	36 4	US-09-082-279B-705
19	195	100.0	36 4	US-09-082-279B-834
20	195	100.0	36 4	US-09-082-279B-1076
21	195	100.0	36 4	US-09-082-279B-1121
22	195	100.0	36 4	US-09-082-279B-1161
23	195	100.0	36 4	US-08-965-056-1
24	195	100.0	36 4	US-08-965-056-108
25	195	100.0	36 4	US-09-045-920-1
26	195	100.0	36 4	US-08-474-349A-1
27	195	100.0	36 4	US-08-474-349A-399

28	195	100.0	36 4	US-08-474-349A-413	Sequence 413, App
29	195	100.0	36 4	US-09-315-304B-15	Sequence 15, Appl
30	195	100.0	36 4	US-09-315-304B-497	Sequence 497, App
31	195	100.0	36 4	US-09-315-304B-498	Sequence 498, App
32	195	100.0	36 4	US-09-315-304B-603	Sequence 603, App
33	195	100.0	36 4	US-09-315-304B-630	Sequence 630, App
34	195	100.0	36 4	US-09-315-304B-631	Sequence 631, App
35	195	100.0	36 4	US-09-315-304B-705	Sequence 705, App
36	195	100.0	36 4	US-09-315-304B-834	Sequence 834, App
37	195	100.0	36 4	US-09-315-304B-1076	Sequence 1076, App
38	195	100.0	36 4	US-09-315-304B-1121	Sequence 1121, App
39	195	100.0	36 4	US-09-315-304B-1161	Sequence 1161, App
40	195	100.0	36 4	US-09-315-304B-1469	Sequence 1469, App
41	195	100.0	36 4	US-09-315-304B-1470	Sequence 1470, App
42	195	100.0	36 4	US-09-315-304B-1486	Sequence 1486, App
43	195	100.0	36 4	US-08-255-208A-1	Sequence 1, Appl
44	195	100.0	37 4	US-09-082-279B-771	Sequence 771, App
45	195	100.0	37 4	US-09-082-279B-775	Sequence 775, App

#### ALIGNMENTS

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RESULT 1
US-08-073-028-1
; Sequence 1, Application US/08073028
; Patent No. 5464933
;
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Mathews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
;
; US-08-073-028-1
;
; Query Match 100.0%; Score 195; DB 1; Length 36;
; Best Local Similarity 100.0%; Pred. No. 5.5e-18;
; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; 1 YTSLSHSLIESQNOEKNEDELLEDKWASLWNF 36
; |||
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Db 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWMPF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Daniel P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pelletier, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWMPF 36

Db 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWMPF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichty, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Marutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

Db 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWMPF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Daniel P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pelletier, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWMPF 36

Db 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWMPF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Daniel P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pelletier, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONQOEKNEQELLELDKWSLWMPF 36

Db 1 YTSLSHLSIESONQOEKNEQELLEDKWSASLWNMF 36

RESULT 5  
US-08-484-223B-1  
Sequence 1, Application US/08484223B  
Patent No. 6020459

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:

## TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESONQOEKNEQELLEDKWSASLWNMF 36  
Db 1 YTSLSHLSIESONQOEKNEQELLEDKWSASLWNMF 36

RESULT 6  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:

## TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHLSIESONQOEKNEQELLEDKWSASLWNMF 36  
Db 1 YTSLSHLSIESONQOEKNEQELLEDKWSASLWNMF 36

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6060065

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIEESQNOEKNEDELLELDKWSLWNMF 36  
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DB 1 YTSLSHLSIEESQNOEKNEDELLELDKWSLWNMF 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/0848551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pelletway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIEESQNOEKNEDELLELDKWSLWNMF 36  
|||||  
DB 1 YTSLSHLSIEESQNOEKNEDELLELDKWSLWNMF 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pelletway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIEESQNOEKNEDELLELDKWSLWNMF 36  
|||||  
DB 1 YTSLSHLSIEESQNOEKNEDELLELDKWSLWNMF 36

RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dant P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8664/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1  
Query Match 100.0%; Score 195; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSLIEESQNOEKNEQELLIDKWSLWNNF 36  
|||||  
DB 1 YTSLSLSLIEESQNOEKNEQELLIDKWSLWNNF 36

RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dant P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pettway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1  
Query Match 100.0%; Score 195; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSLIEESQNOEKNEQELLIDKWSLWNNF 36  
|||||  
DB 1 YTSLSLSLIEESQNOEKNEQELLIDKWSLWNNF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15  
Query Match 100.0%; Score 195; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSLIEESQNOEKNEQELLIDKWSLWNNF 36  
|||||

```
Db      1 YTSLSHSLIESONQOEKNEQELLELDKWSASLWNMF 36
RESULT 13
US-09-082-279B-497
; Sequence 497, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; ID NO 497
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-497
Query Match      100.0%; Score 195; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSLSHSLIESONQOEKNEQELLELDKWSASLWNMF 36
DB      1 YTSLSHSLIESONQOEKNEQELLELDKWSASLWNMF 36
RESULT 14
US-09-082-279B-498
; Sequence 498, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; ID NO 498
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-498
Query Match      100.0%; Score 195; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSLSHSLIESONQOEKNEQELLELDKWSASLWNMF 36
DB      1 YTSLSHSLIESONQOEKNEQELLELDKWSASLWNMF 36
RESULT 15
US-09-082-279B-603
```

```
; Sequence 603, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; ID NO 603
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-603
Query Match      100.0%; Score 195; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 YTSLSHSLIESONQOEKNEQELLELDKWSASLWNMF 36
Search completed: May 16, 2003, 11:22:09
Job time : 11.1928 secs
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GenCore version 5.1.4\_p5\_4578  
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Om protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title:	US-09-623-533A-1
Perfect score:	195
Sequence:	1 YTSLIHSLIEESQNOQEKNEQELLELDKWSIWMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues  
 1 number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_101002.\*

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- 2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*
- 3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*
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- 10: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.\*
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- 20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.\*
- 21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*
- 22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*
- 23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	195	100.0	36	16	AAR64364	DP-178 derived from
2	195	100.0	36	17	AAR98398	DP178 corresponds
3	195	100.0	36	16	AAAI7011	DP178 derived pep
4	195	100.0	36	19	AAV22912	SEQ ID NO. 108 fr
5	195	100.0	36	19	AAV22805	SEQ ID NO. 1 from
6	195	100.0	36	20	AAV31955	Synthetic peptide
7	195	100.0	36	20	AAV31974	HIV-1 LAI gp41 T-T
8	195	100.0	36	21	AAV52655	T20/DP178 peptide
9	195	100.0	36	21	AAV52688	T20/DP178 peptide
10	195	100.0	36	21	AAV52818	T20/DP178 peptide

11	195	100.0	36	21	AA814533	HIV-1 isolate LA
12	195	100.0	36	21	AA88665	Core polypeptide f
13	195	100.0	36	21	AA88729	Core polypeptide f
14	195	100.0	36	21	AA89135	Core polypeptide f
15	195	100.0	36	21	AA89136	Core polypeptide f
16	195	100.0	36	21	AA89242	Core polypeptide f
17	195	100.0	36	21	AA89424	Core polypeptide f
18	195	100.0	36	21	AA89692	Core polypeptide f
19	195	100.0	36	21	AA89735	Core polypeptide f
20	195	100.0	36	21	AA89777	Core polypeptide f
21	195	100.0	36	21	AA89982	Core polypeptide f
22	195	100.0	36	21	AA89983	Core polypeptide f
23	195	100.0	36	21	AA89999	Core polypeptide f
24	195	100.0	36	22	AAU70179	HIV viral envelope
25	195	100.0	36	22	AAU70741	HXB2 transmembrane
26	195	100.0	36	22	AA82961	Anti-HIV peptide T
27	195	100.0	36	22	AA657039	HIV-1 gp41 peptide
28	195	100.0	36	22	AB800024	HIV-1 gp41 peptide
29	195	100.0	36	22	AB800087	HIV-1 gp41 peptide
30	195	100.0	36	22	AB800088	Biotin-labelled HIV
31	195	100.0	36	22	AB800494	Viral DP178/107-11
32	195	100.0	36	22	AB800495	Viral DP178/107-11
33	195	100.0	36	22	AB800600	RSV F1 protein DP1
34	195	100.0	36	22	AB800626	Viral DP178/107-11
35	195	100.0	36	22	AB800627	Viral DP178/107-11
36	195	100.0	36	22	AB800628	Viral DP178/107-11
37	195	100.0	36	22	AB800832	Viral DP178/107-11
38	195	100.0	36	22	AB801100	Viral DP178/107-11
39	195	100.0	36	22	AB801143	Viral DP178/107-11
40	195	100.0	36	22	AB801185	Fluorescein-labelled
41	195	100.0	36	22	AB801391	Viral DP178/107-11
42	195	100.0	36	22	AB801392	Viral DP178/107-11
43	195	100.0	36	22	AB801414	Viral DP178/107-11
44	195	100.0	36	22	AB801488	Viral core polypep
45	195	100.0	36	22	AB801970	Viral core polypep

## RESULT :

ID	AAE64364	standard; Peptide; 36 AA.
XX		
AC	AAE64364;	
XX		
DT	24-AUG-1995	(first entry)
XX		
DE	DP-178	derived from HIV-1 isolate LAI has antiviral activity.
XX		
KW	antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;	
KW	human immunodeficiency virus; transmembrane protein; gp41;	
KW	alpha helix; leucine zipper; DP-185.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Modified-site	1
FT		/note= "optionally has an amino, acetyl,
FT		9-fluorenylmethoxy-carbonyl, hydrophobic or
FT	Modified-site	38
FT		/note= "optionally has a carboxyl, amide, hydrophobic
FT		or macromolecular carrier gp. attached"
XX		
PN	W09428920-A.	
XX		
PD	22-DEC-1994.	
XX		
PF	07-JUN-1994;	94WO-US05739.
XX		
PR	07-JUN-1993;	93US-0073028.
XX		

PR 07-JUN-1993; 93US-0073028

PA (UYDU-) UNIV DUKE.  
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Peteway SR, Wild CT;  
 XX WPI: 1995-036105/05.  
 DR  
 XX Computer search generated synthetic peptides - are inhibitors of  
 PT HIV transmission  
 XX  
 PS Claim 11, Page 132, 182pp; English.  
 XX  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibit transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.

XX Sequence 36 AA:

Query Match 100.0%; Score 195; DB 16; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONOQEKNEQELLELDKNASLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YTSLSHSLIEESONOQEKNEQELLELDKNASLWNMF 36

RESULT 2

XX AAR98398 standard; peptide; 36 AA.

XX AAR98398;

XX 17-FEB-1997 (first entry)

XX DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;

XX ALM0715; 107x178x4; PLZIP search motif; viral transmission; HIV;

XX Influenza virus; hepatitis B virus.

XX Human immunodeficiency virus type 1.

XX WO9619495-A1.

XX 27-JUN-1996.

XX 20-DEC-1995; 95WO-US16733.

XX 06-JUN-1995; 95US-0470896.

XX 20-DEC-1994; 94US-0360107.

XX (TRIM-) TRIMERIS INC.

XX (UYDU-) UNIV DUKE.

XX Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;

XX Matthews TJ, Peteway SR, Wild CT;

XX WPI: 1996-309517/31.

XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALM0715, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX Disclosure; Fig 1; 471pp; English.

CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALM0715,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
 CC hepatitis B virus, to a cell.

XX Sequence 36 AA:

Query Match 100.0%; Score 195; DB 17; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONOQEKNEQELLELDKNASLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YTSLSHSLIEESONOQEKNEQELLELDKNASLWNMF 36

RESULT 3

XX AAW17011 standard; peptide; 36 AA.

XX AAW17011;

XX 30-JUN-1997 (first entry)

XX HIV-1 derived peptide useful for treatment of HIV infection.

XX HIV; SIV; human; simian immunodeficiency virus; glycoprotein 41;

XX transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;

XX replication; transmission.

XX Human immunodeficiency virus type 1 LAI isolate.

XX WO9640191-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US09499.

XX 07-JUN-1995; 95US-0481957.

XX (TRIM-) TRIMERIS INC.

XX Johnson RM, Lambert DM;

XX WPI: 1997-099886/09.

XX Compens. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.

XX Claim 2; Figure 1; 84pp; English.

XX AAW17011 represents a peptide designated DP-178, a peptide derived  
 CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
 CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
 CC derivatives are used in combination with a therapeutic agent, e.g. a  
 CC reverse transcriptase, viral protease, cytokine, glycosylation or viral  
 CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
 CC by inhibiting viral replication or inhibiting transmission. They may  
 CC also be used in vaccines for protecting against HIV infection.

XX Sequence 36 AA:

Query Match 100.0%; Score 195; DB 18; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONOQEKNEQELLELDKNASLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YTSLSHSLIEESONOQEKNEQELLELDKNASLWNMF 36



RESULT 4  
 AAY22912  
 ID AAY22912 standard; Peptide; 36 AA.  
 XX  
 AC AAY22912;  
 XX  
 DT 19-AUG-1999 (first entry)  
 XX  
 DE SEQ ID NO. 108 from WO9820036.  
 XX  
 KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
 KW vaccine; antibody; viral membrane fusion; viral infectivity;  
 KW ligand affinity purification; protein A replacement;  
 KW immunoglobulin purification; epitope mimic.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 PN WO9820036-A1.  
 XX  
 FI 14-MAY-1998.  
 XX  
 FE 05-NOV-1997; 97WO-0520069.  
 XX  
 PR 16-JUN-1997; 97US-0876698.  
 PR 06-NOV-1996; 96US-0743698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 XX  
 DR WPI; 1998-286866/25.  
 XX  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa:peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 XX  
 PS Disclosure; Page 233-234; 279pp; English.  
 XX  
 CC Peptides AAY2805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY2810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY2810, AAY2871, AAY2880, AAY2888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 XX  
 Sequence 36 AA;  
 XX

RESULT 5  
 AAY22805  
 ID AAY22805 standard. Peptide: 36 AA.  
 XX  
 AC AAY22805;  
 XX  
 DT 19-AUG-1999 (first entry)  
 XX  
 SEQ ID NO. 1 from WO9820036.  
 DE  
 XX  
 KW HIV: gp41 protein; constrained helical peptide; HIV infection;  
 KW vaccine; antibody; viral membrane fusion; viral infectivity;  
 KW ligand affinity purification; protein A replacement;  
 KW immunoglobulin purification; epitope mimic.  
 XX  
 OS Human immunodeficiency virus.  
 OS  
 PN WO9820036-A1.  
 PN  
 PD 14-MAY-1998.  
 PD  
 PF 05-NOV-1997; 97WO-US20069.  
 PF  
 PR 16-JUN-1997; 97US-0876698.  
 PR 06-NOV-1996; 96US-0743698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI  
 PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 DR WPT. 1998-286866/25.  
 PT  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa:peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 XX  
 PS Disclosure: Page 143-144; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22993 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to produce two amide bonds.  
 CC Infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 XX  
 Sequence 36 AA:

```

RESULT 6
AAV31955
ID AAV31955 standard; Peptide: 36 AA.
AC AAV31955;
XX
XX 21-DEC-1999 (first entry)
XX
XX Synthetic peptide T-20 (DP-178).
XX
XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
XX
XX Synthetic.
XX
XX Human immunodeficiency virus type 1.
XX
XX Key Modified-site 1 Location/Qualifiers
XX FT Modified-site 1 /note= "N-terminal acetyl"
XX FT Modified-site 36 /note= "C-terminal amide"
XX
XX MO9948513-A1.
XX
XX 30-SEP-1999.
XX
XX 22-MAR-1999; 99WO-US06230.
XX
XX 23-MAR-1998; 98US-0045920.
XX PR 01-MAY-1998; 98US-0071877.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Kang M, Bray B, Lichy M, Mader C, Merutka G;
XX
XX WPI; 1999-591038/50.
XX
XX Methods of peptide synthesis, particularly used to produce T-20 or
XX T-20 like peptides
XX
XX Claim 1; Page 102; 120pp; English.
XX
XX The present sequence represents an N- and C-terminal modified
XX peptide, designated T-20 (or DP-178), corresponding to amino acids
XX 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.
XX The invention relates to methods for the synthesis of peptides,
XX in particular T-20 and T-20-like peptides. The method involves
XX synthesizing specific side-chain protected peptide fragment
XX intermediates of T-20 or a T-20-like peptide on a solid support,
XX coupling the protected fragments in solution to form a protected
XX T-20 or T-20-like peptide, followed by deprotection of the side
XX chains to yield the final T-20 or T-20-like peptide. The invention
XX also relates to individual peptide fragments (see AAV31955-73) which
XX act as intermediates in the synthesis of peptides of interest (e.g.
XX T-20), and to particular groups of peptide fragments which act as
XX intermediates in the synthesis of the peptide of interest. The
XX method allows for the large scale, economical production of high
XX purity peptides.
XX
XX Sequence 36 AA:
SQ
Query Match 100.0%; Score 195; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 4, 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLSHSLIESONQOEKNEDELLELDKWSLWNMF 36
DB 1 YTSLSHSLIESONQOEKNEDELLELDKWSLWNMF 36

```

```

ID AAV31974 standard; Peptide: 36 AA.
XX
XX AAV31974;
AC AAV31974;
XX
XX 21-DEC-1999 (first entry)
XX
XX HIV-1 LAI gp41 T-20 peptide.
XX
XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
XX
XX Human immunodeficiency virus type 1.
XX
XX MO9948513-A1.
XX
XX 30-SEP-1999.
XX
XX 22-MAR-1999; 99WO-US06230.
XX
XX 23-MAR-1998; 98US-0045920.
XX PR 01-MAY-1998; 98US-0071877.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Kang M, Bray B, Lichy M, Mader C, Merutka G;
XX
XX WPI; 1999-591038/50.
XX
XX Methods of peptide synthesis, particularly used to produce T-20 or
XX T-20 like peptides
XX
XX Disclosure: Page 9; 120pp; English.
XX
XX The present sequence represents a peptide, designated T-20 (or
XX DP-178), that corresponds to amino acids 638-673 of the
XX transmembrane protein gp41 of HIV-1 LAI isolate. The invention
XX relates to methods for the synthesis of peptides, in particular
XX C- and N-terminal modified T-20 (see AAV31955) and T-20-like peptides.
XX The method involves synthesizing specific side-chain protected
XX peptide fragment intermediates (see AAV31955-73) of T-20 or a
XX T-20-like peptide on a solid support, coupling the protected
XX fragments in solution to form a protected T-20 or T-20-like peptide,
XX followed by deprotection of the side chains to yield the final T-20
XX or T-20-like peptide. The invention also relates to individual
XX peptide fragments which act as intermediates in the synthesis of
XX peptides of interest (e.g. T-20), and to particular groups of
XX peptide fragments which act as intermediates in the synthesis of
XX the peptide of interest. The method allows for the large scale,
XX economical production of high purity peptides.
XX
XX Sequence 36 AA:
SQ
Query Match 100.0%; Score 195; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 4, 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLSHSLIESONQOEKNEDELLELDKWSLWNMF 36
DB 1 YTSLSHSLIESONQOEKNEDELLELDKWSLWNMF 36

```

RESULT 7  
AAV31974

```

RESULT 8
AAV52655
ID AAV52655 standard; Peptide: 36 AA.
AC AAV52655;
XX
XX 23-FEB-2001 (first entry)
XX
XX T20/DP178 peptide fragment #33.
XX
XX Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;
XX chemottractant.
XX

```

XX Human immunodeficiency virus type 1.  
OS  
XX  
XX WO20006622-A1.  
PN  
XX  
XX 09-NOV-2000.  
PD  
XX 05-MAY-2000; 2000WO-US12371.  
PF  
XX 05-MAY-1999; 99US-0132686.  
PR  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
PI WPI: 2000-656493/63.  
DR  
XX  
XX Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
XX Claim 12; Page 24; 148pp; English.  
XX  
XX The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
XX Sequence 36 AA:  
SQ  
XX  
XX Query Match 100.0%; Score 195; DB 21; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4,1e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLSHSLIESONOQEKNEQELLELDKWSLWNMF 36  
1 YTSLSHSLIESONOQEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLIESONOQEKNEQELLELDKWSLWNMF 36  
RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide: 36 AA.  
XX  
XX AAB52688;  
DI 23-FEB-2001 (first entry)  
XX  
XX T20/Dp178 peptide fragment #66.  
DE  
XX  
XX Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
KW chemoattractant.  
XX  
XX Human immunodeficiency virus type 1.  
OS  
XX  
XX WO20006622-A1.  
PN  
XX 09-NOV-2000.  
PD  
XX 05-MAY-2000; 2000WO-US12371.  
PF  
XX 05-MAY-1999; 99US-0132686.  
PR  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
PI WPI: 2000-656493/63.  
DR

XX Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
XX Claim 12; Page 25; 148pp; English.  
XX  
XX The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
XX Sequence 36 AA:  
SQ  
XX  
XX Query Match 100.0%; Score 195; DB 21; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4,1e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLSHSLIESONOQEKNEQELLELDKWSLWNMF 36  
1 YTSLSHSLIESONOQEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLIESONOQEKNEQELLELDKWSLWNMF 36  
RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide: 36 AA.  
XX  
XX AAB52818;  
DI 23-FEB-2001 (first entry)  
XX  
XX T20/Dp178 peptide fragment #97.  
DE  
XX  
XX Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
KW chemoattractant.  
XX  
XX Human immunodeficiency virus type 1.  
OS  
XX  
XX WO20006622-A1.  
PN  
XX 09-NOV-2000.  
PD  
XX 05-MAY-2000; 2000WO-US12371.  
PF  
XX 05-MAY-1999; 99US-0132686.  
PR  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
PI WPI: 2000-656493/63.  
DR  
XX  
XX Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
XX Claim 14; Page 40; 148pp; English.  
XX  
XX The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.

XX Sequence 36 AA: 100.0%; Score 195; DB 21; Length 36;  
 SQ Query Match Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOEKNEQELLELDKWSLWMNF 36  
 |||||||  
 DB 1 YTSLSHSLIEESQNOEKNEQELLELDKWSLWMNF 36

RESULT 11  
 ID AAB14533 standard; peptide: 36 AA.  
 XX AAB14533;  
 XX 24-NOV-2000 (first entry)

DT HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).

XX HIV-1: gp41 C-helical domain;  
 KM gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KM core 6-helix bundle; viral entry inhibition; immunogenic;  
 KM antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KM envelope glycoprotein; prophylaxis; therapy.

XX Human immunodeficiency virus type 1.  
 XX WO200040616-A1.  
 XX 13-JUL-2000.  
 XX 10-JAN-2000; 2000WO-US00456.  
 XX 08-JAN-1999; 99US-0115404.  
 PR 07-JAN-2000; 2000US-0480336.  
 XX (WILD/) WILD C T.  
 PA (WEIS/) WEISS C D.  
 XX Wild CT, Weiss CD;  
 PI WPI: 2000-465959/40.  
 DR Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -

PS Claim 13; Page 12; 97pp; English.

XX Sequences AAB14532-B14534 and AAB14569-B14602 represent specifically  
 CC claimed peptides derived from the C-helical domain of the gp41  
 CC envelope glycoprotein from a variety of HIV-1 isolates. The invention  
 CC relates to raising a neutralising antibody response to a broad spectrum  
 CC of HIV (human immunodeficiency virus) strains and isolates, comprising  
 CC the administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the process  
 CC of viral entry into host cells. Such peptides can correspond to or  
 CC mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly a  
 CC combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can  
 CC be alternately linked together to form a peptide which mimics the  
 CC core 6-helix bundle. Administration of the peptide(s) generates a  
 CC humoral response, with the production of antibodies against gp41  
 CC structures involved in viral entry. As these portions of gp41 are well  
 CC conserved, such antibodies may be effective against a broad range of

CC HIV strains and isolates. The peptide compositions may be administered  
 CC as a prophylactic or therapeutic vaccine to generate antibodies which  
 CC reduce or inhibit the ability of HIV to infect uninfected cells. A  
 CC composition comprising polyclonal or monoclonal antibodies can be  
 CC administered to reduce HIV infection of uninfected cells. Antibodies  
 CC raised against entry-relevant gp41 structures may also be used  
 CC therapeutically and as tools to further elucidate the mechanism of HIV  
 CC cell entry.

XX Sequence 36 AA: 100.0%; Score 195; DB 21; Length 36;  
 SQ Query Match Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOEKNEQELLELDKWSLWMNF 36  
 |||||||  
 DB 1 YTSLSHSLIEESQNOEKNEQELLELDKWSLWMNF 36

RESULT 12  
 ID AAY88665 standard; peptide: 36 AA.  
 XX AAY88665;  
 AC 23-MAY-2000 (first entry)

DT Core polypeptide fragment T No. 20.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KM anti-fusogenic; differentiation factor; interleukin; interferon;  
 KM colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.  
 OS WO9959615-A1.  
 XX 25-NOV-1999.  
 XX 20-MAY-1999; 99WO-US11219.  
 PF 20-MAY-1998; 98US-0082279.  
 XX (TRIM-) TRIMERIS INC.  
 PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI: 2000-136792/12.  
 DR A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

PS Disclosure; Page 21; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX Sequence 36 AA: 100.0%; Score 195; DB 21; Length 36;  
SO Query Match Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWMWF 36  
Db 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWMWF 36

RESULT 13  
ID AAY88729 standard; peptide: 36 AA.  
XX AAY88729;  
XX 23-MAY-2000 (first entry)  
XX Core polypeptide fragment T No. 84.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KM anti-fusogenic; differentiation factor; interleukin; interferon;  
KM colony stimulating factor; hormone; angiogenic factor.  
XX Unidentified.  
XX OS  
XX PN W0959615-A1.  
XX PD 25-NOV-1999.  
XX PE 20-MAY-1999; 99WO-US11219.  
XX PR 20-MAY-1998; 98US-0082279.  
XX PA (TRIM-) TRIMERIS INC.  
XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI: 2000-136792/12.  
XX DR A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX PT comprises enhancer sequence -  
XX PS Disclosure; Page 22; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
sequence linked to core polypeptides. The enhancer polypeptides are  
derived from various retroviral envelope (gp41) protein sequences,  
especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
pharmacokinetic properties such as increasing the half-life of any core  
polypeptide that they are linked to. The core polypeptides are any  
polypeptide that may be introduced into a living system and that can  
function as a pharmacologically useful peptide for the treatment or  
prevention of a disease. The core polypeptides are bioactive peptides  
selected from a growth factor, cytokine, differentiation factor,  
interleukin, interferon, colony stimulating factor, hormone or  
angiogenic factor. The peptides of the invention can be used for  
inhibiting viral infection and can be used in anti-viral and  
anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
polypeptide fragments that can be used in the invention. Some sequences  
among those indicated also comprise enhancer fragments at terminal ends  
and form hybrid polypeptides.

XX Sequence 36 AA:  
SO Query Match Best Local Similarity 100.0%; Score 195; DB 21; Length 36;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWMWF 36

Db 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWMWF 36  
ID AAY89135 standard; peptide: 36 AA.  
XX AAY89135;  
XX 23-MAY-2000 (first entry)  
XX Core polypeptide fragment T No. 573.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KM anti-fusogenic; differentiation factor; interleukin; interferon;  
KM colony stimulating factor; hormone; angiogenic factor.  
XX Unidentified.  
XX OS  
XX PN W0959615-A1.  
XX PD 25-NOV-1999.  
XX PE 20-MAY-1999; 99WO-US11219.  
XX PR 20-MAY-1998; 98US-0082279.  
XX PA (TRIM-) TRIMERIS INC.  
XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI: 2000-136792/12.  
XX DR A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX PT comprises enhancer sequence -  
XX PS Disclosure; Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
sequence linked to core polypeptides. The enhancer polypeptides are  
derived from various retroviral envelope (gp41) protein sequences,  
especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
pharmacokinetic properties such as increasing the half-life of any core  
polypeptide that they are linked to. The core polypeptides are any  
polypeptide that may be introduced into a living system and that can  
function as a pharmacologically useful peptide for the treatment or  
prevention of a disease. The core polypeptides are bioactive peptides  
selected from a growth factor, cytokine, differentiation factor,  
interleukin, interferon, colony stimulating factor, hormone or  
angiogenic factor. The peptides of the invention can be used for  
inhibiting viral infection and can be used in anti-viral and  
anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
polypeptide fragments that can be used in the invention. Some sequences  
among those indicated also comprise enhancer fragments at terminal ends  
and form hybrid polypeptides.

XX Sequence 36 AA:  
SO Query Match Best Local Similarity 100.0%; Score 195; DB 21; Length 36;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWMWF 36  
Db 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWMWF 36

RESULT 15  
ID AAY89136 standard; peptide: 36 AA.

AC AAY89136;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX

DE Core polypeptide fragment T No. 574.  
 XX

KW Retrovirus; hybrid polypeptide; enhancer; gp41, envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX

XX Unidentified.  
 OS

XX WO9959615-A1.  
 PN

XX 25-NOV-1999.  
 PD

XX 20-MAY-1999; 99WO-US11219.  
 PF

XX 20-MAY-1998; 98US-0082279.  
 XX

XX (TRIM-) TRIMERIS INC.  
 PI

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI

XX WPI; 2000-136792/12.  
 DR

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 XX

PS Disclosure; Page 30; 124pp; English.  
 PS

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y9005 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

SQ Sequence 36 AA;  
 SQ

Query Match 100.0%; Score 195; DB 21; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 4, 1e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESQNOEKNEQELLEDKWSLWNP 36  
 |||||||  
 Db 1 YTSLSHSLIESQNOEKNEQELLEDKWSLWNP 36

Search completed: May 16, 2003, 11:12:00  
 Job time : 33.4578 secs

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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-1

Perfect score: 195  
Sequence: 1 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	851	2 S33985	env polypeptide -
2	195	100.0	854	2 S13288	env polypeptide - huma
3	195	100.0	856	1 VCLJH3	env polypeptide pr
4	195	100.0	861	1 VCLJLV	env polypeptide pr
5	186	95.4	443	2 C41621	env polypeptide p
6	186	95.4	856	1 VCLJVL	env polypeptide pr
7	186	95.4	856	1 VCLJ3W	env polypeptide pr
8	186	95.4	861	1 VCLJSC	env polypeptide pr
9	183	93.8	357	2 S21994	env polypeptide pr
10	183	93.8	358	2 S21998	env polypeptide g
11	182	93.3	357	2 S21996	env polypeptide g
12	179	91.8	847	2 T09448	env polypeptide g
13	179	91.8	847	2 S13289	env polypeptide - huma
14	178	91.3	445	2 A41621	env polypeptide M
15	177	90.8	358	2 S22002	env polypeptide g
16	177	90.8	358	2 S22000	env polypeptide g
17	177	90.8	358	2 S70417	env polypeptide g
18	177	90.8	852	2 T12016	env polypeptide g
19	176	90.3	859	1 VCLJMN	env polypeptide pr
20	176	90.3	357	2 S22004	env polypeptide pr
21	176	90.3	855	1 VCLJAJ2	env polypeptide pr
22	174	89.2	853	2 S54384	env polypeptide pr
23	174	89.2	855	1 VCLJZR	env polypeptide pr
24	173	88.7	357	2 S22006	env polypeptide pr
25	173	88.7	843	1 H44001	env polypeptide pr
26	172	88.2	846	1 VCLJND	env polypeptide pr
27	170	87.2	357	2 S21992	env polypeptide g
28	170	87.2	852	1 VCLJBR	env polypeptide g
29	168	86.2	729	1 VCLJHX	env polypeptide pr

30	168	86.2	861	1 VCLJKB	env polypeptide pr
31	167	85.6	859	2 T01672	env polypeptide pr
32	164	84.1	454	2 B41621	env polypeptide D
33	163	83.6	868	1 VCLJH4	env polypeptide -
34	160	82.1	136	2 J00266	env polypeptide -
35	160	82.1	136	2 J00266	env polypeptide -
36	151	77.4	854	1 VCLJSI	env polypeptide pr
37	149	76.4	856	1 A44963	env polypeptide pr
38	147	75.4	357	2 S21990	env polypeptide pr
39	136	69.7	877	2 S49197	env polypeptide p
40	119	61.0	863	2 A53034	env polypeptide p
41	86	44.1	881	1 VCLJG3	env polypeptide -
42	86	44.1	881	1 S03068	env polypeptide -
43	86	44.1	889	1 VCLJG5	env polypeptide -
44	85	43.6	151	2 S30448	env polypeptide -
45	85	43.6	151	2 S30452	env polypeptide -

## ALIGNMENTS

## RESULT 1

S33985 env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F.  
Submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:211530; NID:g60192; PIDN:CAA7628.1; PID:g60199

C:Superfamily: type E retrovirus env polypeptide

Query Match 100.0%; Score 195; DB 2; Length 851;

Best Local Similarity 100.0%; Pred. No. 2e-15; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 36

DB 633 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 668

## RESULT 2

S13288 env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack,

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; PMID:91043044; PMID:2172833

A:Accession: S13288

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 100.0%; Score 195; DB 2; Length 854;

Best Local Similarity 100.0%; Pred. No. 2e-15; Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 36

DB 636 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 671

## RESULT 3

VCLJH3

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env polypotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polypotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberger, J.A.; Papas, T.S.; Grzyb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <Sig>
F:12-856/Product: exterior membrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 100.0%; Score 195; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTSLSHLSIESONQOEKNEQELLELDKASLWNNF 36
DB 638 YTSLSHLSIESONQOEKNEQELLELDKASLWNNF 673

RESULT 4
env polypotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polypotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberger, J.A.; Papas, T.S.; Grzyb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <KAT>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <Sig>
F:12-856/Product: exterior membrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 100.0%; Score 195; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTSLSHLSIESONQOEKNEQELLELDKASLWNNF 36
DB 643 YTSLSHLSIESONQOEKNEQELLELDKASLWNNF 678

RESULT 5
env polypotein precursor - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polypotein

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N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match 95.4%; Score 186; DB 2; Length 443;
Best Local Similarity 94.4%; Pred. No. 1.1e-14;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTSLSHLSIESONQOEKNEQELLELDKASLWNNF 36
DB 378 YTSLSHLSIESONQOEKNEQELLELDKASLWNNF 413

RESULT 6
env polypotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polypotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberger, J.A.; Papas, T.S.; Grzyb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUR>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <Sig>
F:12-856/Product: exterior membrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 95.4%; Score 186; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 2.4e-14;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YTSLSHLSIESONQOEKNEQELLELDKASLWNNF 35
DB 638 YTSLSHLSIESONQOEKNEQELLELDKASLWNNF 672

RESULT 7
env polypotein precursor - human immunodeficiency virus type 1 (isolate WMCI)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997

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C:Accession: A24774  
 R:Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774, MIMD:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STA>  
 A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match  
 Best Local Similarity 95.4%; Score 186; DB 1; Length 856;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLEESONQOEKNEDELLEDKWASLWMP 36  
 DB 638 YTSLSHLEESONQOEKNEDELLEDKWASLWMP 673

RESULT 8  
 VCLJSC  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Guirao, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
 Virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MIMD:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-861/Product: env polyprotein #status predicted <GP>  
 F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match  
 Best Local Similarity 95.4%; Score 186; DB 1; Length 861;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLEESONQOEKNEDELLEDKWASLWMP 36  
 DB 643 YTSLSHLEESONQOEKNEDELLEDKWASLWMP 678

RESULT 9  
 S21994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 27B  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21994  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STEL>

A:Cross-references: EMBL:X61355; NID:g60179; PID:CAA43622.1; PID:g60180  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MIMD:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Molecule type: preliminary  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140/'X',142-312/'X',314-357 <STEL>  
 A:Cross-references: EMBL:X61355; NID:g60179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match  
 Best Local Similarity 93.8%; Score 183; DB 2; Length 357;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLEESONQOEKNEDELLEDKWASLWMP 36  
 DB 139 YTSLSHLEESONQOEKNEDELLEDKWASLWMP 174

RESULT 10  
 S21998  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 28  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21998; S70425  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21998  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STEL>  
 A:Cross-references: EMBL:X61359; NID:g60182; PID:CAA43630.1; PID:g60183  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MIMD:92144209; PMID:1736940  
 A:Accession: S70425  
 A:Molecule type: preliminary  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222/'X',224-358 <STEL>  
 A:Cross-references: EMBL:X61359; NID:g60182; PID:CAA43630.1; PID:g60183  
 A:Superfamily: type E retrovirus env polyprotein

Query Match  
 Best Local Similarity 93.8%; Score 183; DB 2; Length 358;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLEESONQOEKNEDELLEDKWASLWMP 36  
 DB 140 YTSLSHLEESONQOEKNEDELLEDKWASLWMP 175

RESULT 11  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S70422; S21996  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MIMD:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Molecule type: preliminary  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STEL>  
 A:Cross-references: EMBL:X61356; NID:g60181; PID:CAA43624.1; PID:g1067129  
 A:Experimental source: patient 27L  
 A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polypeptide

Query Match 93.3%; Score 182; DB 2; Length 357;

Best Local Similarity 91.7%; Pred. No. 2,7e-14;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36  
 DB 139 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 174

#### RESULT 12

envelope glycoprotein - human immunodeficiency virus type 1 (strain JFRL)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

C:Accession: T09448

R:Pan, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

Accession number: Z16673

Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-References: EMBL:U63632; NID:91465777; PID:91465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

Query Match 91.8%; Score 179; DB 2; Length 847;

Best Local Similarity 91.7%; Pred. No. 1.6e-13;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36

DB 629 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 664

RESULT 13

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13288; MUID:91043044; PMID:2172833

Accession: S13289

Status: preliminary

A:Molecule type: DNA

A:Residues: 1-847 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 91.8%; Score 179; DB 2; Length 847;

Best Local Similarity 91.7%; Pred. No. 1.6e-13;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36

DB 629 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 664

RESULT 14

env polypeptide M - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypeptide

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

C:Accession: A11621

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A11621; MUID:92107924; PMID:1763038

A:Accession: A11621

A:Molecule type: DNA

A:Residues: 1-445 <BUR>

A:Cross-References: GB:M77228; NID:9328627; PID:AA03790.1; PID:9555013

A:Note: this virus was isolated from the mother

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly

F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:426-445/Domain: transmembrane #status predicted <TMN>

F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding st

Query Match 91.3%; Score 178; DB 2; Length 445;

Best Local Similarity 88.9%; Pred. No. 1e-13;

Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36

DB 380 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 415

RESULT 15

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 3L

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22002; S70418

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22002

A:Molecule type: DNA

A:Residues: 1-358 <STEL>

A:Cross-References: EMBL:X61352; NID:960186; PID:CA443616.1; PID:960187

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70418

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333,'X',335-358 <STEN>

A:Cross-References: EMBL:X61352; NID:960186

C:Superfamily: type E retrovirus env polypeptide

Query Match 90.8%; Score 177; DB 2; Length 358;

Best Local Similarity 88.9%; Pred. No. 1.1e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36

DB 140 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 175

Search completed: May 16, 2003, 11:25:05

Job time: 13.1446 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 6.07229 Seconds  
(without alignments)  
245.895 Million cell updates/sec

Title: US-09-623-533A-1

Perfect score: 195  
Sequence: 1 YTSLIHSLIESSQNOEKNEOELLELDKWSLMMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	195	100.0	851	ENV_HV1B8	P04582 human immun
2	195	100.0	856	ENV_HV1B1	P03375 human immun
3	195	100.0	856	ENV_HV1B2	P04578 human immun
4	195	100.0	856	ENV_HV1B3	P04624 human immun
5	195	100.0	856	ENV_HV1B4	P07626 human immun
6	195	100.0	861	ENV_HV1B5	P03377 human immun
7	192	98.5	853	ENV_HV1B6	P19551 human immun
8	186	95.4	856	ENV_HV1B7	P03376 human immun
9	186	95.4	856	ENV_HV1B8	P05878 human immun
10	186	95.4	856	ENV_HV1B9	P31872 human immun
11	184	94.4	852	ENV_HV1C1	P19549 human immun
12	183	93.8	847	ENV_HV1C2	P19550 human immun
13	180	92.3	847	ENV_HV1C3	P05880 human immun
14	179	91.8	867	ENV_HV1C4	P12489 human immun
15	177	90.8	856	ENV_HV1C5	P05877 human immun
16	176	90.3	855	ENV_HV1C6	P03378 human immun
17	175	89.7	853	ENV_HV1C7	P04581 human immun
18	175	89.7	865	ENV_HV1C8	P04579 human immun
19	174	89.2	853	ENV_HV1C9	P12487 human immun
20	174	89.2	855	ENV_HV1D1	P04580 human immun
21	173	88.7	843	ENV_HV1D2	P35961 human immun
22	172	88.2	846	ENV_HV1D3	P18799 human immun
23	172	88.2	855	ENV_HV1D4	P20888 human immun
24	170	87.2	852	ENV_HV1D5	P12488 human immun
25	169	86.7	848	ENV_HV1D6	P20871 human immun
26	168	86.2	861	ENV_HV1D7	P31819 human immun
27	167	85.6	859	ENV_HV1D8	P04583 human immun
28	163	83.6	868	ENV_HV1D9	P05879 human immun
29	162	83.1	863	ENV_HV1D10	P05882 human immun
30	151	77.4	854	ENV_HV1D11	P12881 chimpanzee
31	149	76.4	856	ENV_HV1D12	P05881 human immun
32	90	46.2	854	ENV_HV1D13	O02837 simian immun
33	86	44.1	881	ENV_HV1D14	P05884 simian immun

34	86	44.1	882	ENV_HV1D15	P05885 simian immun
35	85	43.6	885	ENV_HV1D16	P12492 simian immun
36	84	43.1	859	ENV_HV1D17	P15831 human immun
37	84	43.1	860	ENV_HV1D18	P18094 human immun
38	82	42.1	880	ENV_HV1D19	P11267 simian immun
39	80	41.0	859	ENV_HV1D20	P24105 human immun
40	80	41.0	889	ENV_HV1D21	P19503 simian immun
41	77	39.5	846	ENV_HV1D22	P12449 human immun
42	77	39.5	851	ENV_HV1D23	P17755 human immun
43	77	39.5	851	ENV_HV1D24	P18040 human immun
44	77	39.5	858	ENV_HV1D25	P04577 human immun
45	77	39.5	859	ENV_HV1D26	P20872 human immun

## ALIGNMENTS

RESULT 1	ENV_HV1B8	STANDARD:	PRT:	851 AA.
AC	P04582:			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OC	Human immunodeficiency virus type 1 (B8 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11684;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8511123; PubMed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starich B.R., Joseph S.F., Doran E.R., Katsaki J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Peteway S.R. Jr., Pearson M.D., Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;			
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RL	Nature 313:277-284(1985).			
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CC	EMBL: K02011; AAA44661.1; -			
CC	HIV: K02011; ENV5B8.			
DR	Glycosylated: P04582; -			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	851	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	296	331	BY SIMILARITY.
FT	DISULFID	378	440	BY SIMILARITY.
FT	DISULFID	385	413	BY SIMILARITY.
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644. MW; D16A3C90857785F1 CR64.

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Query Match 100.0%; Score 195; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 YTSLSHSLIEESONOQEKNEQELLELDKVASLWNMF 36
DB 633 YTSLSHSLIEESONOQEKNEQELLELDKVASLWNMF 668

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RESULT 2
ENV_HV1B1 STANDARD: PRT: 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GPI60 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
Viruses; Retrovird viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran F.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Pappas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
Chinese hamster ovary cells.";
RL J. Biol. Chem. 265:10373-10382(1990).
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CC EMBL: M15654; AAA44205.1;
DR PIR: A03973; VCLJH3
DR HIV: M15654; ENVSBI102.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
KW SIGNAL 1 30
FT CHAIN 1 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 366 366
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BF61A18931BB27 CR64;

```

```

Query Match 100.0%; Score 195; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTSLSHSLIEESONOQEKNEQELLELDKVASLWNMF 36
DB 638 YTSLSHSLIEESONOQEKNEQELLELDKVASLWNMF 673

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RESULT 3
ENV_HV1H2 STANDARD: PRT: 856 AA.
AC P04578; 009779;

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[illegible]

FT	CARBOHYD	397	397	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	448	448	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	611	611	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	616	616	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	637	637	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	674	674	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	750	750	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	816	816	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
SO	SEQUENCE	856 AA:	97212 MW:	66AB16AF85107FE0 CRC64:		
	Query Match	100.0%:	Score 195;	DB 1;	Length 856;	
	Best Local Similarity	100.0%:	Pred. No. 3,2e-16;			
	Matches	36;	Conservative	0;	Mismatches	0;
OY	1	YTSLIHSLIEESQNOOEKNEOELLLEDKWASIMWNF	36			
DB	638	YTSLIHSLIEESQNOOEKNEOELLLEDKWASIMWNF	673			
	RESULT 4					
ENV_HV1H3	ENV_HV1H3	STANDARD:	PRT:	856 AA.		
AC	P04624:					
DT	13-AUG-1987 (Rel. 05, Created)					
DT	01-FEB-1996 (Rel. 33, Last sequence update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	Envelope polyprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].					
GN	ENV.					
OS	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).					
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.					
OX	NCBI_Taxid=11707;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=85228248; PubMed=2988795;					
RA	Crowl R., Gauguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;					
RT	"HIV-1-II env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients."					
RL	Cell 41:979-986(1985).					
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CC	-----					
DR	EMBL: M14100; AAA4679.1; -					
DR	HIV: M14100; ENVSHXB3.					
DR	InterPro: IPR000328; Env_Gp41.					
DR	InterPro: IPR000777; Gp120.					
DR	Pfam: PF00516; Gp120.1.					
DR	Pfam: PF00517; Gp41.1.					
KW	AIDS; Coat protein; Polypeptide; Polypeptide; Glycoprotein; Transmembrane; Signal.					
KW	SIGNAL					
FT	CHAIN	1	30			
FT	CHAIN	51	511	EXTERIOR MEMBRANE GLYCOPROTEIN.		
FT	CHAIN	512	856	TRANSMEMBRANE GLYCOPROTEIN.		
FT	DISULFID	119	205	BY SIMILARITY.		
FT	DISULFID	126	196	BY SIMILARITY.		
FT	DISULFID	131	157	BY SIMILARITY.		
FT	DISULFID	218	247	BY SIMILARITY.		
FT	DISULFID	228	239	BY SIMILARITY.		
FT	DISULFID	296	331	BY SIMILARITY.		
FT	DISULFID	378	445	BY SIMILARITY.		
FT	DISULFID	385	418	BY SIMILARITY.		
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .)	(POTENTIAL).	
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .)	(POTENTIAL).	

```

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA: 97188 MW: 3373688B84C1AFC CRC64:

```

```

Query Match 100.0%: Score 195; DB 1; Length 856;
Best Local Similarity 100.0%: Pred. No. 3.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 YTSLSHSLIEESONOQEKNEDELLELDKWSLMMNF 36
Db 638 YTSLSHSLIEESONOQEKNEDELLELDKWSLMMNF 673

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RESULT 5
ENV_HVILM STANDARD: PRT: 856 AA.
AC 070626:
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
ENV Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HIV2.3 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz G.M., Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC
CC EMBL, U12055; AAA76690.1; -
CC DR GLYCOSULEDB: 070626; -
CC DR Interpro: IPR000328; Env_GP41.

```

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DR Interpro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT CHAIN 512 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA: 96938 MW: 0C241332CF7E6687 CRC64:

```

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Query Match 100.0%: Score 195; DB 1; Length 856;
Best Local Similarity 100.0%: Pred. No. 3.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTSLSHSLIEESONOQEKNEDELLELDKWSLMMNF 36
Db 638 YTSLSHSLIEESONOQEKNEDELLELDKWSLMMNF 673

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RESULT 6
ENV_HVILM STANDARD: PRT: 861 AA.
AC P03377:
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
ENV Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 853 AA: 96912 MW: 3377B93B6F22ABA CRC64;

Query Match
Best Local Similarity 98.5%; Score 192; DB 1; Length 853;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSHLSIESQNOOEKNEQELLELDKKNASLWNF 36
|||||:|||||:|||||:|||||:|||||:
636 YTSLSHLSIESQNOOEKNEQELLELDKKNASLWNF 671

RESULT 8
ENV_HV1PV STANDARD: PRT; 856 AA.
ID ENV_HV1PV
AC P03376;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OC Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
AIDS/Lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
CC -----
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or send an email to license@sib.ch).
CC -----
CC EMBL: K02083; AAB59873.1;
DR EMBL: X01762; CA25903.1; ALT_SEQ.
DR PIR: A03974; VCLJVL.
DR HIV: K02083; ENVSPV22.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.

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FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA: 97339 MW: 5FCDB1DC3C1209B3 CRC64;

Query Match
Best Local Similarity 95.4%; Score 186; DB 1; Length 856;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSHLSIESQNOOEKNEQELLELDKKNASLWNF 35
|||||:|||||:|||||:|||||:|||||:
638 YTSLSHLSIESQNOOEKNEQELLELDKKNASLWNF 672

RESULT 9
ENV_HV1SC STANDARD: PRT; 856 AA.
ID ENV_HV1SC
AC P05878;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OC Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
1984 IN SOUTHERN CALIFORNIA.
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CC -----

DR EMBL: M17450; -; NOT\_ANNOTATED\_CDS.

DR PIR: B28922; VCLJ3C.

DR HIV: M17450; ENV5SC.

DR InterPro: IPR000328; Env\_Gp41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KW Signal.

FT SIGNAL 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT SITE 760 760

FT SITE 760 760

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 160

FT DISULFID 219 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 439

FT DISULFID 383 412

FT CARBOHYD 87 129

FT CARBOHYD 129 135

FT CARBOHYD 135 135

FT CARBOHYD 140 140

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 276

FT CARBOHYD 276 276

FT CARBOHYD 295 295

FT CARBOHYD 301 301

FT CARBOHYD 302 302

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 384 384

FT CARBOHYD 394 394

FT CARBOHYD 400 400

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

FT CARBOHYD 674 674

FT CARBOHYD 816 816

SO SEQUENCE 856 AA; 97055 MW; DAFDA600EBA7A08 CRC64;

Query Match

Best Local Similarity 94.4%; Score 186; DB 1; Length 856;

Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHLSIESONOQKNEOELLELDKWSLWNF 36

DB 638 YTSLIHLSIESONOQKNEOELLELDKWSLWNF 673

RESULT 10

ID ENV\_HV1M1 STANDARD; PRT; 856 AA.

AC P1872;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).

DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)).

GN ENV.

OS Human immunodeficiency virus type 1 (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI\_Taxid=31678;

OR [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=66218077; PubMed=2423250.

RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

RT Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.

RT AIDS; 45:637-648(1986).

RL Cell 45:637-648(1986).

CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

CC PIR: A24774; VCLJ3W.

DR InterPro: IPR000328; Env\_Gp41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KW Signal.

FT SIGNAL 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT DISULFID 53 73

FT DISULFID 118 205

FT DISULFID 125 196

FT DISULFID 130 152

FT DISULFID 218 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 444

FT DISULFID 383 417

FT CARBOHYD 87 87

FT CARBOHYD 134 134

FT CARBOHYD 140 140

FT CARBOHYD 151 151

FT CARBOHYD 155 155

FT CARBOHYD 183 183

FT CARBOHYD 197 197

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 289 289

FT CARBOHYD 295 295

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 390 390

FT CARBOHYD 394 394

FT CARBOHYD 404 404

FT CARBOHYD 447 447

FT CARBOHYD 459 459

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

SO SEQUENCE 856 AA; 97526 MW; DB68D1E94C04D69 CRC64;

Query Match

Best Local Similarity 94.4%; Score 186; DB 1; Length 856;

Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHLSIESONOQKNEOELLELDKWSLWNF 36

ID	ENV_HV1S3	STANDARD;	PRT;	852 AA.
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).			
OC	Viruses; Retrovirdae; Retroviridae; Lentivirinae.			
OX	NCBI_TaxID=11690;			
RN	11			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90317906; PubMed=2370688;			
RY	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dana D.;			
RY	"Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";			
RY	J. Virol. 64:4016-4020(1990).			
CC	-----			
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CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; M38427; AAA45067.1; .			
DR	HIV; M38427; ENVSEF3.			
DR	InterPro: IPR000328; Env GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	SIGNAL	1	31	BY SIMILARITY.
FT	CHAIN	32	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	852	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	156	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	331	BY SIMILARITY.
FT	DISULFID	377	439	BY SIMILARITY.
FT	DISULFID	384	412	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	159	159	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	189	189	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	277	277	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	339	339	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	385	385	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	391	391	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	401	401	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	405	405	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	442	442	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	457	457	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	607	607	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	612	612	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	621	621	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	633	633	N-LINKED (GLCNAC . . )	(POTENTIAL).
SO	SEQUENCE	852 AA;	96663 MW;	EETBBB8D23C9910D CRC6d;	(POTENTIAL).
Query Match		94.4%;	Score 184;	DB 1;	Length 852;
Best Local Similarity		91.7%;	Pred. No. 7e-15;		
Matches	33;	Conservative	3;	Mismatches	0; Indels 0; Gaps 0;
OY	1 YTSLSHSLIESQNOEKNEDELLELDKWSLWNF	36			
Dd	634 YTSILYTLLESQNOEKNELLEDKWSLWNF	669			
RESULT 12					
ENV_HV1S1					
ID	ENV_HV1S1	STANDARD:	PRT;	847 AA.	
AC	P19550:				
DT	01-FEB-1991 (Rel. 17,	Created)			
DT	01-FEB-1991 (Rel. 17,	Last sequence update)			
DT	15-JUL-1999 (Rel. 38,	Last annotation update)			
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirinae.				
OX	NCR_TaxID=11691;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90347835; PubMed=2384920;				
RA	Cheng-Mayer C., Quiroga M., Tung J.W., Levy J.:				
RT	"Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation."				
RL	J. Virol. 64:4390-4398(1990).				
CC					
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .				
DR	EMBL; M65024; AAA45072.1; -				
DR	HIV; M38428; ENVSSF162.				
DR	InterPro; IPR000328; Env_GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00517; GP120; 1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.				
FT	SIGNAL.	1	29		
FT	CHAIN	30	502	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	CHAIN	503	847	TRANSMEMBRANE GLYCOPROTEIN.	
FT	DISULFID	53	73	BY SIMILARITY.	
FT	DISULFID	118	203	BY SIMILARITY.	
FT	DISULFID	125	194	BY SIMILARITY.	
FT	DISULFID	130	155	BY SIMILARITY.	
FT	DISULFID	216	245	BY SIMILARITY.	
FT	DISULFID	226	237	BY SIMILARITY.	
FT	DISULFID	294	328	BY SIMILARITY.	
FT	DISULFID	374	435	BY SIMILARITY.	
FT	DISULFID	381	408	BY SIMILARITY.	
FT	CARBOHYD	87	87	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	135	135	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC . . )	(POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC . . )	(POTENTIAL).

```

FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL)
SEQUENCE 847 AA; 96135 MW; 0A901317FD7FE2AB CRC64;

```

```

Query Match 93.8%; Score 183; DB 1; Length 847;
Best Local Similarity 91.7%; Pred. No. 9, 2e-15;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 YTSLSHSLIEESONQOEKNEDELKDKWASLMMNF 36
DB 629 YTNLYTLIEESONQOEKNEDELKDKWASLMMNF 664

```

```

RESULT 13
ENV_HV1W2 STANDARD; PRT; 847 AA.

```

```

AC P05880;
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RX MEDLINE=86235450; PubMed=3012778;
RP Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
"Genetic variation in HTLV-III/LAV over time in patients with AIDS or
at risk for AIDS."
RT Science 232:1548-1553(1986).
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
WAS PERINATALLY INFECTED BY HER MOTHER.

```

```

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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M12507; AAB12990.1;
CC HIV: M12507; ENVSMJ2.
CC InterPro: IPR000328; ENV_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
CC AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.

```

```

FT SIGNAL 1 29
FT CHAIN 30 501
FT CHAIN 502 847
FT DISULFID 53 73
FT DISULFID 118 202
FT DISULFID 125 193
FT DISULFID 130 152
FT DISULFID 215 244
FT DISULFID 225 236
FT DISULFID 293 326
FT DISULFID 372 435
FT DISULFID 379 408
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 140 140
FT CARBOHYD 151 151
FT CARBOHYD 155 155
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FT CARBOHYD 400 400
FT CARBOHYD 438 438
FT CARBOHYD 450 450
FT CARBOHYD 602 602
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FT CARBOHYD 616 616
FT CARBOHYD 628 628
SEQUENCE 847 AA; 96466 MW; C01E33D73A55C8E CRC64;

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```

Query Match 92.3%; Score 180; DB 1; Length 847;
Best Local Similarity 91.7%; Pred. No. 2, 1e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

OY 1 YTSLSHSLIEESONQOEKNEDELKDKWASLMMNF 36
DB 629 YTSLSHSLIEESONQOEKNEDELKDKWASLMMNF 664

```

```

RESULT 14
ENV_HV1J3 STANDARD; PRT; 867 AA.

```

```

AC P12489;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RX MEDLINE=89352108; PubMed=2669897;
RP Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
"Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria."
RT AIDS Res. Hum. Retroviruses 5:411-419(1989).
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```



FT	CARBOHYD	612	612	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	617	617	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	626	626	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	638	638	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	816	816	N-LINKED (GLCNAC. . .)	(POTENTIAL)
SO	SEQUENCE	856 AA;	97140 MM;	D197D80940BE32	CRC64;

Query Match	90.8%	Score 177;	DB 1;	Length 856;
Best Local Similarity	88.9%;	Pred. No. 5e-14;		
Matches	32;	Conservative	3;	Mismatches 1;
				Indels 0;
				Gaps 0;

```

QY      1 YTSLIHSIIIESQNOQEKNEQELLELDKWSLWNWF 36
        |||||:|:|:| ||||| ||||| ||||| |||||
Db      639 YTSLIYSLLEKSTQOEKNEQELLELDKWSLWNWF 674

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Search completed: May 16, 2003, 11:13:31  
Job time : 7.07229 secs

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GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533A-536  
Perfect score: 195  
Sequence: 1 YTSIHSLEESQNOQEKNEDELLELDKWSLWVWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SID52/gcgdata//geneseq//geneseq-emb1/AA1980.DAT:\*  
2: /SID52/gcgdata//geneseq//geneseq-emb1/AA1981.DAT:\*  
3: /SID52/gcgdata//geneseq//geneseq-emb1/AA1982.DAT:\*  
4: /SID52/gcgdata//geneseq//geneseq-emb1/AA1983.DAT:\*  
5: /SID52/gcgdata//geneseq//geneseq-emb1/AA1984.DAT:\*  
6: /SID52/gcgdata//geneseq//geneseq-emb1/AA1985.DAT:\*  
7: /SID52/gcgdata//geneseq//geneseq-emb1/AA1986.DAT:\*  
8: /SID52/gcgdata//geneseq//geneseq-emb1/AA1987.DAT:\*  
9: /SID52/gcgdata//geneseq//geneseq-emb1/AA1988.DAT:\*  
10: /SID52/gcgdata//geneseq//geneseq-emb1/AA1989.DAT:\*  
11: /SID52/gcgdata//geneseq//geneseq-emb1/AA1990.DAT:\*  
12: /SID52/gcgdata//geneseq//geneseq-emb1/AA1991.DAT:\*  
13: /SID52/gcgdata//geneseq//geneseq-emb1/AA1992.DAT:\*  
14: /SID52/gcgdata//geneseq//geneseq-emb1/AA1993.DAT:\*  
15: /SID52/gcgdata//geneseq//geneseq-emb1/AA1994.DAT:\*  
16: /SID52/gcgdata//geneseq//geneseq-emb1/AA1995.DAT:\*  
17: /SID52/gcgdata//geneseq//geneseq-emb1/AA1996.DAT:\*  
18: /SID52/gcgdata//geneseq//geneseq-emb1/AA1997.DAT:\*  
19: /SID52/gcgdata//geneseq//geneseq-emb1/AA1998.DAT:\*  
20: /SID52/gcgdata//geneseq//geneseq-emb1/AA1999.DAT:\*  
21: /SID52/gcgdata//geneseq//geneseq-emb1/AA2000.DAT:\*  
22: /SID52/gcgdata//geneseq//geneseq-emb1/AA2001.DAT:\*  
23: /SID52/gcgdata//geneseq//geneseq-emb1/AA2002.DAT:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.0	36	16	AA64364
2	193	99.0	36	17	AA98398
3	193	99.0	36	18	AA17011
4	193	99.0	36	19	AA122912
5	193	99.0	36	19	AA122805
6	193	99.0	36	20	AA131955
7	193	99.0	36	20	AA131974
8	193	99.0	36	21	AA152655
9	193	99.0	36	21	AA152688
10	193	99.0	36	21	AA152818

11	193	99.0	36	21	AA14533	HIV-1 isolate LAI
12	193	99.0	36	21	AA188655	Core polypeptide f
13	193	99.0	36	21	AA188729	Core polypeptide f
14	193	99.0	36	21	AA189135	Core polypeptide f
15	193	99.0	36	21	AA189136	Core polypeptide f
16	193	99.0	36	21	AA189242	Core polypeptide f
17	193	99.0	36	21	AA189424	Core polypeptide f
18	193	99.0	36	21	AA189692	Core polypeptide f
19	193	99.0	36	21	AA189735	Core polypeptide f
20	193	99.0	36	21	AA189775	Core polypeptide f
21	193	99.0	36	21	AA189892	Core polypeptide f
22	193	99.0	36	21	AA189983	Core polypeptide f
23	193	99.0	36	21	AA189999	Core polypeptide f
24	193	99.0	36	22	AA170179	HIV-1 gp41 peptide
25	193	99.0	36	22	AA170741	HXB2 transmembrane
26	193	99.0	36	22	AA182961	Anti-HIV peptide T
27	193	99.0	36	22	AA187039	HIV-1 gp41 peptide
28	193	99.0	36	22	AA180024	HIV-1 gp41 peptide
29	193	99.0	36	22	AA180087	Biotin-labeled HI
30	193	99.0	36	22	AA180088	Viral DP178/107-11
31	193	99.0	36	22	AA180494	Viral DP178/107-11
32	193	99.0	36	22	AA180495	Viral DP178/107-11
33	193	99.0	36	22	AA180600	RVF F1 protein, DPL
34	193	99.0	36	22	AA180626	Viral DP178/107-11
35	193	99.0	36	22	AA180627	Viral DP178/107-11
36	193	99.0	36	22	AA180628	Viral DP178/107-11
37	193	99.0	36	22	AA180832	Viral DP178/107-11
38	193	99.0	36	22	AA180100	Viral DP178/107-11
39	193	99.0	36	22	AA180143	Viral DP178/107-11
40	193	99.0	36	22	AA180185	Fluorescein-labeled
41	193	99.0	36	22	AA180191	Viral DP178/107-11
42	193	99.0	36	22	AA180192	Viral DP178/107-11
43	193	99.0	36	22	AA1801414	Viral DP178/107-11
44	193	99.0	36	22	AA1801488	Viral core polypep
45	193	99.0	36	22	AA1801970	Viral core polypep

## ALIGNMENTS

RESULT 1  
AA64364  
ID AA64364 standard; Peptide: 36 AA.  
XX  
AC AA64364;  
XX  
DP 24-AUG-1995 (first entry)  
XX  
DE DP-178 derived from HIV-1 isolate LAI has antiviral activity.  
XX  
KW antiviral activity: DP-178; DP-107; diagnostic: HIV-1LAI;  
KW human immunodeficiency virus; transmembrane protein; gp41;  
KW alpha helix; leucine zipper; DP-185.  
XX  
OS Synthetic.  
XX  
FH Key  
FT Modified-site 1 Location/Qualifiers  
FT /note= "optionally has an amino, acetyl,  
FT 9-fluorenylmethoxy-carbonyl, hydrophobic or  
FT macromolecular carrier gp. attached"  
FT  
FT Modified-site 38  
FT /note= "optionally has a carboxyl, amido, hydrophobic  
FT or macromolecular carrier gp. attached"

MO9428920-A.  
22-DEC-1994.  
07-JUN-1994; 94MO-US05739.  
07-JUN-1993; 93US-0073028.

PA (UYDU-) UNIV DUKE.  
 XX  
 PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Peteway SR, Wild CT;  
 XX  
 DR WPI: 1995-036105/05.  
 XX  
 PT Computer search generated synthetic peptides - are inhibitors of  
 PT HIV transmission  
 XX  
 PS Claim 11; Page 132; 182pp; English.  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-598) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibits transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 16; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSIHSLSIESQNOEKNEDELLELDKWSLWNMF 36  
 DB 1 YTSLSHSLSIESQNOEKNEDELLELDKWSLWNMF 36  
 RESULT 2  
 ID AAR98398 standard; peptide: 36 AA.  
 AC AAR98398;  
 XX  
 DT 17-FEB-1997 (first entry)  
 DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.  
 XX  
 KM Antifusogenic activity; antiviral capability; coiled-coil peptide;  
 KM ALLMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;  
 KM Influenza virus; hepatitis B virus.  
 XX  
 XX Human immunodeficiency virus type 1.  
 PN WO9619495-A1.  
 PD 27-JUN-1996.  
 XX  
 PF 20-DEC-1995; 95WO-US16733.  
 XX  
 PR 06-JUN-1995; 95US-0470896.  
 PR 20-DEC-1994; 94US-0360107.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
 PI Matthews TJ, Peteway SR, Wild CT;  
 XX  
 DR WPI: 1996-309517/31.  
 XX  
 XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX  
 PS Disclosure: Fig 1; 471pp; English.

CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALLMOT15,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, Influenza virus, or  
 CC hepatitis B virus, to a cell.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 17; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSIHSLSIESQNOEKNEDELLELDKWSLWNMF 36  
 DB 1 YTSLSHSLSIESQNOEKNEDELLELDKWSLWNMF 36  
 RESULT 3  
 ID AAM17011 standard; peptide: 36 AA.  
 AC AAM17011;  
 XX  
 DT 30-JUN-1997 (first entry)  
 DE HIV-1 derived peptide useful for treatment of HIV infection.  
 XX  
 KM HIV, SIV: human, simian immunodeficiency virus; glycoprotein 41;  
 KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
 KM replication; transmission.  
 XX  
 OS Human immunodeficiency virus type 1 LAI isolate.  
 XX  
 PN WO9640191-A1.  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US09499.  
 XX  
 PR 07-JUN-1995; 95US-0481957.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PA Johnson RM, Lambert DM;  
 XX  
 DR WPI: 1997-099886/09.  
 XX  
 PT Compns. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.  
 XX  
 PS Claim 2; Figure 1; 84pp; English.  
 XX  
 CC AAM17011 represents a peptide designated DP-178, a peptide derived  
 CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
 CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
 CC derivatives are used in combination with a therapeutic agent, e.g. a  
 CC reverse transcriptase, viral protease, cytokine, glycosylation or viral  
 CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
 CC by inhibiting viral replication or inhibiting transmission. They may  
 CC also be used in vaccines for protecting against HIV infection.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 18; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSIHSLSIESQNOEKNEDELLELDKWSLWNMF 36  
 DB 1 YTSLSHSLSIESQNOEKNEDELLELDKWSLWNMF 36



## RESULT 4

AAV22912  
ID AAV22912 standard; Peptide: 36 AA.  
XX  
AC AAV22912;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 108 from WO9820036.  
XX  
KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
MO9820036-A1.  
XX  
PD 14-MAY-1998.  
XX  
PF 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Braisted A, Judice JK, McDowell RS, Pheian JC, Starovasnik MA;  
PI Wells JA;  
XX  
DR WPI: 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on terminal of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure: Page 233-234; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SO Sequence 36 AA:

Query Match 99.0%; Score 193; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,1e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

0Y 1 YTSIHSILIESONQOEKNEDELLELDKWSLWNMF 36  
Db 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36

## RESULT 5

AAV22805  
ID AAV22805 standard; Peptide: 36 AA.  
XX  
AC AAV22805;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 1 from WO9820036.  
XX  
KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
MO9820036-A1.  
XX  
PD 14-MAY-1998.  
XX  
PF 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Braisted A, Judice JK, McDowell RS, Pheian JC, Starovasnik MA;  
PI Wells JA;  
XX  
DR WPI: 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on terminal of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure: Page 143-144; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SO Sequence 36 AA:

Query Match 99.0%; Score 193; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,1e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

0Y 1 YTSIHSILIESONQOEKNEDELLELDKWSLWNMF 36  
Db 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36

RESULT 6  
 AAY31955  
 ID AAY31955 standard; Peptide: 36 AA.  
 AC AAY31955;  
 DT 21-DEC-1999 (first entry)  
 DE Synthetic peptide T-20 (DP-178).  
 XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 FH Key  
 FT Modified-site 1 Location/Qualifiers  
 FT Modified-site /note= "N-terminal acetyl"  
 FT Modified-site 36  
 XX Modified-site /note= "C-terminal amide"  
 XX  
 PN W09948513-A1.  
 PD 30-SEP-1999.  
 XX  
 PF 22-MAR-1999; 99WO-US06230.  
 XX  
 PR 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PI Kang M, Bray B, Lichy M, Mader C, Merutka G;  
 DR WPI: 1999-591038/50.  
 PT Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides  
 XX  
 PS Claim 1; Page 102; 120pp; English.  
 XX  
 CC The present sequence represents an N- and C-terminal modified  
 CC peptide, designated T-20 (or DP-178), corresponding to amino acids  
 CC 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.  
 CC The invention relates to methods for the synthesis of peptides,  
 CC in particular T-20 and T-20-like peptides. The method involves  
 CC synthesizing specific side-chain protected peptide fragment  
 CC intermediates of T-20 or a T-20-like peptide on a solid support,  
 CC coupling the protected fragments in solution to form a protected  
 CC T-20 or T-20-like peptide, followed by deprotection of the side  
 CC chains to yield the final T-20 or T-20-like peptide. The invention  
 CC also relates to individual peptide fragments (see AAY31956-73) which  
 CC act as intermediates in the synthesis of peptides of interest (e.g.  
 CC T-20), and to particular groups of peptide fragments which act as  
 CC intermediates in the synthesis of the peptide of interest. The  
 CC method allows for the large scale, economical production of high  
 CC purity peptides.  
 CC  
 SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6,1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ID AAY31974 standard; Peptide: 36 AA.  
 XX  
 AC AAY31974;  
 XX  
 DT 21-DEC-1999 (first entry)  
 DE HIV-1 LAI gp41 T-20 peptide.  
 XX  
 KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W09948513-A1.  
 PD 30-SEP-1999.  
 XX  
 PF 22-MAR-1999; 99WO-US06230.  
 XX  
 PR 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PI Kang M, Bray B, Lichy M, Mader C, Merutka G;  
 DR WPI: 1999-591038/50.  
 PT Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides  
 XX  
 PS Disclosure: Page 9; 120pp; English.  
 XX  
 CC The present sequence represents a peptide, designated T-20 (or  
 CC DP-178), that corresponds to amino acids 638-673 of the  
 CC transmembrane protein gp41 of HIV-1 LAI isolate. The invention  
 CC relates to methods for the synthesis of peptides, in particular  
 CC C- and N-terminal modified T-20 (see AAY31955) and T-20-like peptides.  
 CC The method involves synthesizing specific side-chain protected  
 CC peptide fragment intermediates (see AAY31956-73) of T-20 or a  
 CC T-20-like peptide on a solid support, coupling the protected  
 CC fragments in solution to form a protected T-20 or T-20-like peptide,  
 CC followed by deprotection of the side chains to yield the final T-20  
 CC or T-20-like peptide. The invention also relates to individual  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC peptides of interest (e.g. T-20), and to particular groups of  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC the peptide of interest. The method allows for the large scale,  
 CC economical production of high purity peptides.  
 CC  
 SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6,1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 AAB52655  
 ID AAB52655 standard; Peptide: 36 AA.  
 AC AAB52655;  
 XX  
 DT 23-FEB-2001 (first entry)  
 DE T20/DP178 peptide fragment #33.  
 XX  
 KW Antiflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemottractant.

XX OS Human immunodeficiency virus type 1.  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR MPI; 2000-656493/63.  
XX PT Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX antagionist is used to modulate inflammation -  
XX Claim 12; Page 24; 148pp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
XX CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
XX CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
XX CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
XX CC interacts with members of the formyl peptide receptor (FPR) family and  
XX CC thereby up-regulates an inflammatory response, and acts as a potent  
XX CC chemoattractant and activator of human peripheral blood phagocytes  
XX CC (but not T cells). The present peptide can be used to modulate an  
XX CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
SQ Query Match 99.0%; Score 193; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,1e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSIIHSLIESQNOOEKNEELLELDKWSLWNWF 36  
Db 1 YTSIIHSLIESQNOOEKNEELLELDKWSLWNWF 36  
RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide; 36 AA.  
XX AAB52688;  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #66.  
XX PA Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX KM chemoattractant.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR MPI; 2000-656493/63.

XX OS Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR MPI; 2000-656493/63.  
XX PT Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX antagionist is used to modulate inflammation -  
XX Claim 12; Page 25; 148pp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
XX CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
XX CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
XX CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
XX CC interacts with members of the formyl peptide receptor (FPR) family and  
XX CC thereby up-regulates an inflammatory response, and acts as a potent  
XX CC chemoattractant and activator of human peripheral blood phagocytes  
XX CC (but not T cells). The present peptide can be used to modulate an  
XX CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
SQ Query Match 99.0%; Score 193; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,1e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSIIHSLIESQNOOEKNEELLELDKWSLWNWF 36  
Db 1 YTSIIHSLIESQNOOEKNEELLELDKWSLWNWF 36  
RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide; 36 AA.  
XX AAB52818;  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #97.  
XX PA Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX KM chemoattractant.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR MPI; 2000-656493/63.  
XX PT Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX antagionist is used to modulate inflammation -  
XX Claim 14; Page 40; 148pp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
XX CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
XX CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
XX CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
XX CC interacts with members of the formyl peptide receptor (FPR) family and  
XX CC thereby up-regulates an inflammatory response, and acts as a potent  
XX CC chemoattractant and activator of human peripheral blood phagocytes  
XX CC (but not T cells). The present peptide can be used to modulate an  
XX CC inflammatory response in a subject.

XX Sequence 36 AA;  
 SQ Query Match 99.0%; Score 193; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36  
 |||:|||||  
 Db 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36

RESULT 11  
 AABI4533  
 ID AABI4533 standard; peptide; 36 AA.  
 AC AABI4533;  
 XX  
 DT 24-NOV-2000 (first entry)

HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).  
 HIV-1; gp41 C-helical domain;  
 KM gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KM core 6-helix bundle; viral entry inhibition; immunogenic;  
 KM antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KM envelope glycoprotein; prophylaxis; therapy.  
 XX  
 OS Human immunodeficiency virus type 1.  
 PN WO200040616-A1.  
 PD 13-JUL-2000.  
 XX  
 PF 10-JAN-2000; 2000MO-US00456.  
 XX  
 PR 08-JAN-1999; 99US-0115404.  
 PR 07-JAN-2000; 2000US-0480336.  
 XX  
 PA (WILD/) WILD C T.  
 PA (WEIS/) WEISS C D.  
 XX  
 PI WILD CT, Weiss CD;  
 PI  
 DR WPI; 2000-465959/40.  
 XX  
 DR  
 PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -  
 PS Claim 13; Page 12; 97pp; English.

Sequences AABI4533-BI4534 and AABI4569-BI4602 represent specifically  
 CC claimed peptides derived from the C-helical domain of the gp41  
 CC envelope glycoprotein from a variety of HIV-1 isolates. The invention  
 CC relates to raising a neutralising antibody response to a broad spectrum  
 CC of HIV (human immunodeficiency virus) strains and isolates, comprising  
 CC the administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the process  
 CC of viral entry into host cells. Such peptides can correspond to or  
 CC mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly a  
 CC combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can  
 CC be alternately linked together to form a peptide which mimics the  
 CC core 6-helix bundle. Administration of the peptide(s) generates a  
 CC humoral response, with the production of antibodies against gp41  
 CC structures involved in viral entry. As these portions of gp41 are well  
 CC conserved, such antibodies may be effective against a broad range of

CC HIV strains and isolates. The peptide compositions may be administered  
 CC as a prophylactic or therapeutic vaccine to generate antibodies which  
 CC reduce or inhibit the ability of HIV to infect uninfected cells. A  
 CC composition comprising polyclonal or monoclonal antibodies can be  
 CC administered to reduce HIV infection of uninfected cells. Antibodies  
 CC raised against entry-relevant gp41 structures may also be used  
 CC therapeutically and as tools to further elucidate the mechanism of HIV  
 CC cell entry.  
 XX  
 SQ Sequence 36 AA;  
 Query Match 99.0%; Score 193; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36  
 |||:|||||  
 Db 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36

RESULT 12  
 AAY88665  
 ID AAY88665 standard; peptide; 36 AA.  
 AC AAY88665;  
 XX  
 DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 20.  
 DE  
 XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KM anti-fusogenic; differentiation factor; interleukin; interferon;  
 KM colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 OS  
 PN WO9959615-A1.  
 PD 25-NOV-1999.  
 XX  
 PF 20-MAY-1999; 99MO-US11219.  
 PF  
 PR 20-MAY-1998; 98US-0082279.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PA  
 PI Barney S, Guthrie KI, Merutka G, Anver MK, Lambert DM;  
 PI  
 DR WPI; 2000-136792/12.  
 XX  
 DR  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 PS Disclosure; Page 21; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX Sequence 36 AA:

Query Match 99.0%; Score 193; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6, 1e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIEESONQOEKNEQLLELDKMASLWNMF 36  
1 YTSIIHSLIEESONQOEKNEQLLELDKMASLWNMF 36

RESULT 13

AA8729  
ID AAY88729 standard; peptide; 36 AA.

AC AAY88729;

DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 84.

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.

Unidentified.

MO9959615-A1.

25-NOV-1999.

20-MAY-1999; 99WO-US11219.

20-MAY-1998; 98US-0082279.

(TRIM-) TRIMERIS INC.

Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

WPI; 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties  
comprises enhancer sequence -

Disclosure; Page 22; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide  
sequence linked to core polypeptides. The enhancer polypeptides are  
derived from various retroviral envelope (gp41) protein sequences,  
especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
pharmacokinetic properties such as increasing the half-life of any core  
polypeptide that they are linked to. The core polypeptides are any  
polypeptide that may be introduced into a living system and that can  
function as a pharmacologically useful peptide for the treatment or  
prevention of a disease. The core polypeptides are bioactive peptides  
selected from a growth factor, cytokine, differentiation factor,  
interleukin, interferon, colony stimulating factor, hormone or  
angiogenic factor. The peptides of the invention can be used for  
inhibiting viral infection and can be used in anti-viral and  
anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
polypeptide fragments that can be used in the invention. Some sequences  
among those indicated also comprise enhancer fragments at terminal ends  
and form hybrid polypeptides.

Sequence 36 AA:

Query Match 99.0%; Score 193; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6, 1e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIEESONQOEKNEQLLELDKMASLWNMF 36

DB 1 YTSIIHSLIEESONQOEKNEQLLELDKMASLWNMF 36

RESULT 14

AA89135  
ID AAY89135 standard; peptide; 36 AA.

AC AAY89135;

DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 573.

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.

Unidentified.

MO9959615-A1.

25-NOV-1999.

20-MAY-1999; 99WO-US11219.

20-MAY-1998; 98US-0082279.

(TRIM-) TRIMERIS INC.

Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

WPI; 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties  
comprises enhancer sequence -

Disclosure; Page 30; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide  
sequence linked to core polypeptides. The enhancer polypeptides are  
derived from various retroviral envelope (gp41) protein sequences,  
especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
pharmacokinetic properties such as increasing the half-life of any core  
polypeptide that they are linked to. The core polypeptides are any  
polypeptide that may be introduced into a living system and that can  
function as a pharmacologically useful peptide for the treatment or  
prevention of a disease. The core polypeptides are bioactive peptides  
selected from a growth factor, cytokine, differentiation factor,  
interleukin, interferon, colony stimulating factor, hormone or  
angiogenic factor. The peptides of the invention can be used for  
inhibiting viral infection and can be used in anti-viral and  
anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
polypeptide fragments that can be used in the invention. Some sequences  
among those indicated also comprise enhancer fragments at terminal ends  
and form hybrid polypeptides.

Sequence 36 AA:

Query Match 99.0%; Score 193; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6, 1e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIEESONQOEKNEQLLELDKMASLWNMF 36  
1 YTSIIHSLIEESONQOEKNEQLLELDKMASLWNMF 36

RESULT 15

AA89136  
ID AAY89136 standard; peptide; 36 AA.

AC AAY89136;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Core polypeptide fragment T No. 574.  
 XX  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN W09595615-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 20-MAY-1999; 99WO-US11219.  
 XX  
 PF 20-MAY-1998; 98US-0082279.  
 XX  
 (TRIM-) TRIMERIS INC.  
 XX  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX  
 DR WPI; 2000-136792/12.  
 XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 XX  
 PS Disclosure; Page 30; 124pp; English.  
 XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.  
 SU Sequence 36 AA;  
 Query Match 99.0%; Score 193; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred No. 6, 1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSIIHSLSIESQNOQEKNEQELLELDKVASLWNMF 36  
 |||:|||||  
 DB 1 YTSIIHSLSIESQNOQEKNEQELLELDKVASLWNMF 36

Search completed: May 16, 2003, 11:12:05  
 Job time : 33.4578 secs

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Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-535

Perfect score: 197  
Sequence: 1 YTNLIHSLEESQNOEKNEDELLDKWASLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	97.5	36	9	US-09-874-475-16
2	192	97.5	36	9	US-10-116-797-1
3	192	97.5	36	9	US-09-493-346-1
4	192	97.5	36	10	US-09-796-202-10
5	192	97.5	36	10	US-09-779-451-5
6	192	97.5	36	10	US-09-834-628-1
7	192	97.5	36	10	US-09-854-816-1
8	192	97.5	36	10	US-09-854-816-108
9	192	97.5	37	9	US-09-848-616-176
10	192	97.5	46	10	US-09-779-451-41
11	192	97.5	56	10	US-09-779-451-4
12	192	97.5	177	9	US-10-040-349B-2
13	192	97.5	221	9	US-10-059-271-84
14	192	97.5	232	9	US-10-059-271-81
15	192	97.5	254	9	US-10-059-271-82
16	192	97.5	256	9	US-10-059-271-97
17	192	97.5	268	10	US-09-854-816-16
18	192	97.5	268	10	US-09-854-816-17
19	192	97.5	268	10	US-09-854-816-18

20	192	97.5	344	9	US-10-040-349B-1	Sequence 1, Appl
21	192	97.5	345	9	US-10-026-741-49	Sequence 49, Appl
22	192	97.5	345	10	US-09-779-451-8	Sequence 8, Appl
23	192	97.5	391	9	US-10-059-271-93	Sequence 93, Appl
24	192	97.5	519	10	US-09-756-551A-8	Sequence 8, Appl
25	192	97.5	853	9	US-10-003-035-33	Sequence 33, Appl
26	192	97.5	856	10	US-09-476-242-1	Sequence 103, App
27	192	97.5	861	9	US-10-026-741-103	Sequence 53, Appl
28	192	97.5	1101	9	US-10-003-035-53	Sequence 55, Appl
29	192	97.5	1186	9	US-10-003-035-55	Sequence 1, Appl
30	189	95.9	36	10	US-09-912-824-1	Sequence 19, Appl
31	189	95.9	268	10	US-09-854-816-13	Sequence 26, Appl
32	188	95.4	268	10	US-09-854-816-26	Sequence 4, Appl
33	188	95.4	619	10	US-09-891-609-4	Sequence 2, Appl
34	188	95.4	646	10	US-09-891-609-2	Sequence 2, Appl
35	188	95.4	847	10	US-09-476-242-2	Sequence 94, Appl
36	186	94.4	1231	9	US-10-059-271-94	Sequence 13, Appl
37	184	93.4	268	10	US-09-854-816-13	Sequence 50, Appl
38	183	92.9	233	10	US-09-854-816-50	Sequence 9, Appl
39	183	92.9	268	10	US-09-854-816-9	Sequence 12, Appl
40	183	92.9	269	10	US-09-854-816-12	Sequence 38, Appl
41	182	92.4	267	10	US-09-854-816-38	Sequence 41, Appl
42	182	92.4	268	10	US-09-854-816-41	Sequence 43, Appl
43	182	92.4	269	10	US-09-854-816-43	Sequence 46, Appl
44	182	92.4	269	10	US-09-854-816-46	Sequence 109, App
45	181	91.9	46	10	US-09-854-816-109	

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
; Sequence 16, Application US/09874475  
; Publication No. US20020182592A1  
; GENERAL INFORMATION:  
; APPLICANT: Petropoulos, Christos J.  
; APPLICANT: Parkin, Neil T.  
; APPLICANT: Whitcomb, Jeanette  
; APPLICANT: Huang, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
; FILE REFERENCE: 2793/65166  
; CURRENT APPLICATION NUMBER: US/09/874,475  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16  
  
Query Match 97.5%; Score 192; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YTNLIHSLEESQNOEKNEDELLDKWASLWNMF 36  
DB 1 YTNLIHSLEESQNOEKNEDELLDKWASLWNMF 36  
  
RESULT 2  
US-10-116-797-1  
; Sequence 1, Application US/10116797  
; Publication No. US20030044411A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen, William C.  
; APPLICANT: Madden, Paul J.  
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
; FILE REFERENCE: 64672-A  
; CURRENT APPLICATION NUMBER: US/10/116,797  
; CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 97.5%: Score 192; DB 9; Length 36;  
Best Local Similarity 97.2%: Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
||:|||||  
DB 1 YTSLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:  
APPLICANT: Olson, William C  
APPLICANT: Madden, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
TITLE OF INVENTION: Infection  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 97.5%: Score 192; DB 9; Length 36;  
Best Local Similarity 97.2%: Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
||:|||||  
DB 1 YTSLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

ULT 4  
US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SOLIDATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 97.5%: Score 192; DB 10; Length 36;  
Best Local Similarity 97.2%: Pred. No. 2.2e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
||:|||||  
DB 1 YTSLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US2002009452A1  
GENERAL INFORMATION:  
APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.030003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 97.5%: Score 192; DB 10; Length 36;  
Best Local Similarity 97.2%: Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
||:|||||  
DB 1 YTSLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 6  
US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US20020119922A1  
GENERAL INFORMATION:  
APPLICANT: YO, YEON GYU  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 97.5%: Score 192; DB 10; Length 36;  
Best Local Similarity 97.2%: Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36  
||:|||||  
DB 1 YTSLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 36



```

RESULT 7
US-09-854-816-1
: Sequence 1, Application US/09854816
: Patent No. US20020151473A1
: GENERAL INFORMATION:
: APPLICANT: Andrew C. Braisted
: J. Kevin Judice
: Robert S. McDowell
: J. Christopher Phelan
: Melissa A. Starovasnik
: James A. Wells
: TITLE OF INVENTION: Constrained Helical Peptides and Methods of
: Making Same
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/854,816
: FILING DATE: 15-May-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/965,056
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, Phd., Timothy E.
: REGISTRATION NUMBER: 36,700
: REFERENCE/DOCKET NUMBER: P1005R2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-8674
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 36 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: MOLECULE TYPE: DP178
: SEQUENCE DESCRIPTION: SEQ ID NO: 1:
9-854-816-1
Query Match 97.5%; Score 192; DB 10; Length 36;
Best Local Similarity 97.2%; Pred. No. 2.2e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

Y 1 YTNLIHSLIEESQNOQEKNEQELFLIDRWASLWNF 36
||:|||||
1 YTSLIHSLIEESQNOQEKNEQELFLIDRWASLWNF 36

RESULT 8
US-09-854-816-108
: Sequence 108, Application US/09854816
: Patent No. US20020151473A1
: GENERAL INFORMATION:
: APPLICANT: Andrew C. Braisted
: J. Kevin Judice
: Robert S. McDowell
: J. Christopher Phelan
: Melissa A. Starovasnik
: James A. Wells
: TITLE OF INVENTION: Constrained Helical Peptides and Methods of
: Making Same
: NUMBER OF SEQUENCES: 113

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1	YTNLIHSLEESQNOOEKNEDELLELDKVASLWNNF	36	97.5%	Score 192;	DB 10;	Length 36;	0;	Gaps 0;
2	1	YTNLIHSLEESQNOOEKNEDELLELDKVASLWNNF	36	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;	
3	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
4	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
5	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
6	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
7	Query Match	Best Local Similarity	97.5%;	Score 192;	DB 10;	Length 36;	0;	Gaps 0;
8	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
9	US-09-848-616-176	SEQUENCE 176, Application US/09848616						
10	Publication No. US20030054010A1	GENERAL INFORMATION:						
11	APPLICANT: Seibel, Peter	APPLICANT: Dunant, Nicolas						
12	APPLICANT: Bachmann, Martin	APPLICANT: Tissot, Alain						
13	APPLICANT: Lechner, Franziska	TITLE OF INVENTION: Molecular Antigen Array						
14	FILE REFERENCE: 1700 0180002	CURRENT FILING DATE: 2001-05-05						
15	CURRENT FILING DATE: 2001-05-05	NUMBER OF SEQ ID NOS: 186						
16	SOFTWARE: PatentIn Ver. 2.1	SEQ ID NO 176						
17	LENGTH: 37	TYPE: PRT						
18	ORGANISM: Artificial Sequence	FEATURE:						
19	OTHER INFORMATION: DP178c peptide	US-09-848-616-176						
20	Query Match	Best Local Similarity	97.5%;	Score 192;	DB 9;	Length 37;	0;	Gaps 0;
21	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
22	1	YTNLIHSLEESQNOOEKNEDELLELDKVASLWNNF	36	97.2%;	Pred No. 2.3e-16;	Indels 0;	Gaps 0;	
23	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
24	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
25	Query Match	Best Local Similarity	97.5%;	Score 192;	DB 10;	Length 36;	0;	Gaps 0;
26	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
27	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
28	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
29	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
30	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
31	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
32	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
33	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
34	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
35	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
36	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
37	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
38	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
39	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
40	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
41	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
42	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
43	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
44	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
45	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
46	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
47	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
48	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
49	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
50	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
51	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
52	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
53	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
54	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						
55	Query Match	Best Local Similarity	97.2%;	Pred No. 2.2e-16;	Indels 0;	Gaps 0;		
56	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
57	US-09-854-816-108	SEQUENCE DESCRIPTION: SEQ ID NO: 108;						

Db 2 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNNF 37

RESULT 10

US-09-779-451-41

Sequence 41, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: WILD, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT APPLICATION NUMBER: US/09/779,451

PRIOR FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 46

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match

Best Local Similarity 97.5%; Score 192; DB 10; Length 46;

Best Local Similarity 97.2%; Pred. No. 2,9e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIESQNOQEKNEQELLELDKWSLWNNF 36

Db 11 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNNF 46

RESULT 11

US-09-779-451-4

Sequence 4, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: WILD, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT APPLICATION NUMBER: US/09/779,451

PRIOR FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match

Best Local Similarity 97.5%; Score 192; DB 10; Length 56;

Best Local Similarity 97.2%; Pred. No. 3.5e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIESQNOQEKNEQELLELDKWSLWNNF 36

Db 16 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNNF 51

RESULT 12

US-10-040-349B-2

Sequence 2, Application US/10040349B

Publication No. US20030082521A1

GENERAL INFORMATION:

APPLICANT: Brasseur, Robert

APPLICANT: Charlotiaux, Benoit

APPLICANT: Chevallier, Michel

APPLICANT: El Habib, Raphaelle

APPLICANT: Krell, Tino

TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

FILE REFERENCE: 01-078-A

CURRENT APPLICATION NUMBER: US/10/040,349B

CURRENT FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)..(177)

OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match

Best Local Similarity 97.5%; Score 192; DB 9; Length 177;

Best Local Similarity 97.2%; Pred. No. 1.2e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIESQNOQEKNEQELLELDKWSLWNNF 36

Db 104 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNNF 139

RESULT 13

US-10-059-271-84

Sequence 84, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

FILE REFERENCE: ALBRE-22

CURRENT APPLICATION NUMBER: US/10/059,271

PRIOR FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: DE 101 06 295

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide

US-10-059-271-84

Query Match

Best Local Similarity 97.5%; Score 192; DB 9; Length 221;

Best Local Similarity 97.2%; Pred. No. 1.5e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIESQNOQEKNEQELLELDKWSLWNNF 36

Db 131 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNNF 166

RESULT 14

US-10-059-271-81

Sequence 81, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

;; TITLE OF INVENTION: BEING IMMOBILIZED  
;; FILE REFERENCE: ALBRE-22  
;; CURRENT APPLICATION NUMBER: US/10/059,271  
;; CURRENT FILING DATE: 2002-01-31  
;; PRIOR APPLICATION NUMBER: DE 101 06 295  
;; PRIOR FILING DATE: 2001-02-02  
;; NUMBER OF SEQ ID NOS: 97  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 81  
;; LENGTH: 232  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
US-10-059-271-81

Query Match 97.5%; Score 192; DB 9; Length 232;  
Best Local Similarity 97.2%; Pred. No. 1.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTNLIHSLSIESONQOEKNEQELLELDKWSLNNWF 36  
11:|||||  
Db 144 YTSLSHSLSIESONQOEKNEQELLELDKWSLNNWF 179

RESULT 15  
US-10-059-271-82  
;; Sequence 82, Application US/10059271  
;; Publication No. US20030082208A1  
;; GENERAL INFORMATION:  
;; APPLICANT: REPKKE, HEINRICH  
;; APPLICANT: BUDE, ECKHARD  
;; APPLICANT: NICOLAUS, STEFAN  
;; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
;; FILE REFERENCE: ALBRE-22  
;; CURRENT APPLICATION NUMBER: US/10/059,271  
;; CURRENT FILING DATE: 2002-01-31  
;; PRIOR APPLICATION NUMBER: DE 101 06 295  
;; PRIOR FILING DATE: 2001-02-02  
;; NUMBER OF SEQ ID NOS: 97  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 82  
;; LENGTH: 254  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
US-10-059-271-82

Query Match 97.5%; Score 192; DB 9; Length 254;  
Best Local Similarity 97.2%; Pred. No. 1.7e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLSIESONQOEKNEQELLELDKWSLNNWF 36  
11:|||||  
Db 166 YTSLSHSLSIESONQOEKNEQELLELDKWSLNNWF 201

Search completed: May 16, 2003, 12:10:24  
Job time : 15.759 secs

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GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-535  
Perfect score: 197  
Sequence: 1 YTNLHSLIESONQOEKNEDELIDKRWASLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCtus.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	97.5	36	1 US-08-073-028-1	Sequence 1, Appli
2	192	97.5	36	3 US-08-486-099-1	Sequence 1, Appli
3	192	97.5	36	3 US-09-071-877-1	Sequence 1, Appli
4	192	97.5	36	3 US-08-360-107A-1	Sequence 1, Appli
5	192	97.5	36	3 US-08-484-223B-1	Sequence 1, Appli
6	192	97.5	36	3 US-08-919-597-1	Sequence 1, Appli
7	192	97.5	36	3 US-08-475-668A-1	Sequence 1, Appli
8	192	97.5	36	3 US-08-485-551A-1	Sequence 1, Appli
9	192	97.5	36	3 US-08-471-913A-1	Sequence 1, Appli
10	192	97.5	36	4 US-08-554-616-1	Sequence 1, Appli
11	192	97.5	36	4 US-08-485-264A-1	Sequence 1, Appli
12	192	97.5	36	4 US-09-082-279B-15	Sequence 15, Appli
13	192	97.5	36	4 US-09-082-279B-497	Sequence 497, App
14	192	97.5	36	4 US-09-082-279B-498	Sequence 498, App
15	192	97.5	36	4 US-09-082-279B-603	Sequence 603, App
16	192	97.5	36	4 US-09-082-279B-630	Sequence 630, App
17	192	97.5	36	4 US-09-082-279B-631	Sequence 631, App
18	192	97.5	36	4 US-09-082-279B-705	Sequence 705, App
19	192	97.5	36	4 US-09-082-279B-834	Sequence 834, App
20	192	97.5	36	4 US-09-082-279B-1076	Sequence 1076, App
21	192	97.5	36	4 US-09-082-279B-1121	Sequence 1121, App
22	192	97.5	36	4 US-09-082-279B-1161	Sequence 1161, App
23	192	97.5	36	4 US-08-965-056-1	Sequence 1, Appli
24	192	97.5	36	4 US-08-965-056-108	Sequence 108, App
25	192	97.5	36	4 US-09-045-920-1	Sequence 1, Appli
26	192	97.5	36	4 US-08-474-349A-1	Sequence 399, App
27	192	97.5	36	4 US-08-474-349A-399	Sequence 399, App

28	192	97.5	36	4 US-08-474-349A-413	Sequence 413, App
29	192	97.5	36	4 US-09-315-304B-15	Sequence 15, Appli
30	192	97.5	36	4 US-09-315-304B-497	Sequence 497, App
31	192	97.5	36	4 US-09-315-304B-498	Sequence 498, App
32	192	97.5	36	4 US-09-315-304B-603	Sequence 603, App
33	192	97.5	36	4 US-09-315-304B-630	Sequence 630, App
34	192	97.5	36	4 US-09-315-304B-631	Sequence 631, App
35	192	97.5	36	4 US-09-315-304B-705	Sequence 705, App
36	192	97.5	36	4 US-09-315-304B-834	Sequence 834, App
37	192	97.5	36	4 US-09-315-304B-1076	Sequence 1076, App
38	192	97.5	36	4 US-09-315-304B-1121	Sequence 1121, App
39	192	97.5	36	4 US-09-315-304B-1161	Sequence 1161, App
40	192	97.5	36	4 US-09-315-304B-1469	Sequence 1469, App
41	192	97.5	36	4 US-09-315-304B-1470	Sequence 1470, App
42	192	97.5	36	4 US-09-315-304B-1486	Sequence 1486, App
43	192	97.5	36	4 US-08-255-208A-1	Sequence 1, Appli
44	192	97.5	37	4 US-09-082-279B-771	Sequence 771, App
45	192	97.5	37	4 US-09-082-279B-775	Sequence 775, App

ALIGNMENTS

RESULT 1  
US-08-073-028-1  
; Sequence 1, Application US/08073028  
; Patent No. 5464933  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-1  
Query Match 97.5%; Score 192; DB 1; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 YTNLHSLIESONQOEKNEDELIDKRWASLWNMF 36  
|||||

Db 1 YTNLIHSLIESQNOEKNEQELLELDKWSIWMNF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmunds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 97.5%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 3.4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTNLIHSLIESQNOEKNEQELLELDKWSIWMNF 36

Db 1 YTNLIHSLIESQNOEKNEQELLELDKWSIWMNF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichty, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Merutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

Db 1 YTNLIHSLIESQNOEKNEQELLELDKWSIWMNF 36

CURRENT APPLICATION NUMBER: US/09/071,877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 36

TYPE: PRT

ORGANISM: Human Immunodeficiency virus

US-09-071-877-1

Query Match 97.5%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 3.4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTNLIHSLIESQNOEKNEQELLELDKWSIWMNF 36

Db 1 YTNLIHSLIESQNOEKNEQELLELDKWSIWMNF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmunds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 97.5%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 3.4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTNLIHSLIESQNOEKNEQELLELDKWSIWMNF 36

Db 1 YTNLHSLIEESONOEKNEDELLELDKWSLWMP 36

RESULT 5  
US-08-484-223B-1  
Sequence 1, Application US/08484223B  
Patent No. 6020459

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 97.5%; Score 192; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLHSLIEESONOEKNEDELLELDKWSLWMP 36  
Db 1 YTNLHSLIEESONOEKNEDELLELDKWSLWMP 36

RESULT 6  
US-08-919-597-1

Sequence 1, Application US/08919597  
Patent No. 6054265

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 97.5%; Score 192; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLHSLIEESONOEKNEDELLELDKWSLWMP 36  
Db 1 YTNLHSLIEESONOEKNEDELLELDKWSLWMP 36

RESULT 7  
US-08-475-668A-1

Sequence 1, Application US/08475668A  
Patent No. 6060065

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNTE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-1

Query Match 97.5% Score 192; DB 3; Length 36;  
Best Local Similarity 97.2% Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONOQEKNEQELLELDKVASLWNWF 36  
1 YTSLSHSLEESONOQEKNEQELLELDKVASLWNWF 36

Db 1 YTSLSHSLEESONOQEKNEQELLELDKVASLWNWF 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNTE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 97.5% Score 192; DB 3; Length 36;  
Best Local Similarity 97.2% Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONOQEKNEQELLELDKVASLWNWF 36  
1 YTSLSHSLEESONOQEKNEQELLELDKVASLWNWF 36

Db 1 YTSLSHSLEESONOQEKNEQELLELDKVASLWNWF 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNTE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 97.5% Score 192; DB 3; Length 36;  
Best Local Similarity 97.2% Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONOQEKNEQELLELDKVASLWNWF 36  
1 YTSLSHSLEESONOQEKNEQELLELDKVASLWNWF 36

Db 1 YTSLSHSLEESONOQEKNEQELLELDKVASLWNWF 36



RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1

Query Match 97.5%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3,4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOEKNEQELLELDKVASLWNMF 36  
DB 1 YTSLIHSLIEESQNOEKNEQELLELDKVASLWNMF 36

RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1

Query Match 97.5%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3,4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOEKNEQELLELDKVASLWNMF 36  
DB 1 YTSLIHSLIEESQNOEKNEQELLELDKVASLWNMF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15

Query Match 97.5%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3,4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOEKNEQELLELDKVASLWNMF 36  
DB 1 YTSLIHSLIEESQNOEKNEQELLELDKVASLWNMF 36

Db 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

## RESULT 13

US-09-082-279B-497

Sequence 497, Application US/09082279B  
Patent No. 6258782

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

Q ID NO 497

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

## Query Match

Best Local Similarity 97.5%; Score 192; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 3.4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36  
DB 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

## RESULT 14

US-09-082-279B-498

Sequence 498, Application US/09082279B

Patent No. 6258782

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 498

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide.

US-09-082-279B-498

## Query Match

Best Local Similarity 97.5%; Score 192; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 3.4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36  
DB 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

RESULT 15  
US-09-082-279B-603

Sequence 603, Application US/09082279B

Patent No. 6258782

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 603

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

## Query Match

Best Local Similarity 97.5%; Score 192; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 3.4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36  
DB 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

Search completed: May 16, 2003, 11:22:12  
Job time : 10.1928 secs

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds

(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-535

Perfect score: 197

Sequence: 1 YTNLHSLIEESQNOEKNEQELLEDKWASLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	97.5	645	15	0993A6 human immun
2	192	97.5	747	15	070607 human immun
3	192	97.5	748	15	070606 human immun
4	192	97.5	752	15	070604 human immun
5	192	97.5	752	15	070605 human immun
6	192	97.5	752	15	070608 human immun
7	192	97.5	851	15	078243 human immun
8	192	97.5	852	15	089797 human immun
9	192	97.5	854	15	085582 human immun
10	192	97.5	854	15	072502 human immun
11	192	97.5	856	15	092877 simian-huma
12	192	97.5	856	15	074599 human immun
13	192	97.5	856	15	074090 human immun
14	188	95.4	122	15	09YX08 human immun
15	188	95.4	684	15	09IK06 human immun
16	188	95.4	854	15	090178 human immun

17	188	95.4	854	15	078705 human immun
18	188	95.4	855	15	09IK00 human immun
19	188	95.4	860	15	09YP43 human immun
20	188	95.4	860	15	09YP50 human immun
21	188	95.4	861	15	09IK05 human immun
22	188	95.4	861	15	09IK04 human immun
23	188	95.4	861	15	09IK03 human immun
24	188	95.4	863	15	09IJ20 human immun
25	188	95.4	863	15	09IJY9 human immun
26	188	95.4	863	15	09IJY8 human immun
27	188	95.4	863	15	09IJY7 human immun
28	188	95.4	863	15	09MUT4 human immun
29	188	95.4	864	15	09YP48 human immun
30	188	95.4	865	15	09IK11 human immun
31	188	95.4	865	15	09IK10 human immun
32	188	95.4	865	15	09IK09 human immun
33	188	95.4	865	15	09IK08 human immun
34	188	95.4	865	15	09IK07 human immun
35	188	95.4	866	15	09IJ24 human immun
36	187	94.9	856	15	090SM7 human immun
37	187	94.9	858	15	071974 human immun
38	187	94.9	859	15	092937 human immun
39	186	94.4	122	15	09YXM9 human immun
40	186	94.4	616	15	0933B0 human immun
41	186	94.4	618	15	0933B2 human immun
42	186	94.4	757	15	090722 human immun
43	186	94.4	848	15	069990 human immun
44	186	94.4	859	15	080863 human immun
45	185	93.9	122	15	09EA89 human immun

## ALIGNMENTS

## RESULT 1

ID 0993A6 PRELIMINARY: PRT; 645 AA.  
AC 0993A6;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4-T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
DR EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW Aids; Coat protein; Envelope protein; Glycoprotein; Polypeptide;  
KW Transmembrane.  
FT NON\_TER 1 1  
SQ SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;

Query Match 97.5%; Score 192; DB 15; Length 645;  
Best Local Similarity 97.2%; Pred. No. 4,9e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLHSLIEESQNOEKNEQELLEDKWASLWNF 36  
DB 607 YTNLHSLIEESQNOEKNEQELLEDKWASLWNF 642

## RESULT 2

ID 070607 PRELIMINARY: PRT: 747 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-LW87-1;

RA MEDLINE-95127297; PubMed-7826699;

RA Relitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,

RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;

RA "Viral variability and serum antibody response in a laboratory worker

RT infected with HIV type 1 (HIV type IIB).";

RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-LW87-1;

RA Mulder K.E.;

RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL: U12034; AAA76669.1; -

DR InterPro: IPR000328; Env\_Gp41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON\_TER 747

FT SEQUENCE 747 AA; 84250 MW; 732E836A52245514 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 747;

Best Local Similarity 97.2%; Pred. No. 5.6e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 633 YTSLSHLSIEESONQOEKNEQLLELDKWSLWNMF 668

QY 1 YTNLSHLSIEESONQOEKNEQLLELDKWSLWNMF 36

DI 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-LW881;

RA MEDLINE-95127297; PubMed-7826699;

RA Relitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,

RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;

RA "Viral variability and serum antibody response in a laboratory worker

RT infected with HIV type 1 (HIV type IIB).";

RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-LW881;

RA Mulder K.E.;

RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.

EMBL: U12032; AAA76668.1; -

DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 748

Query Match 97.5%; Score 192; DB 15; Length 748;  
 Best Local Similarity 97.2%; Pred. No. 5.6e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLSHLSIEESONQOEKNEQLLELDKWSLWNMF 36  
 DB 634 YTSLSHLSIEESONQOEKNEQLLELDKWSLWNMF 669

## RESULT 4

ID 070604 PRELIMINARY: PRT: 752 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-LW851;

RA MEDLINE-95127297; PubMed-7826699;

RA Relitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,

RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;

RA "Viral variability and serum antibody response in a laboratory worker

RT infected with HIV type 1 (HIV type IIB).";

RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-LW851;

RA Mulder K.E.;

RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL: U12030; AAA76666.1; -

DR InterPro: IPR000328; Env\_Gp41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.

FT NON\_TER 752

FT SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 97.5%; Score 192; DB 15; Length 752;

Best Local Similarity 97.2%; Pred. No. 5.7e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 638 YTSLSHLSIEESONQOEKNEQLLELDKWSLWNMF 673

QY 1 YTNLSHLSIEESONQOEKNEQLLELDKWSLWNMF 36

DI 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)

DE Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_Taxid=11676;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U12031; AAA76667.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 97.5%; Score 192; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 5.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 638 YTSLIHSLEESONOEKNEDELLELDKWSLWMP 673

RESULT 6  
 Q70608 PRELIMINARY; PRT; 752 AA.  
 AC 070608;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U12035; AAA76670.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA; 84780 MW; 708672A2DC0E8F8 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 5.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 638 YTSLIHSLEESONOEKNEDELLELDKWSLWMP 673

DB 638 YTSLIHSLEESONOEKNEDELLELDKWSLWMP 673

RESULT 7  
 Q78243 PRELIMINARY; PRT; 851 AA.  
 AC 078243;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Env polyprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai O.,  
 RA Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 chronically infected HUT-78 cellular clone."  
 RL J. Viral Diseases 14:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federic M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Macchi B., Mangiano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 producer clones from HUT-78 infected with a patient HIV isolate."  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Borsetti A., Saglio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 productive clone."  
 RT Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL; Z11530; CAA7628.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 6.4e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 633 YTSLIHSLEESONOEKNEDELLELDKWSLWMP 668

RESULT 8  
 Q89797 PRELIMINARY; PRT; 852 AA.  
 AC 089797;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RT "Viral variability and serum antibody response in a laboratory worker

Query Match 97.5%; Score 192; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 6.4e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RT Infected with HIV type 1 (HTLV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM90-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12053; AAA76685.1;  
 DR EMBL: U12036; AAA76671.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR Pfam: Coat protein; Envelope protein; Glycoprotein; Polypotein;  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;  
 KW Transmembrane.  
 SO SEQUENCE 852 AA; 96347 MW; 4E865229DAEB33CF CRC64;

Query Match 97.5%; Score 192; DB 15; Length 852;  
 Best Local Similarity 97.2%; Pred. No. 6.4e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTNLHSLIEESONOQEKNEDELLELDKWSLWNF 36  
 11:|||||  
 Db 634 YTSLSHSLIEESONOQEKNEDELLELDKWSLWNF 669

RESULT 9  
 ID 085582 PRELIMINARY; PRT; 854 AA.  
 AC 085582;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Envelope polypeptide.  
 GN ENV.  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone."  
 RL J. Virol. 59:284-291(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E.; Buckler-White A.J.; Willey R.L.; McCoy J.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-92219406; PubMed-1373204;  
 RA Dai L.C.; Littau R.; Takahashi K.; Ennis F.A.;  
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
 RT gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T  
 RT lymphocytes."  
 RL J. Virol. 66:3151-3154(1992).  
 DR EMBL: M19921; AAA44992.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR Pfam: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 SO SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;

Query Match 97.5%; Score 192; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 6.4e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 YTNLHSLIEESONOQEKNEDELLELDKWSLWNF 36  
 11:|||||  
 Db 636 YTSLSHSLIEESONOQEKNEDELLELDKWSLWNF 671

RESULT 10  
 ID 072502 PRELIMINARY; PRT; 854 AA.  
 AC 072502;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE ENV polypeptide.  
 GN ENV.  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone."  
 RL J. Virol. 59:284-291(1986).  
 DR EMBL: U26942; AAB0578.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 KW CONFLICT 214 H -> L (IN REF. 2).  
 FT CONFLICT 530 A -> S (IN REF. 2).  
 FT CONFLICT 739 G -> D (IN REF. 2).  
 SO SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 6.4e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTNLHSLIEESONOQEKNEDELLELDKWSLWNF 36  
 11:|||||  
 Db 636 YTSLSHSLIEESONOQEKNEDELLELDKWSLWNF 671

RESULT 11  
 ID 092877 PRELIMINARY; PRT; 856 AA.  
 AC 092877;  
 DT 01-NOV-1998 (TRENBLREL. 08, Created)  
 DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 RT "Simian-human immunodeficiency virus.  
 OS Simian-human immunodeficiency virus.  
 OC Viruses; Retrovirus; Retroviridae; Lentivirus.  
 NCBI\_Taxid=57667;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99098984; PubMed-9882298;

RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodroski J.G.;  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 responsible for the pathogenicity of a multiply passaged simian-human  
 immunodeficiency virus (SHV-HXBc2).";  
 RT Immunodeficiency virus (SHV-HXBc2).";  
 RL J. Virol. 73:976-984(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041850; AAD12142.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00517; Gp41; 1.  
 DR Pfam: PF00516; Gp120; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 856;  
 Best local Similarity 97.2%; Pred. No. 6.5e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIEESONQOEKNEOELLELDKWSLWNMF 36  
 DB 638 YTSLIHSLIEESONQOEKNEOELLELDKWSLWNMF 673

## RESULT 12

ID 074599 PRELIMINARY; PRT; 856 AA.  
 AC 074599;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 RT Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86068; BAA12995.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 856;  
 Best local Similarity 97.2%; Pred. No. 6.5e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIEESONQOEKNEOELLELDKWSLWNMF 36  
 DB 638 YTSLIHSLIEESONQOEKNEOELLELDKWSLWNMF 673

## RESULT 13

074090

ID 074090 PRELIMINARY; PRT; 856 AA.  
 AC 074090;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 RT Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 97.5%; Score 192; DB 15; Length 856;  
 Best local Similarity 97.2%; Pred. No. 6.5e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIEESONQOEKNEOELLELDKWSLWNMF 36  
 DB 638 YTSLIHSLIEESONQOEKNEOELLELDKWSLWNMF 673

## RESULT 14

ID 09YX08 PRELIMINARY; PRT; 122 AA.  
 AC 09YX08;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein immunodominant region (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RJ96BRP029;  
 RA Tanui A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,  
 RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,  
 RA Rayfield M.;  
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";  
 RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF034045; AAC79297.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR Pfam: PF00517; Gp41; 1.  
 KW Transmembrane.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 122 AA; 14767 MW; B0B60F44F72975CB CRC64;

Query Match 95.4%; Score 188; DB 15; Length 122;  
 Best local Similarity 94.4%; Pred. No. 2.7e-15;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIEESONQOEKNEOELLELDKWSLWNMF 36

Db 78 YTNLIYNLIEESONQOEKNEQELLELDKWSLWNMF 113

RESULT 15

Q9IK06 PRELIMINARY; PRT; 684 AA.  
 AC Q9IK06;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=546HC-86;  
 RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;  
 RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from  
 a patient with HIV dementia: evidence for monocyte trafficking into  
 brain.";  
 RL J. Neurovirol. 0:0-0(2000).  
 DR EMBL: AF217161; AAF75503.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; Env\_GP41.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 SQ SEQUENCE 684 AA: 77266 MW; F9E6F3CCAD32E10 CRC64;

Query Match 95.4%; Score 188; DB 15; Length 684;  
 Best Local Similarity 94.4%; Pred. No. 1.6e-14;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
 Db 643 YTNLIYNLIEESONQOEKNEQELLELDKWSLWNMF 678

Search completed: May 16, 2003, 11:19:47  
 Job time : 26.3124 secs



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 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 SQ SEQUENCE 867 AA; 98399 MW; 5F2310146B8E8680 CRC64;

Query Match 89.3%; Score 176; DB 1; Length 867;  
 Best Local Similarity 88.9%; Pred. No. 1.3e-13;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESQNOQEKNEQELLEDDKXASLWNMF 36  
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 Db 649 YTSLIYTLIEESQNOQEKNEQELLEDDKXASLWNMF 684

Search completed: May 16, 2003, 11:13:35  
 Job time : 7.07229 secs



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FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 852 AA; 9663 MW; EETBBF8D23C9910D CRC64;

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Query Match      91.9%; Score 181; DB 1; Length 852;
Best Local Similarity 88.9%; Pred. No. 3,3e-14;
Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTNLIHSLEESONOEKNEOELELDKWSLWMP 36
DB 634 YTNLIHSLEESONOEKNEOELELDKWSLWMP 669

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RESULT 13
ENV_HV1A2 STANDARD; PRT; 855 AA.
AC P03378;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11685;
RN [1]
RP MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
(RARV-2).";
RL Science 227:484-492(1985).

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CC DR EMBL: K02007; AAB59882.1; -
CC DR PIR: A03976; VCLJ42.
CC DR HIV: K02007; ENVSSE2.
CC DR InterPro: IPR000328; ENV_GP41.
CC DR InterPro: IPR000777; GP120.
CC DR Pfam: PF00516; GP120.1.
CC DR Pfam: PF00517; GP41.1.
CC DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC Signal.
FT SIGNAL 1 29

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FT CHAIN 30 509
FT CHAIN 510 855
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FT DISULFID 118 208
FT DISULFID 125 199
FT DISULFID 130 155
FT DISULFID 221 250
FT DISULFID 231 242
FT DISULFID 299 333
FT DISULFID 380 442
FT DISULFID 387 415
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 154 154
FT CARBOHYD 158 158
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FT CARBOHYD 304 304
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FT CARBOHYD 445 445
FT CARBOHYD 458 458
FT CARBOHYD 461 461
FT CARBOHYD 610 610
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FT CARBOHYD 815 815
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Query Match      91.9%; Score 181; DB 1; Length 855;
Best Local Similarity 88.9%; Pred. No. 3,3e-14;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTNLIHSLEESONOEKNEOELELDKWSLWMP 36
DB 637 YTNLIHSLEESONOEKNEOELELDKWSLWMP 672

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RESULT 14
ENV_HV1A2 STANDARD; PRT; 847 AA.
AC P05880;
DT 01-NOV-1988 (rel. 09, Created)
DT 01-NOV-1988 (rel. 09, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11705;
RN [1]
RP MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
at risk for AIDS.";

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FT	CARBONHD	155	159	N-LINKED	(GLCNAC	(POTENTI
FT	CARBONHD	155	159	N-LINKED <td>(GLCNAC</td> <td>(POTENTI</td>	(GLCNAC	(POTENTI
FT	CARBONHD	155	159	N-LINKED <td>(GLCNAC</td> <td>(POTENTI</td>	(GLCNAC	(POTENTI
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DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
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 FT CARBOHYD 197 197  
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 FT CARBOHYD 241 241  
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 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97339 MW; 5FCD81DC3C1209B3 CRC64;  
 Query Match 92.9%; Score 183; DB 1; Length 856;  
 Best Local Similarity 94.3%; Pred. No. 1.9e-14;  
 Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 YNLIHSLEESONQOEKNEDELLDKWASLMMN 35  
 Db 638 YTSLSHSLEESONQOEKNEDELLDKWASLMMN 672  
 RESULT 10  
 ENV\_HVISC STANDARD; PRT: 856 AA.  
 AC P05878;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OC NCB1\_Taxid=11702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88219542; PubMed=3369091;

RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;  
 RT "Envelope sequences of two new United States HIV-1 isolates";  
 RL Virology 164:531-536(1988)  
 CC -i- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.  
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 CC -----  
 CC EMBL: M17450; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: B28922; VCLJSC.  
 DR HIV: M17450; ENVSSC.  
 DR InterPro: IPR000328; ENV\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 510  
 FT CHAIN 511 856  
 FT STYPE 760 760  
 FT DISULFID 53 73  
 FT DISULFID 118 206  
 FT DISULFID 125 197  
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 FT DISULFID 296 330  
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 FT DISULFID 383 412  
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 SO SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;  
 Query Match 92.9%; Score 183; DB 1; Length 856;  
 Best Local Similarity 91.7%; Pred. No. 1.9e-14;

DR Pfam; PF00516; GPI20; 1.





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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SO SEQUENCE 836 AA; 97188 MW; 3373C68B84C1AFC CRC64;

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Query Match 97.5%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTNLHSLIESQNOEKNEQLLELDKWSLWNMF 36
Db 638 YTNLHSLIESQNOEKNEQLLELDKWSLWNMF 673

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RESULT 5
ENV_HVILW STANDARD; PRT; 856 AA.
ID ENV_HVILW STANDARD; PRT; 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HTLV type IIIB)."
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL: U12055; AAA76690.1;
CC GlycoSiteDB: Q70626;
CC InterPro: IPR000328; ENV_GP41.
DR

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 131 247
FT DISULFID 218 257
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
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FT CARBOHYD 616 616
FT CARBOHYD 624 624
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FT CARBOHYD 674 674
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FT CARBOHYD 816 816
SO SEQUENCE 836 AA; 96938 MW; 0C241332CF7E687 CRC64;

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Query Match 97.5%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTNLHSLIESQNOEKNEQLLELDKWSLWNMF 36
Db 638 YTNLHSLIESQNOEKNEQLLELDKWSLWNMF 673

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RESULT 6
ENV_HVILW STANDARD; PRT; 861 AA.
ID ENV_HVILW STANDARD; PRT; 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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[illegible]

Query Match	Best Local Similarity	Score	DB 1:	Length	DB 2:	Score	DB 3:	Length	DB 4:	Score	DB 5:	Length	DB 6:	Score	DB 7:	Length	DB 8:	Score	DB 9:	Length	DB 10:	Score	DB 11:	Length	DB 12:	Score	DB 13:	Length	DB 14:	Score	DB 15:	Length	DB 16:	Score	DB 17:	Length	DB 18:	Score	DB 19:	Length	DB 20:	Score	DB 21:	Length	DB 22:	Score	DB 23:	Length	DB 24:	Score	DB 25:	Length	DB 26:	Score	DB 27:	Length	DB 28:	Score	DB 29:	Length	DB 30:	Score	DB 31:	Length	DB 32:	Score	DB 33:	Length	DB 34:	Score	DB 35:	Length	DB 36:	Score	DB 37:	Length	DB 38:	Score	DB 39:	Length	DB 40:	Score	DB 41:	Length	DB 42:	Score	DB 43:	Length	DB 44:	Score	DB 45:	Length	DB 46:	Score	DB 47:	Length	DB 48:	Score	DB 49:	Length	DB 50:	Score	DB 51:	Length	DB 52:	Score	DB 53:	Length	DB 54:	Score	DB 55:	Length	DB 56:	Score	DB 57:	Length	DB 58:	Score	DB 59:	Length	DB 60:	Score	DB 61:	Length	DB 62:	Score	DB 63:	Length	DB 64:	Score	DB 65:	Length	DB 66:	Score	DB 67:	Length	DB 68:	Score	DB 69:	Length	DB 70:	Score	DB 71:	Length	DB 72:	Score	DB 73:	Length	DB 74:	Score	DB 75:	Length	DB 76:	Score	DB 77:	Length	DB 78:	Score	DB 79:	Length	DB 80:	Score	DB 81:	Length	DB 82:	Score	DB 83:	Length	DB 84:	Score	DB 85:	Length	DB 86:	Score	DB 87:	Length	DB 88:	Score	DB 89:	Length	DB 90:	Score	DB 91:	Length	DB 92:	Score	DB 93:	Length	DB 94:	Score	DB 95:	Length	DB 96:	Score	DB 97:	Length	DB 98:	Score	DB 99:	Length	DB 100:	Score	DB 101:	Length	DB 102:	Score	DB 103:	Length	DB 104:	Score	DB 105:	Length	DB 106:	Score	DB 107:	Length	DB 108:	Score	DB 109:	Length	DB 110:	Score	DB 111:	Length	DB 112:	Score	DB 113:	Length	DB 114:	Score	DB 115:	Length	DB 116:	Score	DB 117:	Length	DB 118:	Score	DB 119:	Length	DB 120:	Score	DB 121:	Length	DB 122:	Score	DB 123:	Length	DB 124:	Score	DB 125:	Length	DB 126:	Score	DB 127:	Length	DB 128:	Score	DB 129:	Length	DB 130:	Score	DB 131:	Length	DB 132:	Score	DB 133:	Length	DB 134:	Score	DB 135:	Length	DB 136:	Score	DB 137:	Length	DB 138:	Score	DB 139:	Length	DB 140:	Score	DB 141:	Length	DB 142:	Score	DB 143:	Length	DB 144:	Score	DB 145:	Length	DB 146:	Score	DB 147:	Length	DB 148:	Score	DB 149:	Length	DB 150:	Score	DB 151:	Length	DB 152:	Score	DB 153:	Length	DB 154:	Score	DB 155:	Length	DB 156:	Score	DB 157:	Length	DB 158:	Score	DB 159:	Length	DB 160:	Score	DB 161:	Length	DB 162:	Score	DB 163:	Length	DB 164:	Score	DB 165:	Length	DB 166:	Score	DB 167:	Length	DB 168:	Score	DB 169:	Length	DB 170:	Score	DB 171:	Length	DB 172:	Score	DB 173:	Length	DB 174:	Score	DB 175:	Length	DB 176:	Score	DB 177:	Length	DB 178:	Score	DB 179:	Length	DB 180:	Score	DB 181:	Length	DB 182:	Score	DB 183:	Length	DB 184:	Score	DB 185:	Length	DB 186:	Score	DB 187:	Length	DB 188:	Score	DB 189:	Length	DB 190:	Score	DB 191:	Length	DB 192:	Score	DB 193:	Length	DB 194:	Score	DB 195:	Length	DB 196:	Score	DB 197:	Length	DB 198:	Score	DB 199:	Length	DB 200:	Score	DB 201:	Length	DB 202:	Score	DB 203:	Length	DB 204:	Score	DB 205:	Length	DB 206:	Score	DB 207:	Length	DB 208:	Score	DB 209:	Length	DB 210:	Score	DB 211:	Length	DB 212:	Score	DB 213:	Length	DB 214:	Score	DB 215:	Length	DB 216:	Score	DB 217:	Length	DB 218:	Score	DB 219:	Length	DB 220:	Score	DB 221:	Length	DB 222:	Score	DB 223:	Length	DB 224:	Score	DB 225:	Length	DB 226:	Score	DB 227:	Length	DB 228:	Score	DB 229:	Length	DB 230:	Score	DB 231:	Length	DB 232:	Score	DB 233:	Length	DB 234:	Score	DB 235:	Length	DB 236:	Score	DB 237:	Length	DB 238:	Score	DB 239:	Length	DB 240:	Score	DB 241:	Length	DB 242:	Score	DB 243:	Length	DB 244:	Score	DB 245:	Length	DB 246:	Score	DB 247:	Length	DB 248:	Score	DB 249:	Length	DB 250:	Score	DB 251:	Length	DB 252:	Score	DB 253:	Length	DB 254:	Score	DB 255:	Length	DB 256:	Score	DB 257:	Length	DB 258:	Score	DB 259:	Length	DB 260:	Score	DB 261:
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FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
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Query Match 97.5%; Score 192; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTNLIHSLEESONOENKNEOELLELDKVASLWNMF 36
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DB 633 YTSLIHSLEESONOENKNEOELLELDKVASLWNMF 668

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RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
ID ENV_HV1B1 STANDARD; PRT; 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
SV Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;

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RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patara R., Lyak K.J., Starich B.R.,
RA Joseph S.F., Doran E.R., Ratslisk J.A., Whitehorn E.A.,
RA Baumanister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Launberger J.A., Pappas T.S., Ghayee J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RL Nature 313:277-284(1985).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
Chinese hamster ovary cells."
RL J. Biol. Chem. 265:10373-10382(1990).
CC -----
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CC EMBL; M15654; AAA44205.1;
CC PIR; A03973; VCLJH3.
CC HIV; M15654; ENVSBI102.
CC InterPro; IPR000328; ENV GP41.
CC InterPro; IPR00777; GP120.
CC Pfam; PF00516; GP41; 1.
CC AIDS; Coat protein; Glycoprotein; Transmembrane;
CC Signal.
CC CHAIN 1 30
CC CHAIN 512 856
CC DISULFID 54 74
CC DISULFID 119 205
CC DISULFID 126 196
CC DISULFID 131 157
CC DISULFID 218 247
CC DISULFID 228 239
CC DISULFID 296 331
CC DISULFID 378 445
CC DISULFID 385 418
CC CARBOHYD 88 88
CC CARBOHYD 136 136
CC CARBOHYD 141 141
CC CARBOHYD 156 156
CC CARBOHYD 160 160
CC CARBOHYD 186 186
CC CARBOHYD 197 197
CC CARBOHYD 230 230
CC CARBOHYD 241 241
CC CARBOHYD 262 262
CC CARBOHYD 276 276
CC CARBOHYD 289 289
CC CARBOHYD 295 295
CC CARBOHYD 301 301
CC CARBOHYD 332 332
CC CARBOHYD 339 339
CC CARBOHYD 356 356
CC CARBOHYD 386 386
CC CARBOHYD 392 392
CC CARBOHYD 397 397
CC CARBOHYD 406 406
CC CARBOHYD 448 448
CC CARBOHYD 463 463
CC CARBOHYD 611 611
CC CARBOHYD 616 616
CC CARBOHYD 625 625
CC CARBOHYD 637 637
CC CARBOHYD 674 674
CC CARBOHYD 750 750
CC CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931BB27 CRC64;

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Query Match 97.5%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

OY 1 YTNLIHSLEESONOENKNEOELLELDKVASLWNMF 36
    ||:|||||
DB 638 YTSLIHSLEESONOENKNEOELLELDKVASLWNMF 673

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RESULT 3
ENV_HV1H2 STANDARD; PRT; 856 AA.
ID ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; O09779;

```



XX :



RESULT 4  
AAV22912  
ID AAV22912 standard; Peptide: 36 AA.  
XX  
AC AAV22912;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 108 from WO9820036.  
XX  
KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
PD WO9820036-A1.  
XX  
PD 14-MAY-1998.  
XX  
PE 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH) GENENTECH INC.  
PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovashnik MA;  
PI Wells JA;  
PI  
DR WPI: 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on terminus of octa-peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure; Page 233-234; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SO Sequence 36 AA;

Query Match 97.5%; Score 192; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTNLIHSIIIESQNOQEKNEQELLELDKWSLWMWF 36  
1 YTSLIHSIIIESQNOQEKNEQELLELDKWSLWMWF 36

RESULT 5  
AAV22805  
ID AAV22805 standard; Peptide: 36 AA.  
XX  
AC AAV22805;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 1 from WO9820036.  
XX  
KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
PD WO9820036-A1.  
XX  
PD 14-MAY-1998.  
XX  
PE 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH) GENENTECH INC.  
PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovashnik MA;  
PI Wells JA;  
PI  
DR WPI: 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on terminus of octa-peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure; Page 143-144; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SO Sequence 36 AA;

Query Match 97.5%; Score 192; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTNLIHSIIIESQNOQEKNEQELLELDKWSLWMWF 36  
1 YTSLIHSIIIESQNOQEKNEQELLELDKWSLWMWF 36

RESULT 6  
 AAY31955  
 ID AAY31955 standard; Peptide: 36 AA.  
 AC AAY31955;  
 XX  
 DT 21-DEC-1999 (first entry)  
 XX  
 DE Synthetic peptide T-20 (DP-178).  
 XX  
 XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 FH Key  
 FT Modified-site 1 Location/Qualifiers  
 FT Modified-site 36 /note= "N-terminal acetyl"  
 FT Modified-site 36 /note= "C-terminal amide"  
 XX  
 PN WO9948513-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PF 22-MAR-1999; 99WO-US06230.  
 XX  
 PR 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Kang M, Bray B, Lichy M, Mader C, Merutka G;  
 PI WPI: 1999-591038/50.  
 DR  
 PT Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides  
 PS Claim 1: Page 102; 120pp; English.  
 XX  
 CC The present sequence represents an N- and C-terminal modified  
 CC peptide, designated T-20 (or DP-178), corresponding to amino acids  
 CC 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.  
 CC The invention relates to methods for the synthesis of peptides,  
 CC in particular T-20 and T-20-like peptides. The method involves  
 CC synthesizing specific side-chain protected peptide fragment  
 CC intermediates of T-20 or a T-20-like peptide on a solid support,  
 CC coupling the protected fragments in solution to form a protected  
 CC T-20 or T-20-like peptide, followed by deprotection of the side  
 CC chains to yield the final T-20 or T-20-like peptide. The invention  
 CC also relates to individual peptide fragments (see AAY31956-73) which  
 CC act as intermediates in the synthesis of peptides of interest (e.g.  
 CC T-20), and to particular groups of peptide fragments which act as  
 CC intermediates in the synthesis of the peptide of interest. The  
 CC method allows for the large scale, economical production of high  
 CC purity peptides.  
 CC  
 SQ Sequence 36 AA:  
 Query Match 97.5%; Score 192; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTNLIHSLEESQNOEKNEOELLELDKWSLWNMF 36  
 DB 1 YTSLIHSLEESQNOEKNEOELLELDKWSLWNMF 36

RESULT 7  
 AAY31974  
 ID AAY31974 standard; Peptide: 36 AA.  
 AC AAY31974;  
 XX  
 DT 21-DEC-1999 (first entry)  
 XX  
 DE HIV-1 LAI gp41 T-20 peptide.  
 XX  
 XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 XX  
 OS Human immunodeficiency virus type 1.  
 PN WO9948513-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PF 22-MAR-1999; 99WO-US06230.  
 XX  
 PR 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Kang M, Bray B, Lichy M, Mader C, Merutka G;  
 PI WPI: 1999-591038/50.  
 DR  
 PT Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides  
 PS Disclosure: Page 9; 120pp; English.  
 XX  
 CC The present sequence represents a peptide, designated T-20 (or  
 CC DP-178), that corresponds to amino acids 638-673 of the  
 CC transmembrane protein gp41 of HIV-1 LAI isolate. The invention  
 CC relates to methods for the synthesis of peptides, in particular  
 CC C- and N-terminal modified T-20 (see AAY31955) and T-20-like peptides.  
 CC The method involves synthesizing specific side-chain protected  
 CC peptide fragment intermediates (see AAY31956-73) of T-20 or a  
 CC T-20-like peptide on a solid support, coupling the protected  
 CC fragments in solution to form a protected T-20 or T-20-like peptide,  
 CC followed by deprotection of the side chains to yield the final T-20  
 CC or T-20-like peptide. The invention also relates to individual  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC peptides of interest (e.g. T-20), and to particular groups of  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC the peptide of interest. The method allows for the large scale,  
 CC economical production of high purity peptides.  
 CC  
 SQ Sequence 36 AA:  
 Query Match\* 97.5%; Score 192; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTNLIHSLEESQNOEKNEOELLELDKWSLWNMF 36  
 DB 1 YTSLIHSLEESQNOEKNEOELLELDKWSLWNMF 36

RESULT 8  
 AAB52655  
 ID AAB52655 standard; Peptide: 36 AA.  
 AC AAB52655;  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DE T20/DP178 peptide fragment #33.  
 XX  
 XX Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemottractant.





XX Sequence 36 AA;  
 SQ Query Match 97.5%; Score 192; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIESONOQKNEOELLELDKMASLWNMF 36  
 1 YTSLIHSLIESONOQKNEOELLELDKMASLWNMF 36

Db 1 YTSLIHSLIESONOQKNEOELLELDKMASLWNMF 36

RESULT 11  
 AAB14533  
 ID AAB14533 standard; peptide; 36 AA.  
 XX AAB14533;  
 XX  
 DT 24-NOV-2000 (first entry)

HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).

KM HIV-1: gp41 C-helical domain;  
 KM gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KM core 6-helix bundle; viral entry inhibition; immunogenic;  
 KM antibody; humoral response; broad spectrum vaccine; anti-HIV-  
 KM envelope glycoprotein; prophylaxis; therapy.

OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200040616-A1.  
 XX  
 PD 13-JUL-2000.  
 XX  
 PF 10-JAN-2000; 2000MO-US00456.  
 XX  
 PR 08-JAN-1999; 99US-0115404.  
 PR 07-JAN-2000; 2000US-0480336.  
 XX  
 PA (WILD/) WILD C T.  
 PA (WEIS/) WEISS C D.  
 XX  
 PI Wild CT, Weiss CD;  
 XX  
 DR WPI: 2000-465959/40.

Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -

PS Claim 13; Page 12; 97pp; English.

XX Sequences AAB14532-B14534 and AAB14569-B14602 represent specifically  
 CC claimed peptides derived from the C-helical domain of the gp41  
 CC envelope glycoprotein from a variety of HIV-1 isolates. The invention  
 CC relates to raising a neutralising antibody response to a broad spectrum  
 CC of HIV (human immunodeficiency virus) strains and isolates, comprising  
 CC the administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the process  
 CC of viral entry into host cells. Such peptides can correspond to or  
 CC mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly a  
 CC combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can  
 CC be alternately linked together to form a peptide which mimics the  
 CC core 6-helix bundle. Administration of the peptide(s) generates a  
 CC humoral response, with the production of antibodies against gp41  
 CC structures involved in viral entry. As these portions of gp41 are well  
 CC conserved, such antibodies may be effective against a broad range of

CC HIV strains and isolates. The peptide compositions may be administered  
 CC as a prophylactic or therapeutic vaccine to generate antibodies which  
 CC reduce or inhibit the ability of HIV to infect uninfected cells. A  
 CC composition comprising polyclonal or monoclonal antibodies can be  
 CC administered to reduce HIV infection of uninfected cells. Antibodies  
 CC raised against entry-relevant gp41 structures may also be used  
 CC therapeutically and as tools to further elucidate the mechanism of HIV  
 CC cell entry.

QY 1 YTNLIHSLIESONOQKNEOELLELDKMASLWNMF 36  
 1 YTSLIHSLIESONOQKNEOELLELDKMASLWNMF 36

Db 1 YTSLIHSLIESONOQKNEOELLELDKMASLWNMF 36

RESULT 12  
 AAY88665  
 ID AAY88665 standard; peptide; 36 AA.  
 XX AAY88665;  
 XX  
 DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 20.

DE Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KM anti-fusogenic; differentiation factor; interleukin; interferon;  
 KM colony stimulating factor; hormone; angiogenic factor.

XX  
 OS Unidentified.  
 XX  
 PN WO9959615-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 20-MAY-1999; 99MO-US11219.  
 XX  
 PR 20-MAY-1998; 98US-0082279.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PI Barney S. Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX  
 DR WPI: 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

PS Disclosure; Page 21; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX Sequence 36 AA: 97.5%; Score 192; DB 21; Length 36;  
Query Match Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLSIESONQOEKNEQELLELDKWSLWNMF 36  
||:|||||  
1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 13  
ID AAY88729 standard; peptide: 36 AA.  
XX AAY88729;  
XX 23-MAY-2000 (first entry)  
DT Core polypeptide fragment T No. 84.

XX Core polypeptide fragment T No. 84.  
XX Retrovirus: hybrid polypeptide; enhancer: gp41; envelope protein; HIV-1;  
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX Unidentified.  
OS  
XX WO959615-A1.  
PN 25-NOV-1999.  
PD 20-MAY-1999; 99WO-US11219.  
PF 20-MAY-1998; 98US-0082279.  
PR (TRIM-) TRIMERIS INC.  
PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
PI WPI: 2000-136792/12.  
DR A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence -  
PS Disclosure: Page 22; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.  
XX  
XX Sequence 36 AA:

Query Match 97.5%; Score 192; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36  
||:|||||  
1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 14  
ID AAY89135 standard; peptide: 36 AA.  
XX AAY89135;  
XX 23-MAY-2000 (first entry)  
DT Core polypeptide fragment T No. 573.

XX Core polypeptide fragment T No. 573.  
XX Retrovirus: hybrid polypeptide; enhancer: gp41; envelope protein; HIV-1;  
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX Unidentified.  
OS  
XX WO959615-A1.  
PN 25-NOV-1999.  
PD 20-MAY-1999; 99WO-US11219.  
PF 20-MAY-1998; 98US-0082279.  
PR (TRIM-) TRIMERIS INC.  
PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
PI WPI: 2000-136792/12.  
DR A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence -  
PS Disclosure: Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.  
XX  
XX Sequence 36 AA:

Query Match 97.5%; Score 192; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLSIESONQOEKNEQELLELDKWSLWNMF 36  
||:|||||  
1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 15  
ID AAY89136 standard; peptide: 36 AA.  
XX

AC AAY89136;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Core polypeptide fragment T No. 574.  
 XX  
 KW Retrovirus: hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN WO959615-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 20-MAY-1999; 99WO-US11219.  
 XX  
 PR 20-MAY-1998; 980S-0082279.  
 XX  
 (TRIM-) TRIMERIS INC.  
 XX  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX  
 DR WPI; 2000-136792/12.  
 XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 XX  
 PS Disclosure; Page 30; 124pp; English.  
 XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.  
 CC  
 CC Sequence 36 AA;  
 CC  
 CC Query Match 97.5%; Score 192; DB 21; Length 36;  
 CC Best Local Similarity 97.2%; Pred. No. 1,3e-16;  
 CC Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 YTNLIHSLSIESQNOQEKNEQLLELDKWSLNNWF 36  
 CC ||:|||||  
 CC Db 1 YTSLSHSLSIESQNOQEKNEQLLELDKWSLNNWF 36

Search completed: May 16, 2003, 11:12:04  
 Job time : 32.4578 secs

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TITLE OF INVENTION: BEING IMMOBILIZED  
FILE REFERENCE: ALBRE-22  
CURRENT APPLICATION NUMBER: US/10/059,271  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: DE 101 06 295  
PRIOR FILING DATE: 2001-02-02  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 81  
LENGTH: 232  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-059-271-81

Query Match 97.0%; Score 191; DB 9; Length 232;  
Best Local Similarity 97.2%; Pred. No. 6.5e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
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Db 144 YTSLSHSLEESQNOEKNEQELLELDKWSLWNMF 179

RESULT 15  
US-10-059-271-82  
Sequence 82, Application US/10059271  
Publication No. US20030082208A1  
GENERAL INFORMATION:  
APPLICANT: REPKE, HEINRICH  
APPLICANT: BUDDÉ, ECKHARD  
APPLICANT: NICOLAUS, STEFAN  
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
FILE REFERENCE: ALBRE-22  
CURRENT APPLICATION NUMBER: US/10/059,271  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: DE 101 06 295  
PRIOR FILING DATE: 2001-02-02  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 82  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-059-271-82

Query Match 97.0%; Score 191; DB 9; Length 254;  
Best Local Similarity 97.2%; Pred. No. 7.2e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
|||  
Db 166 YTSLSHSLEESQNOEKNEQELLELDKWSLWNMF 201

Search completed: May 16, 2003, 12:10:24  
Job time : 15.759 secs

Db 2 YTSLHSLIEESONQOEKNEQELLELDKWSLWNMF 37

RESULT 10

US-09-779-451-41

Sequence 41, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT APPLICATION NUMBER: US/09/779,451

PRIOR FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 46

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match

Best Local Similarity 97.0%; Score 191; DB 10; Length 46;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGLHSLIEESONQOEKNEQELLELDKWSLWNMF 36

Db 11 YTSLHSLIEESONQOEKNEQELLELDKWSLWNMF 46

RESULT 11

US-09-779-451-4

Sequence 4, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT APPLICATION NUMBER: US/09/779,451

PRIOR FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match

Best Local Similarity 97.0%; Score 191; DB 10; Length 56;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGLHSLIEESONQOEKNEQELLELDKWSLWNMF 36

Db 16 YTSLHSLIEESONQOEKNEQELLELDKWSLWNMF 51

RESULT 12

US-10-040-349B-2

Sequence 2, Application US/10040349B

Publication No. US20030082521A1

GENERAL INFORMATION:

APPLICANT: Brasseur, Robert

APPLICANT: Charlotiaux, Benoit

APPLICANT: Chevalier, Michel

APPLICANT: El Habib, Raphaelle

APPLICANT: Krell, Tino

TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

FILE REFERENCE: 01-078-A

CURRENT APPLICATION NUMBER: US/10/040,349B

CURRENT FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)..(177)

OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match

Best Local Similarity 97.0%; Score 191; DB 9; Length 177;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGLHSLIEESONQOEKNEQELLELDKWSLWNMF 36

Db 104 YTSLHSLIEESONQOEKNEQELLELDKWSLWNMF 139

RESULT 13

US-10-059-271-84

Sequence 84, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

FILE REFERENCE: ALBRE-22

CURRENT APPLICATION NUMBER: US/10/059,271

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: DE 101 06 295

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-059-271-84

Query Match

Best Local Similarity 97.0%; Score 191; DB 9; Length 221;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGLHSLIEESONQOEKNEQELLELDKWSLWNMF 36

Db 131 YTSLHSLIEESONQOEKNEQELLELDKWSLWNMF 166

RESULT 14

US-10-059-271-81

Sequence 81, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

RESULT 7  
US-09-854-816-1  
Sequence 1, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: DP178  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
09-854-816-1  
Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
CY 1 YTGILHSLEESONOQEKNEQELLELDKASLWNMF 36  
DB 1 YTSLHSLEESONOQEKNEQELLELDKASLWNMF 36  
RESULT 8  
US-09-854-816-108  
Sequence 108, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108  
Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
CY 1 YTGILHSLEESONOQEKNEQELLELDKASLWNMF 36  
DB 1 YTSLHSLEESONOQEKNEQELLELDKASLWNMF 36  
RESULT 9  
US-09-848-616-176  
Sequence 176, Application US/09848616  
Publication No. US20030054010A1  
GENERAL INFORMATION:  
APPLICANT: Seibel, Peter  
APPLICANT: Dunant, Nicolas  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Lechner, Franziska  
TITLE OF INVENTION: Molecular Antigen Array  
FILE REFERENCE: 1700.0180002  
CURRENT APPLICATION NUMBER: US/09/848,616  
CURRENT FILING DATE: 2001-05-05  
NUMBER OF SEQ ID NOS: 186  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 176  
LENGTH: 37  
TYPE: PPT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: DP178c peptide  
US-09-848-616-176  
Query Match 97.0%; Score 191; DB 9; Length 37;  
Best Local Similarity 97.2%; Pred. No. 9,4e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
CY 1 YTGILHSLEESONOQEKNEQELLELDKASLWNMF 36  
DB 1 YTGILHSLEESONOQEKNEQELLELDKASLWNMF 36



NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 97.0%; Score 191; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEDELELDKWSLWNF 36  
DB 1 YTSLSHSLEESQNOQEKNEDELELDKWSLWNF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Olson, William C  
APPLICANT: Maddon, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
TITLE OF INVENTION: Infection  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 97.0%; Score 191; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEDELELDKWSLWNF 36  
DB 1 YTSLSHSLEESQNOQEKNEDELELDKWSLWNF 36

ULT 4

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)...(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTGILHSLEESQNOQEKNEDELELDKWSLWNF 36  
DB 1 YTSLSHSLEESQNOQEKNEDELELDKWSLWNF 36

RESULT 5  
US-09-779-451-5

Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:  
APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900 0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEDELELDKWSLWNF 36  
DB 1 YTSLSHSLEESQNOQEKNEDELELDKWSLWNF 36

RESULT 6  
US-09-834-628-1

Sequence 1, Application US/09834628  
Patent No. US2002011922A1  
GENERAL INFORMATION:  
APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEDELELDKWSLWNF 36  
DB 1 YTSLSHSLEESQNOQEKNEDELELDKWSLWNF 36

GenCore version 5.1.4\_p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
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Title: US-09-623-533a-534  
Perfect score: 197  
Sequence: 1 YTGILHSLEESQNOEKNEDELELDKWSLWNNF 36

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Gapop 10.0 , Gapext 0.5

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1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/PC1\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	97.0	36	9 US-09-874-475-16	Sequence 16, Appl
2	191	97.0	36	9 US-10-116-797-1	Sequence 1, Appl
3	191	97.0	36	9 US-09-493-346-1	Sequence 1, Appl
4	191	97.0	36	10 US-09-796-202-10	Sequence 10, Appl
5	191	97.0	36	10 US-09-451-5	Sequence 5, Appl
6	191	97.0	36	10 US-09-834-628-1	Sequence 1, Appl
7	191	97.0	36	10 US-08-854-816-1	Sequence 1, Appl
8	191	97.0	36	10 US-09-854-816-108	Sequence 108, App
9	191	97.0	37	9 US-09-848-616-176	Sequence 176, App
10	191	97.0	46	10 US-09-779-451-41	Sequence 41, Appl
11	191	97.0	56	10 US-09-779-451-4	Sequence 4, Appl
12	191	97.0	177	9 US-10-040-349B-2	Sequence 2, Appl
13	191	97.0	221	9 US-10-059-271-84	Sequence 84, Appl
14	191	97.0	232	9 US-10-059-271-81	Sequence 81, Appl
15	191	97.0	234	9 US-10-059-271-82	Sequence 82, Appl
16	191	97.0	256	9 US-10-059-271-97	Sequence 97, Appl
17	191	97.0	268	10 US-09-854-816-16	Sequence 16, Appl
18	191	97.0	268	10 US-09-854-816-17	Sequence 17, Appl
19	191	97.0	268	10 US-09-854-816-18	Sequence 18, Appl

20	191	97.0	344	9 US-10-040-349B-1	Sequence 1, Appl
21	191	97.0	345	9 US-10-026-741-49	Sequence 49, Appl
22	191	97.0	345	10 US-09-779-451-8	Sequence 8, Appl
23	191	97.0	391	9 US-10-059-271-93	Sequence 93, Appl
24	191	97.0	519	10 US-09-756-551A-8	Sequence 8, Appl
25	191	97.0	853	9 US-10-003-035-33	Sequence 33, Appl
26	191	97.0	856	10 US-09-476-242-1	Sequence 1, Appl
27	191	97.0	861	9 US-10-026-741-103	Sequence 103, App
28	191	97.0	1101	9 US-10-003-035-53	Sequence 53, Appl
29	191	97.0	1186	9 US-10-003-035-55	Sequence 55, Appl
30	188	95.4	36	10 US-09-912-824-1	Sequence 1, Appl
31	188	95.4	267	10 US-09-854-816-38	Sequence 38, Appl
32	188	95.4	268	10 US-09-854-816-19	Sequence 19, Appl
33	188	95.4	268	10 US-09-854-816-41	Sequence 41, Appl
34	188	95.4	269	10 US-09-854-816-43	Sequence 43, Appl
35	185	93.9	1231	9 US-10-059-271-94	Sequence 94, Appl
36	183	92.9	268	10 US-09-854-816-13	Sequence 13, Appl
37	182	92.4	233	10 US-09-854-816-50	Sequence 50, Appl
38	182	92.4	268	10 US-09-854-816-9	Sequence 9, Appl
39	182	92.4	268	10 US-09-854-816-26	Sequence 26, Appl
40	182	92.4	269	10 US-09-854-816-12	Sequence 12, Appl
41	182	92.4	619	10 US-09-891-609-4	Sequence 4, Appl
42	182	92.4	646	10 US-09-891-609-2	Sequence 2, Appl
43	182	92.4	847	10 US-09-476-242-2	Sequence 2, Appl
44	181	91.9	46	10 US-09-854-816-109	Sequence 109, App
45	181	91.9	269	10 US-09-854-816-6	Sequence 6, Appl

## ALIGNMENTS

```

RESULT 1
US-09-874-475-16
; Sequence 16, Application US/09874475
; Publication No. US20020182592A1
GENERAL INFORMATION:
; APPLICANT: Petropoulos, Christos J.
; APPLICANT: Parkin, Neil T.
; APPLICANT: Whitcomb, Jeanette
; APPLICANT: Huang, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE
; FILE REFERENCE: 2793/65166
; CURRENT APPLICATION NUMBER: US/09/874.475
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 36
; TYPE: PRN
; ORGANISM: Fusion Inhibitor Peptide
US-09-874-475-16

Query Match          97.0%  Score 191; DB 9; Length 36;
Best Local Similarity 97.2%  Pred. No. 9.2e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YTGILHSLEESQNOEKNEDELELDKWSLWNNF 36
|||||||
DB      1 YTGILHSLEESQNOEKNEDELELDKWSLWNNF 36

RESULT 2
US-10-116-797-1
; Sequence 1, Application US/10116797
; Publication No. US2003004411A1
GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672-A
; CURRENT APPLICATION NUMBER: US/10/116.797
; CURRENT FILING DATE: 2002-10-15

```

Db 1 YTSLIHSLEESQNOEKNEQELLELDKWSLWNMF 36

## RESULT 13

Sequence 497, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 497  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-497

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLIHSLEESQNOEKNEQELLELDKWSLWNMF 36

## RESULT 14

US-09-082-279B-498  
Sequence 498, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 498  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-498

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLIHSLEESQNOEKNEQELLELDKWSLWNMF 36

RESULT 15  
US-09-082-279B-603

Sequence 603, Application US/09082279B

Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 603  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-603

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLIHSLEESQNOEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:22:12  
Job time : 10.1928 secs

RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554.616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1  
Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGILHSLEESQNOEKNEDELLDKWASLWNF 36  
DB 1 YTSLSHSLEESQNOEKNEDELLDKWASLWNF 36  
RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Felleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGILHSLEESQNOEKNEDELLDKWASLWNF 36  
DB 1 YTSLSHSLEESQNOEKNEDELLDKWASLWNF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGILHSLEESQNOEKNEDELLDKWASLWNF 36  
DB 1 YTSLSHSLEESQNOEKNEDELLDKWASLWNF 36

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/08485551A  
Patent No. 6068973

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6093794

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLEESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLEESQNOEKNEQELLELDKWSLWNMF 36

RESULT 5  
US-08-484-223B-1  
Sequence 1, Application US/08484223B

Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLIHSLEESQNOEKNEQELLELDKWSLWNMF 36

RESULT 6  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLIHSLEESQNOEKNEQELLELDKWSLWNMF 36

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6060065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 2

US-08-486-099-1  
Sequence 1, Application US/08486099  
Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
TITLE OF INVENTION: B VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,099  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-099-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGSLHLSIESQNOQEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 3

US-09-071-877-1  
Sequence 1, Application US/09071877  
Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol  
APPLICANT: Bray, Brian  
APPLICANT: Lichty, Maynard  
APPLICANT: Mader, Catherine  
APPLICANT: Merutka, Gene  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS  
FILE REFERENCE: 7872-050

CURRENT APPLICATION NUMBER: US/09/071,877  
CURRENT FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO: 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus  
US-09-071-877-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGSLHLSIESQNOQEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 4

US-08-360-107A-1  
Sequence 1, Application US/08360107A  
Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 149  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,107A  
FILING DATE: 20-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-013  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-360-107A-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGSLHLSIESQNOQEKNEQELLELDKWSLWNMF 36

GenCore version 5.1.4\_P5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-534

Perfect score: 197  
Sequence: 1 YTGILHSIESONQOEKNEOELLELDKWSLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2.6/ptodata/1/1aa/PCUTS.COMB.pep.\*  
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	97.0	36	1 US-08-073-028-1	Sequence 1, Appli
2	191	97.0	36	3 US-08-486-099-1	Sequence 1, Appli
3	191	97.0	36	3 US-09-071-877-1	Sequence 1, Appli
4	191	97.0	36	3 US-08-360-107A-1	Sequence 1, Appli
5	191	97.0	36	3 US-08-484-223B-1	Sequence 1, Appli
6	191	97.0	36	3 US-08-919-597-1	Sequence 1, Appli
7	191	97.0	36	3 US-08-475-668A-1	Sequence 1, Appli
8	191	97.0	36	3 US-08-485-551A-1	Sequence 1, Appli
9	191	97.0	36	3 US-08-471-913A-1	Sequence 1, Appli
10	191	97.0	36	4 US-08-554-616-1	Sequence 1, Appli
11	191	97.0	36	4 US-08-485-264A-1	Sequence 1, Appli
12	191	97.0	36	4 US-09-082-279B-15	Sequence 15, Appli
13	191	97.0	36	4 US-09-082-279B-497	Sequence 497, App
14	191	97.0	36	4 US-09-082-279B-498	Sequence 498, App
15	191	97.0	36	4 US-09-082-279B-603	Sequence 603, App
16	191	97.0	36	4 US-09-082-279B-630	Sequence 630, App
17	191	97.0	36	4 US-09-082-279B-631	Sequence 631, App
18	191	97.0	36	4 US-09-082-279B-705	Sequence 705, App
19	191	97.0	36	4 US-09-082-279B-834	Sequence 834, App
20	191	97.0	36	4 US-09-082-279B-1076	Sequence 1076, App
21	191	97.0	36	4 US-09-082-279B-1121	Sequence 1121, App
22	191	97.0	36	4 US-09-082-279B-1161	Sequence 1161, App
23	191	97.0	36	4 US-08-965-056-1	Sequence 1, Appli
24	191	97.0	36	4 US-08-965-056-108	Sequence 108, App
25	191	97.0	36	4 US-09-045-920-1	Sequence 1, Appli
26	191	97.0	36	4 US-08-474-349A-1	Sequence 1, Appli
27	191	97.0	36	4 US-08-474-349A-399	Sequence 399, App

28	191	97.0	36	4 US-08-474-349A-413	Sequence 413, App
29	191	97.0	36	4 US-09-315-304B-15	Sequence 15, Appli
30	191	97.0	36	4 US-09-315-304B-497	Sequence 497, App
31	191	97.0	36	4 US-09-315-304B-498	Sequence 498, App
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33	191	97.0	36	4 US-09-315-304B-630	Sequence 630, App
34	191	97.0	36	4 US-09-315-304B-631	Sequence 631, App
35	191	97.0	36	4 US-09-315-304B-705	Sequence 705, App
36	191	97.0	36	4 US-09-315-304B-834	Sequence 834, App
37	191	97.0	36	4 US-09-315-304B-1076	Sequence 1076, App
38	191	97.0	36	4 US-09-315-304B-1121	Sequence 1121, App
39	191	97.0	36	4 US-09-315-304B-1161	Sequence 1161, App
40	191	97.0	36	4 US-09-315-304B-1469	Sequence 1469, App
41	191	97.0	36	4 US-09-315-304B-1470	Sequence 1470, App
42	191	97.0	36	4 US-09-315-304B-1486	Sequence 1486, App
43	191	97.0	36	4 US-09-315-304B-1520	Sequence 1520, App
44	191	97.0	36	4 US-08-255-208A-1	Sequence 1, Appli
45	191	97.0	37	4 US-09-082-279B-771	Sequence 771, App

## ALIGNMENTS

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RESULT 1
US-08-073-028-1
; Sequence 1, Application US/08073028
; Patent No. 5464933
;
GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-073-028-1
;
Query Match 97.0%; Score 191; DB 1; Length 36;
Best Local Similarity 97.2%; Pred. No. 9.3e-18;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 YTGILHSIESONQOEKNEOELLELDKWSLWNMF 36

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F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.9%; Score 181; DB 1; Length 855;

Best Local Similarity 88.9%; Pred. No. 1,1e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEOELLELDKMASLWNMF 36  
DB 637 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 672

## RESULT 12

S21998 envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: S21998; #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Status: preliminary

A:Residues: 1-358 <STE1>

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Status: preliminary

A:Residues: 1-222, 'X', 224-358 <STE2>

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

C:Superfamily: type E retrovirus env polyprotein

Query Match 91.4%; Score 180; DB 2; Length 358;

Best Local Similarity 88.9%; Pred. No. 5,6e-14;

Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEOELLELDKMASLWNMF 36

DB 140 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 175

RESULT 13

S22004 envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: S22004; #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

A:Reference number: S21990

A:Accession: S22004

A:Status: preliminary

A:Residues: 1-357 <STE1>

A:Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by PCR

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70419

A:Status: preliminary

A:Residues: 1-292, 'X', 294-357 <STE2>

A:Cross-references: EMBL:X61353; NID:g60188

C:Superfamily: type E retrovirus env polyprotein

Query Match 89.8%; Score 177; DB 2; Length 357;

Best Local Similarity 88.9%; Pred. No. 1,3e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEOELLELDKMASLWNMF 36

DB 139 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 174

## RESULT 14

T09448 envelope glycoprotein - human immunodeficiency virus type 1 (strain JRF1)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: T09448

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz

A:Reference number: Z16673

A:Accession: T09448

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-847 <PAN>

A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781

C:Genetics:

A:Superfamily: type E retrovirus env polyprotein

Query Match 89.3%; Score 176; DB 2; Length 847;

Best Local Similarity 88.9%; Pred. No. 4,4e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEOELLELDKMASLWNMF 36

DB 629 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 664

## RESULT 15

S13289 env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack,

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13289

A:Status: preliminary

A:Residues: 1-847 <OBK>

A:Superfamily: type E retrovirus env polyprotein

Query Match 89.3%; Score 176; DB 2; Length 847;

Best Local Similarity 88.9%; Pred. No. 4,4e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEOELLELDKMASLWNMF 36

DB 629 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 664

Search completed: May 16, 2003, 11:25:09

Job time: 12.1446 secs

C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the en  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STAN>  
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
A:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <Sig>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 92.9%; Score 183; DB 1; Length 856;  
Best Local Similarity 91.7%; Pred. No. 6, 6e-14;  
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLHSLIEESONOEKNEDELLEDKWASLWMP 36  
DB 638 YTSLYTLIEESONOEKNEDELLEDKWASLWMP 673

RESULT 8  
VCLJ2C  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
R:Guirao, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
Virology 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091  
A:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
F:1-29/Domain: signal sequence #status predicted <Sig>  
F:30-861/Product: env polyprotein #status predicted <EP>  
F:129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 92.9%; Score 183; DB 1; Length 861;  
Best Local Similarity 91.7%; Pred. No. 6, 6e-14;  
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLHSLIEESONOEKNEDELLEDKWASLWMP 36  
DB 643 YTSLYTLIEESONOEKNEDELLEDKWASLWMP 678

RESULT 9  
S21994  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 278  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ  
A:Reference number: S21990  
A:Accession: S21994  
A:Molecule type: DNA  
A:Residues: 1-357 <STEL>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAAA3622.1; PID:g60180  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70421  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STEL>  
A:Cross-references: EMBL:X61355; NID:g60179  
C:Superfamily: type E retrovirus env polyprotein

Query Match 92.4%; Score 182; DB 2; Length 357;  
Best Local Similarity 91.7%; Pred. No. 3, 2e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTNLHSLIEESONOEKNEDELLEDKWASLWMP 36  
DB 139 YTSLYTLIEESONOEKNEDELLEDKWASLWMP 174

RESULT 10  
S21996  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70422  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAAA3624.1; PID:g1067129  
A:Experimental source: patient 27L  
A:Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type E retrovirus env polyprotein

Query Match 92.4%; Score 182; DB 2; Length 357;  
Best Local Similarity 91.7%; Pred. No. 3, 2e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTNLHSLIEESONOEKNEDELLEDKWASLWMP 36  
DB 139 YTSLYTLIEESONOEKNEDELLEDKWASLWMP 174

RESULT 11  
VCLJ22  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown  
Science 227, 484-492, 1985  
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453; PMID:2578227  
A:Accession: A03976  
A:Molecule type: DNA  
A:Residues: 1-855 <SAN>  
A:Cross-references: GB:K02007; NID:g328658; PIDN:AA59882.1; PID:g328666  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>  
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,

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env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Retner, L.; Haseilane, W.; Patarca, R.; Liyak, K.J.; Starcich, B.; Josephs, S.F.; Dorra
berger, J.A.; Papas, T.S.; Grayed, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <STIC>
F:1-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:2-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 97.5%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5,6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESONOEKNEOELLELDKASLWNMF 36
DB 638 YTSLIHSLEESONOEKNEOELLELDKASLWNMF 673

RESULT 4
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Main-Hodson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAI>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <STIC>
F:1-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 97.5%; Score 192; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 5,6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESONOEKNEOELLELDKASLWNMF 36
DB 643 YTSLIHSLEESONOEKNEOELLELDKASLWNMF 678

RESULT 5
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
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N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: CA1621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Glibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: CA1621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-51/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match 92.9%; Score 183; DB 2; Length 443;
Best Local Similarity 91.7%; Pred. No. 3,1e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESONOEKNEOELLELDKASLWNMF 36
DB 378 YTSLIHSLEESONOEKNEOELLELDKASLWNMF 413

RESULT 6
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <STIC>
F:1-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 92.9%; Score 183; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 6,6e-14;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESONOEKNEOELLELDKASLWNMF 35
DB 638 YTSLIHSLEESONOEKNEOELLELDKASLWNMF 672

RESULT 7
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WM11)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
```

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284,970 Million cell updates/sec

Title: US-09-623-533a-535

Perfect score: 197  
Sequence: 1 YTNLIHSLIEESONOQEKNEDELLELDKWSLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	97.5	851	2 S33985	env polyprotein -
2	192	97.5	854	2 S13288	env protein - huma
3	192	97.5	856	1 VCLJH3	env polyprotein pr
4	192	97.5	861	1 VCLJLV	env polyprotein pr
5	183	92.9	443	2 C41621	env polyprotein pr
6	183	92.9	856	1 VCLJVL	env polyprotein pr
7	183	92.9	856	1 VCLJ3W	env polyprotein pr
8	183	92.9	856	1 VCLJ3C	env polyprotein pr
9	182	92.4	357	2 S21994	env polyprotein pr
10	182	92.4	357	2 S21996	env polyprotein pr
11	181	91.9	855	1 VCLJAZ	env polyprotein pr
12	180	91.4	358	2 S21998	env polyprotein pr
13	176	89.8	357	2 S22004	env polyprotein pr
14	176	89.3	847	2 T09448	env polyprotein pr
15	176	89.3	847	2 S13289	env polyprotein pr
16	175	88.8	357	2 S21992	env polyprotein pr
17	175	88.8	445	2 A41621	env polyprotein pr
18	175	88.8	843	1 H44001	env polyprotein pr
19	175	88.8	852	1 VCLJBR	env polyprotein pr
20	174	88.3	357	2 S22006	env polyprotein pr
21	174	88.3	358	2 S22002	env polyprotein pr
22	174	88.3	358	2 S22000	env polyprotein pr
23	174	88.3	358	2 S70417	env polyprotein pr
24	174	88.3	852	2 T12016	env polyprotein pr
25	174	88.3	853	2 S54384	env polyprotein pr
26	174	88.3	855	2 VCLJZR	env polyprotein pr
27	174	88.3	859	1 VCLJMN	env polyprotein pr
28	173	87.8	729	1 VCLJTX	env polyprotein pr
29	173	87.8	861	1 VCLJKB	env polyprotein pr

30	172	87.3	846	1 VCLJND	env polyprotein pr
31	167	84.8	859	2 T01672	env polyprotein pr
32	165	83.6	136	2 J00266	env polyprotein pr
33	165	83.8	136	2 J00954	env polyprotein pr
34	165	83.8	154	2 B41621	env polyprotein pr
35	165	83.8	868	1 VCLJH4	env polyprotein pr
36	151	76.6	854	1 VCLJ3I	env polyprotein pr
37	149	75.6	856	1 A44963	env polyprotein pr
38	144	73.1	357	2 S21990	env polyprotein pr
39	133	67.5	877	2 S49197	env polyprotein pr
40	116	58.9	863	2 A53034	env polyprotein pr
41	86	43.7	881	1 VCLJG3	env polyprotein pr
42	86	43.7	881	2 S03068	env polyprotein pr
43	86	43.7	889	1 VCLJG5	env polyprotein pr
44	85	43.1	151	2 S30448	env polyprotein pr
45	85	43.1	151	2 S30452	env polyprotein pr

## ALIGNMENTS

## RESULT 1

S33985  
env polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F.

Submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CCAR>

A:Cross-references: EMBL:211530; NID:g60192; PIDN:CAA7628.1; PID:g60199

C:Superfamily: type E retrovirus env polyprotein

Query Match  
Best local similarity 97.5%; Score 192; DB 2; Length 851;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONOQEKNEDELLELDKWSLWMP 36  
DB 633 YTNLIHSLIEESONOQEKNEDELLELDKWSLWMP 668

## RESULT 2

S13288  
env polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Nambale, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <COBR>

C:Superfamily: type E retrovirus env polyprotein

Query Match  
Best local similarity 97.5%; Score 192; DB 2; Length 854;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONOQEKNEDELLELDKWSLWMP 36  
DB 636 YTNLIHSLIEESONOQEKNEDELLELDKWSLWMP 671

## RESULT 3

VCLJH3

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## RESULT 12

VCLJZR

env polyprotein precursor - human immunodeficiency virus Zr-6

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus Zr-6

C&gt;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999

C:Accession: D26192

R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

Gene 52, 71-82, 1987

A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot

A:Reference number: A26192; M0ID:87248097; PMID:3036660

A:Accession: D26192

A:Molecule type: DNA

A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F:19/Domain: signal sequence #status predicted &lt;Sig&gt;

F:20-855/Product: env polyprotein #status predicted &lt;Mat&gt;

F:501-855/Product: transmembrane glycoprotein #status predicted &lt;TM&gt;

F:87,129,140,145,154,158,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match : 91.4%; Score 180; DB 1; Length 855;

Best Local Similarity 91.7%; Pred. No. 8.6e-14;

Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLEDKWASLWNMF 36

Db 637 YTGILYSLIEESQTOOEKNEDELLEDKWASLWNMF 672

## RESULT 13

S21998

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 28

C&gt;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S21998; S70425

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ

A:Reference number: S21990

A:Accession: S21998

A:Molecule type: DNA

A:Residues: 1-358 &lt;STE1&gt;

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb

A:Reference number: S70417; M0ID:92144209; PMID:1736940

A:Accession: S70425

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-222, 'X', 224-358 &lt;STE2&gt;

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

C:Superfamily: type E retrovirus env polyprotein

Query Match : 90.9%; Score 179; DB 2; Length 358;

Best Local Similarity 88.9%; Pred. No. 4.2e-14;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLEDKWASLWNMF 36

Db 140 YTGILYSLIEESONQOEKNEDELLEDKWASLWNMF 175

## RESULT 14

VCLJND

env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)

N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C&gt;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C:Accession: J00066

R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,

Gene 81, 275-284, 1989

A:Title: Nucleotide sequence of HIV-1-NK: a highly cytopathic strain of the human imm

A:Reference number: J00065; M0ID:90034200; PMID:2806517

A:Accession: J00066

A:Molecule type: DNA

A:Residues: 1-846 &lt;SPI&gt;

A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA44873.1; PID:g328162

A:Note: the authors translated the codon GCG for residue 523 as Arg

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly

F:1-29/Domain: signal sequence #status predicted &lt;Sig&gt;

F:30-501/Product: coat protein gp120 #status predicted &lt;CP1&gt;

F:502-846/Product: coat protein gp41 #status predicted &lt;CP2&gt;

F:674-692/Domain: transmembrane #status predicted &lt;TM2&gt;

F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,

Query Match : 90.4%; Score 178; DB 1; Length 846;

Best Local Similarity 91.7%; Pred. No. 1.5e-13;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLEDKWASLWNMF 36

Db 628 YTGILYSLIEESQIOOEKNEDELLEDKWASLWNMF 663

## RESULT 15

S22004

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 4B

C&gt;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22004; S70419

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22004

A:Molecule type: DNA

A:Residues: 1-357 &lt;STE1&gt;

A:Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70419; M0ID:92144209; PMID:1736940

A:Accession: S70419

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-292, 'X', 294-357 &lt;STE2&gt;

A:Cross-references: EMBL:X61353; NID:g60188

C:Superfamily: type E retrovirus env polyprotein

Query Match : 88.8%; Score 175; DB 2; Length 357;

Best Local Similarity 88.9%; Pred. No. 1.3e-13;

Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLEDKWASLWNMF 36

Db 139 YTGILYSLIEESONQOEKNEDELLEDKWASLWNMF 174

Search completed: May 16, 2003, 11:25:09  
Job time : 13.1446 secs

A:Molecule type: DNA  
A:Residues: 1-856 <MDE>  
A:Cross-references: GB:K02083; NID:9555008; PIDN:AAB59873.1; PID:g328559  
C:Genetics:

A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-51/Product: exterior membrane glycoprotein #status predicted <TM>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted

## Query Match

Best Local Similarity 92.4%; Score 182; DB 1; Length 856;  
Pred. No. 4.9e-14;  
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKASLWNMF 35  
638 YTSILYRLIEESONQOEKNEDELLELDKASLWNMF 672

## RESULT 8

env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
C:Accession: A24774  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the env  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774

A:Molecule type: DNA

A:Residues: 1-856 <STA>

A:Cross-references: GB:K03455; GB:M88432; NID:g1906382

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-501/Product: coat protein gp120 #status predicted <GP2>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

## Query Match

Best Local Similarity 92.4%; Score 182; DB 1; Length 856;  
Pred. No. 4.9e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKASLWNMF 36  
638 YTSILYRLIEESONQOEKNEDELLELDKASLWNMF 673

## RESULT 9

env polypeptide precursor - human immunodeficiency virus type 1 (isolate SC)  
N:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922  
R:Guirao, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
Virology 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091  
A:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane pr  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-861/Product: env polypeptide #status predicted <EP>  
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,

## Query Match

Best Local Similarity 92.4%; Score 182; DB 1; Length 861;  
Pred. No. 5e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKASLWNMF 36  
Db 643 YTSILYRLIEESONQOEKNEDELLELDKASLWNMF 678

## RESULT 10

env polypeptide precursor - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 27B  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21994; S70421  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
A:Reference number: S21990  
A:Accession: S21994

A:Molecule type: DNA

A:Residues: 1-357 <STE>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70421; MUID:92144209; PMID:1736940

A:Accession: S70421

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>

A:Cross-references: EMBL:X61355; NID:g60179

C:Superfamily: type E retrovirus env polypeptide

Query Match

Best Local Similarity 91.4%; Score 180; DB 2; Length 357;  
Pred. No. 3.2e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKASLWNMF 36  
Db 139 YTSILYRLIEESONQOEKNEDELLELDKASLWNMF 174

## RESULT 11

env polypeptide precursor - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
R:Theodore, T.; Buckler-White, A.J.  
submitted to the EMBL Data Library, July 1989  
A:Reference number: S54377  
A:Accession: S54384  
A>Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-853 <RHE>  
A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA5370.1; PID:g329385  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: polypeptide

## Query Match

Best Local Similarity 91.4%; Score 180; DB 2; Length 853;  
Pred. No. 8.6e-14;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKASLWNMF 36  
Db 635 YTSILYRLIEESONQOEKNEDELLELDKASLWNMF 670



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env polypotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polypotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Papastefanou, W.; Patarca, R.; Liyak, K.J.; Starcich, B.; Josephs, S.F.; Dore
nberger, J.A.; Pappas, T.S.; Chirayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A03353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAAA42
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypot
E:1-30/Domain: signal sequence #status predicted <SIG>
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:2-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,301,332,339,356,386,392,397,406
F:611,616,625,637,674,730,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 97.0%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 4e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

RESULT 4

```

env polypotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polypotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A0866; MUID:8509333; PMID:298135
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <WAI>
A:Cross-references: GB:K02013; NID:9326417; PIDN:AAB5951.1; PID:9326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypot
E:1-30/Domain: signal sequence #status predicted <SIG>
F:1-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,161,197,202,233,241,264,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 97.0%; Score 191; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 4.1e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

RESULT 5

```

env polypotein precursor - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1

```

```

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: EMBL:X61356; NID:960181; PIDN:CA43624.1; PID:91067129
A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypotein
Query Match 95.4%; Score 188; DB 2; Length 357;
Best Local Similarity 94.4%; Pred. No. 3.5e-15;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 6

```

env polypotein P - human immunodeficiency virus type 1 (fragment)
C:Accession: C41621
N:Alternate names: coat polypotein
M:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi
A:Reference number: A41621; MUID:92107924; PMID:1765038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
E:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match 92.4%; Score 182; DB 2; Length 443;
Best Local Similarity 91.7%; Pred. No. 2.3e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

RESULT 7

```

env polypotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polypotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/Tymphadenopathy retr
A:Reference number: A03355; MUID:85111157; PMID:2982104
A:Accession: A03974

```

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds

(Without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-534

Perfect score: 197

Sequence: 1 YTGILHSLEESQNOQEKNEQELLELDKWSLMMNF 36

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	97.0	851	2 S33985	env polypeptide - huma
2	191	97.0	854	2 S13288	env polypeptide - huma
3	191	97.0	856	1 VCLJH3	env polypeptide pr
4	191	97.0	861	1 VCLJLV	env polypeptide pr
5	188	95.4	357	2 S21996	env polypeptide pr
6	182	92.4	443	2 C41621	env polypeptide pr
7	182	92.4	856	1 VCLJVL	env polypeptide pr
8	182	92.4	856	1 VCLJ3W	env polypeptide pr
9	182	92.4	861	1 VCLJSC	env polypeptide pr
10	180	91.4	357	2 S21994	env polypeptide pr
11	180	91.4	855	2 S54384	env polypeptide pr
12	180	91.4	855	1 VCLJZR	env polypeptide pr
13	179	90.9	358	2 S21998	env polypeptide pr
14	178	90.4	846	1 VCLJND	env polypeptide pr
15	175	88.8	357	2 S22004	env polypeptide pr
16	175	88.8	847	2 T09448	env polypeptide pr
17	175	88.8	847	2 S13289	env polypeptide pr
18	175	88.8	845	1 VCLJJA	env polypeptide pr
19	174	88.3	445	2 A41621	env polypeptide pr
20	173	87.8	358	2 S22002	env polypeptide pr
21	173	87.8	358	2 S22000	env polypeptide pr
22	173	87.8	358	2 S70417	env polypeptide pr
23	173	87.8	852	2 T12016	env polypeptide pr
24	173	87.8	859	1 VCLJMN	env polypeptide pr
25	173	87.8	859	2 T01672	env polypeptide pr
26	172	87.3	357	2 S22006	env polypeptide pr
27	172	87.3	843	1 H44001	env polypeptide pr
28	169	85.8	357	2 S21992	env polypeptide pr
29	169	85.8	852	1 VCLJBR	env polypeptide pr

30	167	84.8	729	1 VCLJXX	env polypeptide pr
31	167	84.8	861	1 VCLJKB	env polypeptide pr
32	163	82.7	454	2 B41621	env polypeptide pr
33	162	82.2	868	1 VCLJH4	env polypeptide pr
34	159	80.7	136	2 J10266	env polypeptide pr
35	159	80.7	136	2 J10954	env polypeptide pr
36	157	79.7	854	1 VCLJST	env polypeptide pr
37	147	74.6	856	1 A44963	env polypeptide pr
38	143	72.6	357	2 S21990	env polypeptide pr
39	132	67.0	877	2 S49197	env polypeptide pr
40	115	58.4	863	2 A53034	env polypeptide pr
41	86	43.7	881	1 VCLJG3	env polypeptide pr
42	86	43.7	881	2 S03068	env polypeptide pr
43	86	43.7	889	1 VCLJG5	env polypeptide pr
44	85	43.1	151	2 S30448	env polypeptide pr
45	85	43.1	151	2 S30452	env polypeptide pr

## ALIGNMENTS

RESULT 1  
S33985  
env polypeptide - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
Submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <C>  
A:Cross-references: EMBL:211530; NID:g60192; PIDN:CAA77628.1; PID:g60199  
C:Superfamily: type E retrovirus env polypeptide

Query Match  
Best Local Similarity 97.0%; Score 191; DB 2; Length 851;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEQELLELDKWSLMMNF 36  
DB 633 YTSILHSLEESQNOQEKNEQELLELDKWSLMMNF 668

RESULT 2  
S13288  
env polypeptide - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack,  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <C>  
C:Superfamily: type E retrovirus env polypeptide

Query Match  
Best Local Similarity 97.0%; Score 191; DB 2; Length 854;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEQELLELDKWSLMMNF 36  
DB 636 YTSILHSLEESQNOQEKNEQELLELDKWSLMMNF 671

RESULT 3  
VCLJH3

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FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 SQ SEQUENCE 853 AA; 97043 MW; 849B08CBFAFF7008 CRC64;

Query Match 91.4%; Score 180; DB 1; Length 853;  
 Best Local Similarity 91.7%; Pred. No. 1.5e-14;

Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGILHSITFEESQNOOEKNEOELELDKWSLWMPF 36  
 DB 635 YTGILIRLIEESQTOOEKNEOELELDKWSLWMPF 670

Search completed: May 16, 2003, 11:13:34  
 Job time : 6.07229 secs

"Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome." J. Virol. 64:4016-4020(1990).

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DR EMBL: M38427; AAA5067.1; -  
 DR HIV: M38427; ENV5SF33.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 Signal.

FT	CHAIN	1	31	BY SIMILARITY.
FT	CHAIN	32	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	507	852	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	156	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	331	BY SIMILARITY.
FT	DISULFID	377	439	BY SIMILARITY.
FT	DISULFID	384	412	BY SIMILARITY.
FT	CARBOHYD	87	129	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	129	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	CARBOHYD	263	277	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	277	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	CARBOHYD	385	391	N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	CARBOHYD	397	401	N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	CARBOHYD	633	812	N-LINKED (GLCNAC. . .) (POTENTIAL).
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SEQUENCE 852 AA; 9663 MW; EE7BFB8D23C9910D CMC64;

Query Match 91.4%; Score 180; DB 1; Length 852;  
 Best Local Similarity 88.9%; Pred. No. 1.5e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTGILHSIIIEESONOEKNELELDKASLIMNF 36  
 |||:::|||||  
 Db 634 YTSLYTLLIESONOEKNELELDKASLIMNF 669

RESULT 15  
 ID ENV\_HV122 STANDARD: PRT: 853 AA.  
 AC P12487; 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 CN ENV.  
 OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11683;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Theodore T., Buckler-White A.;  
 RL Submitted (NOV-1988) to the HIV data bank.  
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DR EMBL: M22639; AAA5370.1; -  
 DR HIV: M22639; ENV5Z226.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 Signal.

FT	CHAIN	1	31	BY SIMILARITY.
FT	CHAIN	32	508	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	509	853	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	154	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
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FT	CARBOHYD	87	137	N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAAD07A5 CRC64;

Query Match 91.9%; Score 181; DB 1; Length 853;
Best Local Similarity 91.7%; Pred. No. 1,2e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTGILHSILIESONOQEKNEQELLELDKWSLWNMF 36
Db 635 YTGILHSILIESONOQEKNEQELLELDKWSLWNMF 670

RESULT 13
ENV_HV1RH STANDARD: PRT: 865 AA.
ID ENV_HV1RH STANDARD: PRT: 865 AA.
AC P04579;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11701;
PN [1]
SEQUENCE FROM N.A.
MEDLINE=66218077; Pubmed=2423250;
RA Starck B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable of
regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS";
RT AIDS;
RL Cell 45:637-648(1986).
CC -----
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CC -----
CC EMBL: M17451; AAA45057.1; -.
CC DR HIV: M17451; ENVSRF.
CC DR InterPro: IPR000328; ENV_GP41.
CC DR InterPro: IPR000777; GP120.
CC DR Pfam: PF00516; GP120; 1.
CC DR Pfam: PF00517; GP41; 1.
CC DR AIDS; Coat protein; Glycoprotein; Glycoprotein; Transmembrane;
KW Signal.

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FT SIGNAL 1 29
FT CHAIN 30 519
FT CHAIN 520 865
FT DISULFID 53 73
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FT DISULFID 125 209
FT DISULFID 130 157
FT DISULFID 231 260
FT DISULFID 241 252
FT DISULFID 309 343
FT DISULFID 389 452
FT DISULFID 396 425
FT DISULFID 87 87
FT CARBOHYD 129 129
FT CARBOHYD 136 136
FT CARBOHYD 139 139
FT CARBOHYD 156 156
FT CARBOHYD 193 193
FT CARBOHYD 194 194
FT CARBOHYD 197 197
FT CARBOHYD 198 198
FT CARBOHYD 203 203
FT CARBOHYD 210 210
FT CARBOHYD 247 247
FT CARBOHYD 254 254
FT CARBOHYD 275 275
FT CARBOHYD 289 289
FT CARBOHYD 302 302
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FT CARBOHYD 314 314
FT CARBOHYD 344 344
FT CARBOHYD 351 351
FT CARBOHYD 367 367
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FT CARBOHYD 403 403
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FT CARBOHYD 418 418
FT CARBOHYD 455 455
FT CARBOHYD 471 471
FT CARBOHYD 620 620
FT CARBOHYD 625 625
FT CARBOHYD 634 634
FT CARBOHYD 646 646
FT CARBOHYD 825 825
SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;

Query Match 91.9%; Score 181; DB 1; Length 865;
Best Local Similarity 86.18%; Pred. No. 1,2e-14;
Matches 31; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTGILHSILIESONOQEKNEQELLELDKWSLWNMF 36
Db 647 YTGILHSILIESONOQEKNEQELLELDKWSLWNMF 682

RESULT 14
ENV_HV1S3 STANDARD: PRT: 852 AA.
ID ENV_HV1S3 STANDARD: PRT: 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11690;
PN [1]
SEQUENCE FROM N.A.
MEDLINE=90317906; Pubmed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;

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DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 512 856  
 FT DISULFID 34 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 236 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 160  
 FT CARBOHYD 166 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 234 224  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 289 289  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97339 MW; 5FCBD1DC3C1209B3 CRC64;

Query Match  
 Best Local Similarity 92.4%; Score 182; DB 1; Length 856;  
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILSLIEESNOOEKNEDELLEKKNASLNMW 35  
 DB 638 YTSILSLIEESNOOEKNEDELLEKKNASLNMW 672

RESULT 10  
 ENV\_HVISC STANDARD; PRT; 856 AA.  
 AC P05678;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88219542; PubMed=3369091;

RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.,  
 RL "Envelope sequences of two new United States HIV-1 isolates."  
 VIROLOGY 164:531-536(1988).  
 CC -1 MISCELLANEOUS; THE SC ISOLATE WAS TAKEN FROM AN ANC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: M17450; NOT\_ANNOTATED\_CDS.  
 DR PIR: B28922; VCLISC.  
 DR HIV: M17450; ENV5SC.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 510  
 FT SITE 511 856  
 FT SITE 760 760  
 FT DISULFID 53 73  
 FT DISULFID 118 206  
 FT DISULFID 125 197  
 FT DISULFID 130 160  
 FT DISULFID 219 247  
 FT DISULFID 228 239  
 FT DISULFID 296 330  
 FT DISULFID 376 439  
 FT DISULFID 383 412  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
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 FT CARBOHYD 140 140  
 FT CARBOHYD 143 143  
 FT CARBOHYD 159 159  
 FT CARBOHYD 163 163  
 FT CARBOHYD 189 189  
 FT CARBOHYD 198 198  
 FT CARBOHYD 234 234  
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 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 295 295  
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 FT CARBOHYD 302 302  
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 FT CARBOHYD 338 338  
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 FT CARBOHYD 405 405  
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 FT CARBOHYD 457 457  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 625 625  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97055 MW; DAF4DA600DBA7A08 CRC64;

Query Match  
 Best Local Similarity 92.4%; Score 182; DB 1; Length 856;  
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 95.4%; Score 188; DB 1; Length 853;
Best Local Similarity 94.4%; Pred. No. 1.6e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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1 YTGILHSLEESONQOEKNEDELLELDKWSLMMNF 36
|||||:|||||:|||||:|||||:|||||:|||||:
636 YTSLSHSLEESONQOEKNEDELLELDKWSLMMNF 671

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## RESULT 8

ENV\_HV1S1 STANDARD; PRT: 847 AA.

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ID ENV_HV1S1 STANDARD; PRT: 847 AA.
AC P19550:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11691;
RN [1]
RP MEDLINE=90347835; PubMed=2384920;
RX Cheng-Mayer C., Outroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M65024; AAA45072.1; -
DR HIV; M38428; ENV5SFI62.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KM AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT CHAIN 1 29
FT SIGNAL 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFD 53 73
FT DISULFD 118 203
FT DISULFD 125 194
FT DISULFD 130 155
FT DISULFD 130 155
FT DISULFD 216 245
FT DISULFD 226 237
FT DISULFD 294 328
FT DISULFD 374 435
FT DISULFD 381 408 BY SIMILARITY.

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FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 847 AA; 96135 MW; 0A901317FD7FE2AB CRC64;

Query Match 92.4%; Score 182; DB 1; Length 847;
Best Local Similarity 91.7%; Pred. No. 8.6e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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1 YTGILHSLEESONQOEKNEDELLELDKWSLMMNF 36
|||||:|||||:|||||:|||||:|||||:|||||:
629 YTNLTLYLEESONQOEKNEDELLELDKWSLMMNF 664

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## RESULT 9

ENV\_HV1PV STANDARD; PRT: 856 AA.

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ID ENV_HV1PV STANDARD; PRT: 856 AA.
AC P03376:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV2 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11700;
RN [1]
RP MEDLINE=85111157; PubMed=2982104;
RX Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.;
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: K02083; AAB59873.1; -
DR EMBL: X01762; CAA25903.1; ALT_SEQ.
DR PIR: A03974; VCLPV.
DR HIV; K02083; ENVSPV2.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;

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Query Match          97.0%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 6,8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTGILHSLEESQNOEKNEDELLEDKWASLWNF 36
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DB 638 YTSILHSLEESQNOEKNEDELLEDKWASLWNF 673

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RESULT 5
ENV_HVILW STANDARD; PRT; 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
    glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OC Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
OX NCBI_TaxID=82834;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
  Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIIB)."
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
CC -----
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CC -----
CC EMBL: U12055; AAA76690.1;
DR GLYCOsuiteDB: Q70626;
DR InterPro: IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
  Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CE7E6687 CRC64;

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Query Match          97.0%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 6,8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTGILHSLEESQNOEKNEDELLEDKWASLWNF 36
    ||||||||||||||||||||||||||||
DB 638 YTSILHSLEESQNOEKNEDELLEDKWASLWNF 673

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RESULT 6
ENV_HVILW STANDARD; PRT; 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
    glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OC Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OX NCBI_TaxID=11686;
OX NCBI_TaxID=11686;
RN [1]

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FT	CARBOHYD	397	397	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	406	406	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	448	448	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	463	463	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	611	611	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	616	616	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	624	624	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	637	637	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	674	674	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	750	750	N-LINKED (GLCNAC . .)	(POTENTIAL).					
FT	CARBOHYD	816	816	N-LINKED (GLCNAC . .)	(POTENTIAL).					
SQ	SEQUENCE	856 AA:	97212 MW:	6FABI6AF85107FED CRC64:						
Query Match		97.0%:	Score 191:	DB 1:	Length 856:					
Best Local Similarity		97.2%:	Pred. No.	6.8e-16:						
Matches 35:		Conservative 0:	Mismatches 1:	Indels 0:	Gaps 0:					
OY	1 YTGLHSLIEESONOEKNEOELLELDKWSIWNMF 36 									
Db	638 YTSLHLSIESQNQEKNQEELELDKWSIWNMF 673									
RESULT 4 -										
ENV_HV1H3	ID	ENV_HV1H3	STANDARD:	PRT:	856 AA.					
AC	P04624; .									
DT	13-AUG-1987 (Rel. 05, Created)									
DT	01-FEB-1996 (Rel. 33, Last sequence update)									
DT	15-JUL-1999 (Rel. 38, Last annotation update)									
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].									
CN	ENV.									
OC	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).									
OS	Viruses; Retrovird viruses; Retroviridae; Lentivirus.									
OX	NCBI_TaxID=11707;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RX	MEDLINE=85228248; PubMed=2988795;									
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P. ;									
RT	"HIV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";									
RL	Cell 41:979-986(1985).									
CC	-----									
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CC	-----									
DR	EMBL: M1A100; AAA44679.1; .									
DR	HIV: M1A100; ENVSHXB3.									
DR	InterPro: IPR000328; Env_GP41.									
DR	InterPro: IPR000777; GP120.									
DR	PIfam: PF00516; GP120.1.									
DR	PIfam: PF00517; GP41.1.									
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.									
FT	SIGNAL	1	30							
FT	CHAIN	31	511		EXTERIOR MEMBRANE GLYCOPROTEIN.					
FT	CHAM	512	856		TRANSMEMBRANE GLYCOPROTEIN.					
FT	DISULFD	119	205		BY SIMILARITY.					
FT	DISULFD	126	196		BY SIMILARITY.					
FT	DISULFD	131	157		BY SIMILARITY.					
FT	DISULFD	218	247		BY SIMILARITY.					
FT	DISULFD	228	239		BY SIMILARITY.					
FT	DISULFD	296	331		BY SIMILARITY.					
FT	DISULFD	378	445		BY SIMILARITY.					
FT	DISULFD	385	418		BY SIMILARITY.					
FT	CARBOHD	88	88		N-LINKED (GLCNAC . .) (POTENTIAL).					
FT	CARBOHD	136	136		N-LINKED (GLCNAC . .) (POTENTIAL).					

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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C9085785F1 CRC64;

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Query Match 97.0%; Score 191; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 6,8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 YTGILHSLEESONQOEKNEDELLELDKWSLWNF 36
Db 633 YTSILHSLEESONQOEKNEDELLELDKWSLWNF 668

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RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
ID ENV_HV1B1
AC P03375;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
VIRUSES: Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumanister K., Ivanoff L., Pelteway S.R., Jr., Pearson M.L.,
RA Lautenberger J.A., Pappas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RA Nature 313:277-284 (1985).
RL Nature 313:277-284 (1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RA "Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
Chinese hamster ovary cells.";
RA J. Biol. Chem. 265:10373-10382 (1990).
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CC EMBL: M15654; AAA44205.1; -.
CC PIR: A03973; VCLQJ3.
CC HIV: M15654; ENV5BH102.
CC InterPro: IPR000328; Env_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00517; GP41; 1.
CC Pfam: PF00517; GP41; 1.
CC AIDS: Coat protein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 30
FT CHAIN 512 856
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 366 366
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFPBIA8931BB27 CRC64;

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Query Match 97.0%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 6,8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Oy 1 YTGILHSLEESONQOEKNEDELLELDKWSLWNF 36
Db 638 YTSILHSLEESONQOEKNEDELLELDKWSLWNF 673

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```

RESULT 3
ENV_HV1H2 STANDARD; PRT; 856 AA.
ID ENV_HV1H2
AC P04578; 009779;

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Db 78 YTGIIYSLEESQNOEKNEQELLELDKWSLWNMF 113

RESULT 15

090IWO ID 090IWO PRELIMINARY: PRT: 122 AA.  
AC 090IWO;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses: Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-GP41ERRJ1;  
RC Caride E., Hertogs K., Larder B., Dehertogh P., Brindelro R.,  
Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,  
Calzans A.R., Tanuri A.;  
RT "Genotyping and phenotyping analysis of B and non-B Human  
immunodeficiency virus type 1 subtypes from patients under HAART";  
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF165544; AAF08489.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR pfam: PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14716 MW; CB39CE85DADE28FE CRC64;

Query Match 95.9%; Score 189; DB 15; Length 122;  
Best Local Similarity 94.4%; Pred. No. 1.1e-15;  
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYSLEESQNOEKNEQELLELDKWSLWNMF 36  
Db 78 YTGIIYSLEESQNOEKNEQELLELDKWSLWNMF 113

Search completed: May 16, 2003, 11:19:47  
Job time : 27.3124 secs

RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
RA Sodroski J.G.:  
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
RT responsible for the pathogenicity of a multiply passaged simian-human  
RT immunodeficiency virus (SHV-HXB2)."  
RL J. Virol. 73:976-984(1999).  
RN [12]  
RP SEQUENCE FROM N.A.  
RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.:  
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF041850; AAD12142.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 97151 MW; C50BE038FB73659 CRC64;

Query Match 97.0%; Score 191; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONQOEKNEDELLELDKWSLWMNF 36  
DB 638 YTSLSHSLEESONQOEKNEDELLELDKWSLWMNF 673

## RESULT 12

ID Q74599 PRELIMINARY; PRT; 856 AA.  
AC Q74599;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.:  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates."  
DE Virology 174:103-116(1990).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RA Iwatani Y.:  
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
DR EMBL: D86068; BAA12995.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 97287 MW; 238042A23AC56685 CRC64;

Query Match 97.0%; Score 191; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONQOEKNEDELLELDKWSLWMNF 36  
DB 638 YTSLSHSLEESONQOEKNEDELLELDKWSLWMNF 673

## RESULT 13

O74090

ID Q74090 PRELIMINARY; PRT; 856 AA.  
AC Q74090;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM213;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.:  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates."  
DE Virology 174:103-116(1990).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PM213;  
RA Iwatani Y.:  
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
DR EMBL: D86069; BAA13003.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 97.0%; Score 191; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONQOEKNEDELLELDKWSLWMNF 36  
DB 638 YTSLSHSLEESONQOEKNEDELLELDKWSLWMNF 673

## RESULT 14

ID Q9YXR6 PRELIMINARY; PRT; 122 AA.  
AC Q9YXR6;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE Envelope glycoprotein immunodominant region (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RJ96BRP004;  
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,  
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Plenzak D.,  
RA Rayfield M.:  
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."  
RT Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF034037; AAC97289.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR Pfam: PF00517; GP41.1.  
KW AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 122 AA; 14702 MW; 873C9A28AE14BA78 CRC64;

Query Match 95.9%; Score 189; DB 15; Length 122;  
Best Local Similarity 94.4%; Pred. No. 1.1e-15;  
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONQOEKNEDELLELDKWSLWMNF 36



RT Infected with HIV type 1 (HTLV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U12053; AAA7665.1;  
 DR EMBL; U12036; AAA7667.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF CRC64;

Query Match 97.0%; Score 191; DB 15; Length 852;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 YTGILSLIEESONQOEKNEQLLELDKASLWNMF 36  
 634 YTSILSLIEESONQOEKNEQLLELDKASLWNMF 669

RESULT 9  
 ID 085582 PRELIMINARY; PRT; 854 AA.  
 AC 085582;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope polypeptide.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 [1]  
 RX MEDLINE=86281827; PubMed=3016298;  
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
 Martin M.A.;  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone.";  
 RL J. Virol. 59:284-291(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92219406; PubMed=1373204;  
 RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;  
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
 RT gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T  
 RT lymphocytes.";  
 RL J. Virol. 66:3151-3154(1992).  
 DR EMBL; M1921; AAA44992.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 KW SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;

Query Match 97.0%; Score 191; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 YTGILSLIEESONQOEKNEQLLELDKASLWNMF 36  
 636 YTSILSLIEESONQOEKNEQLLELDKASLWNMF 671

RESULT 10  
 ID 072502 PRELIMINARY; PRT; 854 AA.  
 AC 072502;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE ENV polypeptide.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NL4-3;  
 RX MEDLINE=96036482; PubMed=7483282;  
 RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
 Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
 RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
 RT from primary virus cultures using the polymerase chain reaction.";  
 RL Virology 213:80-86(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NL4-3;  
 RX MEDLINE=86281827; PubMed=3016298;  
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
 Martin M.A.;  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone.";  
 RL J. Virol. 59:284-291(1986).  
 DR EMBL; U26942; AAB60578.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT CONFLICT 214 H -> L (IN REF. 2).  
 FT CONFLICT 530 A -> S (IN REF. 2).  
 FT CONFLICT 739 G -> D (IN REF. 2).  
 SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match 97.0%; Score 191; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 YTGILSLIEESONQOEKNEQLLELDKASLWNMF 36  
 636 YTSILSLIEESONQOEKNEQLLELDKASLWNMF 671

RESULT 11  
 ID 092877 PRELIMINARY; PRT; 856 AA.  
 AC 092877;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Simian-human immunodeficiency virus.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=57667;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9098984; PubMed=9882298;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW852:
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
RL infected with HIV type 1 (HIV type IIB).";
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW852:
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12031; AAA76667.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.
NON_TER 752
SEQUENCE 752 AA: 84894 MW: 8830AB94013B45A CRC64:

Query Match 97.0%; Score 191; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 4e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWMNF 36
DB 638 YTSILHSLEESQNOEKNEQELLELDKWSLWMNF 673

RESULT 6
O70608 PRELIMINARY: PRT: 752 AA.
AC O70608:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-2:
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
RL infected with HIV type 1 (HIV type IIB).";
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-2:
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12035; AAA76670.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.
NON_TER 752
SEQUENCE 752 AA: 84780 MW: 708672A2D0C0E8F8 CRC64:

Query Match 97.0%; Score 191; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 4e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWMNF 36
DB 638 YTSILHSLEESQNOEKNEQELLELDKWSLWMNF 673

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DB 638 YTSILHSLEESQNOEKNEQELLELDKWSLWMNF 673

RESULT 7
O78243 PRELIMINARY: PRT: 851 AA.
AC O78243:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Env polypotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai O.,
RA Verani P., Rossi G.B.;
RT "Sequence analysis of HIV-1 proviral DNA from a non producer
RL chronically infected HUT-78 cellular clone.";
RN J. Viral Diseases 1:40-55(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352106; PubMed=2765297;
RA Federic M., Tilti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Macchi B., Mangiano N., Verani P., Rossi G.;
RT "Biological and molecular characterization of producer and non
RL producer clones from HUT-78 infected with a patient HIV isolate.";
RN AIDS Res. Hum. Retroviruses 5:385-396(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tilti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,
RA Borselli A., Saggio I., Verani P., Rossi G.;
RT "Variability of HIV-1 virus: characteristics of an infected but not
RT productive clone.";
RL Int. J. Immunopharmacol. 3:17-23(1990).
DR EMBL: Z11530; CAA77628.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.
NON_TER 851
SEQUENCE 851 AA: 96630 MW: 1A3767B9B7E98027 CRC64:

Query Match 97.0%; Score 191; DB 15; Length 851;
Best Local Similarity 97.2%; Pred. No. 4.5e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWMNF 36
DB 633 YTSILHSLEESQNOEKNEQELLELDKWSLWMNF 668

RESULT 8
O89797 PRELIMINARY: PRT: 852 AA.
AC O89797:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW90-2:
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Viral variability and serum antibody response in a laboratory worker
RL infected with HIV type 1 (HIV type IIB).";
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker

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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-534

Perfect score: 197  
Sequence: 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL\_21:\*  
1: sp.\_archaea:\*  
2: sp.\_bacteria:\*  
3: sp.\_fungi:\*  
4: sp.\_human:\*  
5: sp.\_invertebrate:\*  
6: sp.\_mammal:\*  
7: sp.\_mhc:\*  
8: sp.\_organelle:\*  
9: sp.\_phage:\*  
10: sp.\_plant:\*  
11: sp.\_rodent:\*  
12: sp.\_virus:\*  
13: sp.\_vertebrate:\*  
14: sp.\_unclassified:\*  
15: sp.\_virus:\*  
16: sp.\_bacteriophage:\*  
17: sp.\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	97.0	645	15	0993A6 human immun
2	191	97.0	747	15	070607 human immun
3	191	97.0	748	15	070606 human immun
4	191	97.0	752	15	070604 human immun
5	191	97.0	752	15	070605 human immun
6	191	97.0	752	15	070608 human immun
7	191	97.0	851	15	078243 human immun
8	191	97.0	852	15	089797 human immun
9	191	97.0	854	15	085582 human immun
10	191	97.0	854	15	072502 human immun
11	191	97.0	856	15	092877 simian-huma
12	191	97.0	856	15	074599 human immun
13	191	97.0	856	15	074090 human immun
14	189	95.9	122	15	09YXR6 human immun
15	189	95.9	122	15	09Q1W0 human immun
16	188	95.4	122	15	09YXR2 human immun

17	188	95.4	122	15	09YXR0	Q9YXP0 human immun
18	188	95.4	122	15	091JR0	Q91JR0 human immun
19	188	95.4	122	15	091JO3	Q91JO3 human immun
20	188	95.4	122	15	091JP2	Q91JP2 human immun
21	188	95.4	357	15	078119	Q78119 human immun
22	188	95.4	843	15	070008	Q70008 human immun
23	188	95.4	847	15	069996	Q69996 human immun
24	188	95.4	854	15	040222	Q40222 human immun
25	188	95.4	855	15	080367	Q80367 human immun
26	188	95.4	859	15	097013	Q97013 human immun
27	187	94.9	851	15	0994B6	Q994B6 human immun
28	187	94.9	854	15	090178	Q90178 human immun
29	187	94.9	854	15	078705	Q78705 human immun
30	186	94.4	122	15	09YXP1	Q9YXP1 human immun
31	186	94.4	122	15	091JN5	Q91JN5 human immun
32	186	94.4	123	15	09EAA3	Q9EAA3 human immun
33	186	94.4	727	15	090KJ3	Q90KJ3 human immun
34	186	94.4	789	15	090KJ4	Q90KJ4 human immun
35	186	94.4	837	15	090KJ5	Q90KJ5 human immun
36	186	94.4	837	15	092761	Q92761 human immun
37	186	94.4	852	15	092761	Q92761 human immun
38	186	94.4	852	15	073303	Q73303 human immun
39	186	94.4	854	15	065656	Q65656 human immun
40	186	94.4	856	15	090SM7	Q90SM7 human immun
41	186	94.4	861	15	056109	Q56109 human immun
42	185	93.9	122	15	09Q1V1	Q9Q1V1 human immun
43	185	93.9	122	15	091JN6	Q91JN6 human immun
44	185	93.9	127	15	09YXX0	Q9YXX0 human immun
45	185	93.9	129	15	09YR25	Q9YR25 human immun

## ALIGNMENTS

## RESULT 1

ID	Q993A6	PRELIMINARY:	PRT:	645 AA.
AC	Q993A6			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	Truncated envelope glycoprotein (fragment).			
GN	ENV.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=1007;			
RX	MEDLINE=21192672; PubMed=11287644;			
RA	Suman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,			
RA	White S.W., Doherty P.C., Hurwitz J.L.;			
RT	"Localization of CD4+ T cell epitope hotspots to exposed strands of			
RT	HIV envelope glycoprotein suggests structural influences on antigen			
RT	processing."			
RT	Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).			
RL	EMBL: AF321563; AK18810.1;			
DR	InterPro: IPR000328; Env.GP41.			
DR	InterPro: IPR000777; GP120.			
DR	PIfam: PF00516; GP120; 1.			
KW	AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;			
KW	Transmembrane.			
FT	NON_TER			
SQ	SEQUENCE 645 AA: 72485 MW: B076514BE93362EC CRC64:			
Query Match	97.0%;	Score 191;	DB 15;	Length 645;
Best Local Similarity	97.2%;	Pred. No. 3.4e-15;		
Matches	35;	Conservative 0;	Mismatches 1;	Indels 0;

QY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNP 36  
DB 607 YTGILHSLEESQNOEKNEQELLELDKWSLWNP 642

PF	07-JUN-1994;	94WO-US05739
XX		
PR	07-JUN-1993;	93US-0073028
XX		

Query Match	100.0%;	Score 179;	DB 21;	Length 33;
Best Local Similarity	100.0%;	Pred. No. 1.6e-15;		
Matches 33;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	LIHSLIEESQNOQEKNEQELLELDKASLMMNF	33		
1	LIHSLIEESQNOQEKNEQELLELDKASLMMNF	33		
RESULT 3				
AAB52819				
ID	AAB52819	standard; Peptide: 33	AA.	
AC	AAB52819;			
DT	23-FEB-2001	(first entry)		
DE	T716	peptide fragment.		
XX	Antiinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion; T21/DP107;			
XX	formyl peptide receptor family; FPR; inflammatory response up-regulation;			
XX	chemoattractant.			
XX				
OS	Human immunodeficiency virus type 1.			
PN	WO20066622-A1.			
PD	09-NOV-2000.			
XX				
PF	05-MAY-2000; 2000WO-US12371.			
XX				
PR	05-MAY-1999; 99US-0132686.			
XX				
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.			
PI	Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;			
XX				
DR	WPI; 2000-656493/63.			
XX				
PT	Administration of peptide agents with a sequence corresponding to a			
PT	partial-length T20/DP178 or T21/DP107 formyl peptide receptor			
PT	antagonist is used to modulate inflammation			
XX				
PS	Example 1; Page 40; 148pp; English.			
XX				
CC	The present invention relates to peptide fragments of T20/DP178 and			
CC	T21/DP107 (see helical segments of the ectodomain of HIV-1 protein gp41.			
CC	T21/DP107 are helical segments of the ectodomain of HIV-1 protein gp41.			
CC	gp41 plays a critical role in the fusion of HIV-1 and host cell			
CC	membranes. T20/DP178 and T21/DP107 interact with members of the formyl			
CC	peptide receptor (FPR) family and thereby up-regulate an inflammatory			
CC	response, and act as potent chemoattractants and activators of human			
CC	peripheral blood phagocytes (but not T cells). The peptides of the			
CC	present invention can be used to modulate an inflammatory response in a			
CC	subject. The present sequence is a peptide isolated in the present			
CC	invention.			
XX				
SQ	Sequence 33	AA;		
Query Match	100.0%;	Score 179;	DB 21;	Length 33;
Best Local Similarity	100.0%;	Pred. No. 1.6e-15;		
Matches 33;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Sequence 33	AA;			

OY 1 LHSLSIESONOEKNEQELLELDKWSLWNMF 33  
 ||||||||||||||||||  
 DB 1 LHSLSIESONOEKNEQELLELDKWSLWNMF 33

RESULT 4  
 AAB14668  
 AAB14668 standard; peptide; 33 AA.

AC AAB14668;

DT 24-NOV-2000 (first entry)

DE HIV-1 isolate LAI gp41 C-helical domain peptide P-18, fragment #62.

OS HIV-1; gp41 C-helical domain;  
 KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KW core 6-helix bundle; viral entry inhibition; immunogenic;  
 KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;  
 isolate LAI.

OS Human immunodeficiency virus type 1.

PN WO200040616-A1.

PD 13-JUL-2000.

PE 10-JAN-2000; 2000WO-US00456.

PR 08-JAN-1999; 9905-0115404.

PR 07-JAN-2000; 2000US-0480336.

PA (WILD/) WILD C.T.

PI (WEISS/) WEISS C.D.

PI WILD CT, Weiss CD;

DR WPI; 2000-465959/40.

PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -

PS Disclosure: Page 33; 97pp; English.

CC Sequences AAB14604-B14606 and AAB14607-B14670 represent peptides derived  
 CC from the C-helical domain of the gp41 envelope glycoprotein from  
 CC HIV-1 group M, subtype B, isolate LAI. The invention relates to raising  
 CC a neutralising antibody response to a broad spectrum of HIV (human  
 CC immunodeficiency virus) strains and isolates, comprising the  
 CC administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the  
 CC process of viral entry into host cells. Such peptides can correspond  
 CC to or mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly  
 CC a combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can be  
 CC alternately linked together to form a peptide which mimics the core  
 CC 6-helix bundle. Administration of the peptide(s) generates a humoral  
 CC response, with the production of antibodies against gp41 structures  
 CC involved in viral entry. As these portions of gp41 are well conserved,  
 CC such antibodies may be effective against a broad range of HIV strains  
 CC and isolates. The peptide compositions may be administered as a  
 CC prophylactic or therapeutic vaccine to generate antibodies which reduce  
 CC or inhibit the ability of HIV to infect uninfected cells. A composition  
 CC comprising polyclonal or monoclonal antibodies can be administered to  
 CC reduce HIV infection of uninfected cells. Antibodies raised against  
 CC entry-relevant gp41 structures may also be used therapeutically and as

CC tools to further elucidate the mechanism of HIV cell entry.

SO Sequence 33 AA:

Query Match 100.0%; Score 179; DB 21; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1,66-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONOEKNEQELLELDKWSLWNMF 33  
 ||||||||||||||||||  
 DB 1 LHSLSIESONOEKNEQELLELDKWSLWNMF 33

RESULT 5  
 AAY88710  
 AAY88710 standard; peptide; 33 AA.

AC AAY88710;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 65.

OS Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

OS Unidentified.

PN WO9959615-A1.

PD 25-NOV-1999.

PE 20-MAY-1999; 99WO-US11219.

PR 20-MAY-1998; 98US-0082279.

PA (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

PS Disclosure: Page 22; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

SO Sequence 33 AA:

Query Match 100.0%; Score 179; DB 21; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1,66-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESQNOQEKNEQELLELDKWSLWNMF 33  
 Db 1 LIHSLIEESQNOQEKNEQELLELDKWSLWNMF 33

RESULT 6  
 AAY89390  
 ID AAY89390 standard; peptide: 33 AA.

AC AAY89390;

DF 23-MAY-2000 (first entry)

DE Core polypeptide fragment T NO. 925.

XX Retrovirus: hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KM anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

PN W09959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI: 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

XX Disclosure: Page 35; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX Sequence 33 AA:

Query Match 100.0%; Score 179; DB 21; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESQNOQEKNEQELLELDKWSLWNMF 33  
 Db 1 LIHSLIEESQNOQEKNEQELLELDKWSLWNMF 33

RESULT 7  
 ABB00069  
 ID ABB00069 standard; peptide: 33 AA.

XX ABB00069;

XX 03-JAN-2002 (first entry)

DE Viral DP178/107-like region peptide T65.

KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KM infection.

XX Virididae.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal is substituted by Ac"

FT Modified-site 33 /note= "C-terminal amide"

PN W0200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US03988.

XX 29-FEB-2000; 2000US-0515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

DR WPI: 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -

XX Disclosure: Page 34; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX Sequence 33 AA:

Query Match 100.0%; Score 179; DB 22; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESQNOQEKNEQELLELDKWSLWNMF 33  
 Db 1 LIHSLIEESQNOQEKNEQELLELDKWSLWNMF 33

RESULT 8  
 ABB00635  
 ID ABB00635 standard; peptide: 33 AA.

XX ABB00635;  
 AC ABB00635;  
 XX 03-JAN-2002 (first entry)

XX Viral DP178/107-like region peptide T716.  
 DE Viral DP178/107-like region peptide T716.  
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;



KM	virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;
KW	infection.
XX	
OS	Viridiae.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 1 /note= "N-terminal is substituted by Ac"
FT	Modified-site 33 /note= "C-terminal amide"
FT	
XX	
PN	MO200164013-A2.
XX	
PD	07-SEP-2001.
XX	
PF	07-FEB-2001; 2001WO-US03988.
XX	
PR	29-FEB-2000; 2000US-0515965.
XX	
XX	(TRIM-) TRIMERIS INC.
XX	
DR	Aniczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P; WPI: 2001-514829/56.
XX	
PT	Heptad repeat region peptide analogs useful for inhibiting virus/cells fusion, useful for treating HIV and Respiratory Syncytial Virus infection -
PT	
PS	Disclosure; Page 45; 587pp; English.
XX	
CC	The invention relates to isolated analogues of the heptad repeat region peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1) respectively, of HIV-1/tat transmembrane protein gp41. The HRI and HR2 regions of proteins interact non-covalently with each other and/or with peptides derived from them. This interaction is required for normal infectivity of viruses such as RSV and HIV. The heptad repeat region peptide analogues may be used to inhibit respiratory syncytial virus (RSV) infection in a cell. They may also be used to inhibit HIV infection. The present sequence is a peptide provided in the specification.
CC	
CC	
CC	
CC	
XX	
SO	Sequence 33 AA:
Query Match	100.0%; Score 179; DB 22; Length 33;
Best Local Similarity	100.0%; Pred. No. 1.6e-15;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 LIHSLIESONQEKNEDELLDLKWSLWNMF 33	
1 LIHSLIESONQEKNEDELLDLKWSLWNMF 33	
Db	
RESULT 9	
ABB00798	
ID	ABB00798 standard; Peptide: 33 AA.
XX	
AC	ABB00798;
XX	
DT	03-JAN-2002 (first entry)
XX	
DE	Viral DP178/107-like region peptide T925.
XX	
KW	Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW	virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;
XX	infection.
XX	
OS	Viridiae.
XX	
XX	
FH	Key Location/Qualifiers
FT	Modified-site 33 /note= "C-terminal amide"
FT	

```

XX      WO200164013-A2.
PN
XX      07-SEP-2001.
PD
XX      07-FEB-2001; 2001WO-US03988.
PE
XX      29-FEB-2000; 2000US-0515965.
PR
XX      (TRIM-) TRIMERIS INC.
PA
XX      Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
PI
XX      WPI; 2001-514829/56.
DX
XX      Hepfad repeat region peptide analogs useful for inhibiting virus/cells
PT      fusion, useful for treating HIV and Respiratory Syncytial Virus
PF      infection -
PS
XX      Disclosure; Page 49; 567pp; English.
FS
XX
XX      The invention relates to isolated analogues of the heptad repeat region
CC      peptides DP178 and DP107. DP178 and DP107 correspond to amino acids
CC      638-673 (hepfad repeat region HR2) and 558-595 (hepfad repeat region
CC      HRI) respectively, of HIV-1LAI transmembrane protein gp41. The HRI
CC      and/or regions of proteins interact non-covalently with each other
CC      and/or with peptides derived from them. This interaction is required for
CC      normal infectivity of viruses such as RSV and HIV. The hepfad
CC      repeat region peptide analogues may be used to inhibit respiratory
CC      syncytial virus (RSV) infection in a cell. They may also be used to
CC      inhibit HIV infection. The present sequence is a peptide provided in
CC      the specification.
SQ      Sequence      33 AA:

Query Match          100.0%; Score 179; DB 22; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.0e-15;
Matches    33; Conservative   0; Mismatches    0; Indels    0; Gaps    0;

OY      1 LIHSLSIESONQOEKNEOFLELDKWSLMMNF 33
         |||||||
DB      1 LIHSLSIESQNQEKNBOELLELDKWSLMMNF 33

RESULT 10
ABR01534
ID      ABR01534 standard; Peptide; 33 AA.
XX
XX      ABR01534;
AC
XX      03-JAN-2002 (first entry)
DT
XX
DE      Viral core polypeptide, SEQ ID NO: 61.
XX
XX      Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW      vitucude; hepfad repeat region; transmembrane protein; gp41; HRI; HR2;
RV      infection.
XX
XX      Virididae.
OS
XX      WO200164013-A2.
PN
XX
XX      07-SEP-2001.
PD
XX
XX      07-FEB-2001; 2001WO-US03988.
PE
XX      29-FEB-2000; 2000US-0515965.
PR
XX      (TRIM-) TRIMERIS INC.
PA
XX
XX      Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
PI
XX      WPI; 2001-514829/56.
DX
XX

```

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection -  
XX  
XX PS Disclosure: Page 182; 587pp; English.  
XX  
XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1/IIAI transmembrane protein gp41. The HR1  
CC and HR2 regions of proteins interact non-covalently with each other  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.  
XX  
XX Sequence 33 AA:  
XX  
XX  
XX Query Match 100.0%; Score 179; DB 22; Length 33;  
XX Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LHSLSIESONQOEKNEDELLELDKWSLWMPF 33  
DB 1 LHSLSIESONQOEKNEDELLELDKWSLWMPF 33  
RESULT 11  
AB02112  
ID AB02112 standard; Peptide: 33 AA.  
XX  
XX ABB02112;  
XX  
XX 03-JAN-2002 (first entry)  
XX  
XX Viral core polypeptide, SEQ ID NO: 639.  
XX  
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
XX virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
XX infection.  
XX  
XX Viridiae.  
XX  
XX WO200164013-A2.  
XX  
XX 07-SEP-2001.  
XX  
XX 07-FEB-2001; 2001WO-US03988.  
XX  
XX 29-FEB-2000; 2000US-0515965.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
XX MPI; 2001-514829/56.  
XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection -  
XX  
XX Disclosure: Page 336; 587pp; English.  
XX  
XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1/IIAI transmembrane protein gp41. The HR1  
CC and HR2 regions of proteins interact non-covalently with each other  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.

CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.  
XX  
XX Sequence 33 AA:  
XX  
XX  
XX Query Match 100.0%; Score 179; DB 22; Length 33;  
XX Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LHSLSIESONQOEKNEDELLELDKWSLWMPF 33  
DB 1 LHSLSIESONQOEKNEDELLELDKWSLWMPF 33  
RESULT 12  
AB02274  
ID AB02274 standard; Peptide: 33 AA.  
XX  
XX ABB02274;  
XX  
XX 03-JAN-2002 (first entry)  
XX  
XX Viral core polypeptide, SEQ ID NO: 801.  
XX  
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
XX virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
XX infection.  
XX  
XX Viridiae.  
XX  
XX WO200164013-A2.  
XX  
XX 07-SEP-2001.  
XX  
XX 07-FEB-2001; 2001WO-US03988.  
XX  
XX 29-FEB-2000; 2000US-0515965.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
XX MPI; 2001-514829/56.  
XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection -  
XX  
XX Disclosure: Page 380; 587pp; English.  
XX  
XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1/IIAI transmembrane protein gp41. The HR1  
CC and HR2 regions of proteins interact non-covalently with each other  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.  
XX  
XX Sequence 33 AA:  
XX  
XX  
XX Query Match 100.0%; Score 179; DB 22; Length 33;  
XX Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LHSLSIESONQOEKNEDELLELDKWSLWMPF 33  
DB 1 LHSLSIESONQOEKNEDELLELDKWSLWMPF 33

RESULT 13  
AAU12618  
ID AAU12618 standard; peptide; 33 AA.  
XX  
AC AAU12618;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE DP178-like/DP107-like peptide T-65.  
XX  
KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
XX antifusogenic; antiviral; HIV transmission; mutant; mutain.  
OS  
OS Human immunodeficiency virus 1 isolate LAI.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FH Modified-site 1 /note="N-terminal is substituted by Ac"  
FT Modified-site 33 /note="C-terminal amide"  
FT  
PN WO200151673-A2.  
XX  
PD 19-JUL-2001.  
XX  
PE 05-JUL-2000; 2000WO-US35727.  
XX  
PR 09-JUL-1999; 99US-0350841.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
XX  
DR WPI: 2001-442157/47.  
XX  
PT Identifying a compound that inhibits the formation of or disrupts a  
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
PT or intracellular modulatory activity, by detecting the formation of a  
PT DP107/DP178 complex -  
XX  
PS Disclosure; Page 54; 259pp; English.  
XX  
XX The present invention relates to peptides which exhibit anti-retroviral  
XX activity. The peptides of the invention (AAU12559-AAU14009) comprise  
XX DP178-like and DP107-like peptides. The DP178 peptide corresponds  
XX to amino acids 639-673 of the transmembrane protein gp41 from human  
XX immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
XX corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
XX also relates to a method of identifying compounds that inhibit the  
XX formation of or disrupts a DP107/DP178 complex. The method comprises  
XX detecting the formation of a DP107/DP178 complex, both in the presence  
XX or absence of a test compound, in a reaction mixture containing DP107  
XX and DP178 peptides. The method is useful for identifying compounds,  
XX including small molecule compounds, which may themselves exhibit  
XX antifusogenic, antiviral or intracellular modulatory activity. The  
XX DP178-like/DP107-like peptides are useful to inhibit human and non-human  
XX retroviral, particularly HIV, transmission to uninfected cells. The  
XX present sequence represents one of the DP178-like/DP107-like peptides  
XX of the invention.  
XX  
SQ Sequence 33 AA;  
XX

Query Match 100.0%; Score 179; DB 22; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1,6e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTHSLIEESQNOEKNEDELLELDKWSLWNNF 33  
DB 1 LTHSLIEESQNOEKNEDELLELDKWSLWNNF 33

RESULT 14  
AAU13183  
ID AAU13183 standard; peptide; 33 AA.  
XX  
AC AAU13183;  
XX  
DT 21-NOV-2001 (first entry)  
XX  
DE DP178-like/DP107-like peptide T-716.  
XX  
KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
XX antifusogenic; antiviral; HIV transmission; mutant; mutain.  
OS  
OS Human immunodeficiency virus 1 isolate LAI.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FH Modified-site 1 /note="N-terminal is substituted by Ac"  
FT Modified-site 33 /note="C-terminal amide"  
FT  
PN WO200151673-A2.  
XX  
PD 19-JUL-2001.  
XX  
PE 05-JUL-2000; 2000WO-US35727.  
XX  
PR 09-JUL-1999; 99US-0350841.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
XX  
DR WPI: 2001-442157/47.  
XX  
PT Identifying a compound that inhibits the formation of or disrupts a  
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
PT or intracellular modulatory activity, by detecting the formation of a  
PT DP107/DP178 complex -  
XX  
PS Disclosure; Page 65; 259pp; English.  
XX  
XX The present invention relates to peptides which exhibit anti-retroviral  
XX activity. The peptides of the invention (AAU12559-AAU14009) comprise  
XX DP178-like and DP107-like peptides. The DP178 peptide corresponds  
XX to amino acids 639-673 of the transmembrane protein gp41 from human  
XX immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
XX corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
XX also relates to a method of identifying compounds that inhibit the  
XX formation of or disrupts a DP107/DP178 complex. The method comprises  
XX detecting the formation of a DP107/DP178 complex, both in the presence  
XX or absence of a test compound, in a reaction mixture containing DP107  
XX and DP178 peptides. The method is useful for identifying compounds,  
XX including small molecule compounds, which may themselves exhibit  
XX antifusogenic, antiviral or intracellular modulatory activity. The  
XX DP178-like/DP107-like peptides are useful to inhibit human and non-human  
XX retroviral, particularly HIV, transmission to uninfected cells. The  
XX present sequence represents one of the DP178-like/DP107-like peptides  
XX of the invention.  
XX  
SQ Sequence 33 AA;  
XX

Query Match 100.0%; Score 179; DB 22; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1,6e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTHSLIEESQNOEKNEDELLELDKWSLWNNF 33  
DB 1 LTHSLIEESQNOEKNEDELLELDKWSLWNNF 33



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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 11.1325 seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-119  
Perfect score: 179  
Sequence: 1 LIHSLIESQNOEKNEQELLELDKWSLWNVF 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	100.0	851	2 S33985	env polypeptide -
2	179	100.0	854	2 S13288	env polypeptide - huma
3	179	100.0	856	1 VCLJH3	env polypeptide pr
4	179	100.0	861	1 VCLJLV	env polypeptide pr
5	170	95.0	357	2 S21994	env polypeptide pr
6	170	95.0	357	2 S21996	env polypeptide pr
7	170	95.0	443	2 C41621	env polypeptide pr
8	170	95.0	856	1 VCLJVL	env polypeptide pr
9	170	95.0	856	1 VCLJW	env polypeptide pr
10	170	95.0	861	1 VCLJSC	env polypeptide pr
11	167	93.3	358	2 S21998	env polypeptide pr
12	166	92.7	847	2 T09448	env polypeptide pr
13	166	92.7	847	2 S13289	env polypeptide pr
14	164	91.6	357	2 S22004	env polypeptide pr
15	164	91.6	855	1 VCLJAJ	env polypeptide pr
16	162	90.5	445	2 A41621	env polypeptide pr
17	162	90.5	843	1 H44001	env polypeptide pr
18	162	90.5	853	1 S54384	env polypeptide pr
19	162	89.5	357	2 S22005	env polypeptide pr
20	161	89.9	357	2 S22006	env polypeptide pr
21	161	89.9	358	2 S22002	env polypeptide pr
22	161	89.9	358	2 S22000	env polypeptide pr
23	161	89.9	358	2 S70417	env polypeptide pr
24	161	89.9	852	2 T12016	env polypeptide pr
25	161	89.9	859	1 VCLJMN	env polypeptide pr
26	160	89.4	846	1 VCLJND	env polypeptide pr
27	157	87.7	357	2 S21992	env polypeptide pr
28	157	87.7	852	1 VCLJBR	env polypeptide pr
29	153	86.6	729	1 VCLJRX	env polypeptide pr

30	155	86.6	859	2 T01672	envelope polypeptide
31	155	86.6	861	1 VCLJKB	env polypeptide pr
32	154	86.0	454	2 B41621	env polypeptide pr
33	152	84.9	868	1 VCLJH4	env polypeptide pr
34	147	82.1	136	2 J00266	env polypeptide pr
35	147	82.1	136	2 J00266	env polypeptide pr
36	141	78.8	854	1 VCLJST	env polypeptide pr
37	137	76.5	856	1 A44963	env polypeptide pr
38	131	73.2	357	2 S21990	env polypeptide pr
39	131	73.2	877	2 S49197	env polypeptide pr
40	115	64.2	863	2 A53034	env polypeptide pr
41	86	48.0	881	1 VCLJG3	env polypeptide pr
42	86	48.0	881	2 S03068	env polypeptide pr
43	86	48.0	889	1 VCLJG5	env polypeptide pr
44	85	47.5	151	2 S30448	env polypeptide pr
45	85	47.5	151	2 S30452	env polypeptide pr

## ALIGNMENTS

RESULT 1  
S33985  
env polypeptide - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
Submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-references: EMBL:Z11530; NID:G60192; PIDN:CAA77628.1; PID:G60199  
C:Superfamily: type E retrovirus env polypeptide

Query Match  
Best Local Similarity 100.0%; Score 179; DB 2; Length 851;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIESQNOEKNEQELLELDKWSLWNVF 33  
DB 636 LIHSLIESQNOEKNEQELLELDKWSLWNVF 668

RESULT 2  
S13288  
env polypeptide - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polypeptide

Query Match  
Best Local Similarity 100.0%; Score 179; DB 2; Length 854;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIESQNOEKNEQELLELDKWSLWNVF 33  
DB 639 LIHSLIESQNOEKNEQELLELDKWSLWNVF 671

RESULT 3  
VCLJH3

```
env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran-
berger, J.A.; Papas, T.S.; Chirgwin, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A>Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2576615
A:Accession: A03973
A:Molecule type: DNA
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept
E:1-30/Domain: signal sequence #status predicted <SIG>
E:1-511/Product: exterior membrane glycoprotein #status predicted <TM>
E:1-856/Product: transmembrane glycoprotein #status predicted <TM>
E:18,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,366,392,397,406
E:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 100.0%; Score 179; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LHSLSIESQNOOEKNEOELLELDKWSLWNP 33
DB 641 LHSLSIESQNOOEKNEOELLELDKWSLWNP 673
RESULT 4
VCLUTV
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran-
berger, J.A.; Papas, T.S.; Chirgwin, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A>Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2576615
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAT>
A:Cross-references: GB:K02013; NID:9326417; PIDN:AAB59751.1; PID:9326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept
E:1-30/Domain: signal sequence #status predicted <SIG>
E:1-511/Product: exterior membrane glycoprotein #status predicted <TM>
E:1-856/Product: transmembrane glycoprotein #status predicted <TM>
E:18,136,141,156,161,191,202,233,246,267,281,294,300,306,337,344,361,391,397,402,411
E:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 100.0%; Score 179; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LHSLSIESQNOOEKNEOELLELDKWSLWNP 33
DB 646 LHSLSIESQNOOEKNEOELLELDKWSLWNP 678
RESULT 5
S21994
env polypeptide precursor - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
```

```
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21994
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STEL>
A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:960180
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STEL>
A:Cross-references: EMBL:X61355; NID:960179
C:Superfamily: type E retrovirus env polypeptide
Query Match 95.0%; Score 170; DB 2; Length 357;
Best Local Similarity 93.9%; Pred. No. 4.7e-13;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 LHSLSIESQNOOEKNEOELLELDKWSLWNP 33
DB 142 LHSLSIESQNOOEKNEOELLELDKWSLWNP 174
RESULT 6
S21996
env polypeptide precursor - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STEL>
A:Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:91067129
A:Experimental source: patient 27L
A>Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypeptide
Query Match 95.0%; Score 170; DB 2; Length 357;
Best Local Similarity 93.9%; Pred. No. 4.7e-13;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 LHSLSIESQNOOEKNEOELLELDKWSLWNP 33
DB 142 LHSLSIESQNOOEKNEOELLELDKWSLWNP 174
RESULT 7
C41621
env polypeptide precursor - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polypeptide
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
```

A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:q328631; PIDN:AAB03792.1; PID:q555015  
A:Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:424-443/Domain: transmembrane #status predicted <TM>  
F:9,23,36,48,78,101,107,131,137,143,147,153,186,200,203,351,356,365,377/Binding site: ca

Query Match 95.0%; Score 170; DB 1; Length 443;  
Best Local Similarity 93.9%; Pred. No. 6e-13;  
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLEDKNASLWNMF 33  
||:|||||  
381 LITNLEESONQOEKNEDELLEDKNASLWNMF 413

RESULT 8  
VCLJVL  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03974  
R:Wensing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A:Title: Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retrov  
A:Reference number: A93355; MUID:85111157; PMID:2982104  
A:Molecule type: DNA  
A:Residues: 1-856 <MUR>  
A:Cross-references: GB:K02083; NID:q555008; PIDN:AAB59873.1; PID:q328559  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status predic

Query Match 95.0%; Score 170; DB 1; Length 856;  
Best Local Similarity 96.9%; Pred. No. 1.2e-12;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLEDKNASLWNMF 32  
||:|||||  
Db 641 LITNLEESONQOEKNEDELLEDKNASLWNMF 672

RESULT 9  
VCLJ3W  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the en  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:q1906382  
C:Genetics:

A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <Sig>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,

Query Match 95.0%; Score 170; DB 1; Length 856;  
Best Local Similarity 93.9%; Pred. No. 1.2e-12;  
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLEDKNASLWNMF 33  
||:|||||  
Db 641 LITNLEESONQOEKNEDELLEDKNASLWNMF 673

RESULT 10  
VCLJSC  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922  
R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-  
Virology 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091  
A:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane pr  
F:1-29/Domain: signal sequence #status predicted <Sig>  
F:30-861/Product: env polyprotein #status predicted <EP>  
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,

Query Match 95.0%; Score 170; DB 1; Length 861;  
Best Local Similarity 93.9%; Pred. No. 1.2e-12;  
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLEDKNASLWNMF 33  
||:|||||  
Db 646 LITNLEESONQOEKNEDELLEDKNASLWNMF 678

RESULT 11  
S21998  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: Isolate 28  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21998; S70425  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL data library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
A:Reference number: S21990  
A:Accession: S21998  
A:Molecule type: DNA  
A:Residues: 1-358 <STE1>  
A:Cross-references: EMBL:X61359; NID:q60182; PIDN:CAA43630.1; PID:q60183  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209; PMID:1736940.  
A:Accession: S70425  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-222, X, 224-358 <STE2>  
A:Cross-references: EMBL:X61359; NID:q60182; PIDN:CAA43630.1; PID:q60183

C:Superfamily: type E retrovirus env polypeptide

Query Match 93.3%; Score 167; DB 2; Length 358;

Best Local Similarity 90.9%; Pred. No. 1.1e-12;

Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 143 LITLIESONQOEKNEDELLELDKMASLWNF 175

RESULT 12

T09448 envelope glycoprotein - human immunodeficiency virus type 1 (strain JFL)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

C:Accession: T09448

R:Panig, S.; Vinters, H.V.; Akshat, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09448

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

Query Match 92.7%; Score 166; DB 2; Length 847;

Best Local Similarity 93.8%; Pred. No. 3.7e-12;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 633 IYTLIESONQOEKNEDELLELDKMASLWNF 664

RESULT 13

S13289 env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13288; PMID:91043044; PMID:2172833

A:Accession: S13289

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-847 <COBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 92.7%; Score 166; DB 2; Length 847;

Best Local Similarity 93.8%; Pred. No. 3.7e-12;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 633 IYTLIESONQOEKNEDELLELDKMASLWNF 664

RESULT 14

S22004 envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: Isolate 4B

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22004; S70419

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi

A:Reference number: S21990

A:Accession: S22004

A:Molecule type: DNA

A:Residues: 1-357 <STP1>

A:Cross-references: EMBL:X61353; NID:g60188; PID:CAA43618.1; PID:g60189

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; PMID:92144209; PMID:1736940

A:Accession: S70419

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-292, 'X', 294-357 <STP2>

A:Cross-references: EMBL:X61353; NID:g60188

C:Superfamily: type E retrovirus env polypeptide

Query Match 91.6%; Score 164; DB 2; Length 357;

Best Local Similarity 90.9%; Pred. No. 2.5e-12;

Matches 30; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 142 LITLIESONQOEKNEDELLELDKMASLWNF 174

RESULT 15

VCJLA2

env polypeptide precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: Host Homo sapiens (man)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03976

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown

Science 227, 484-492, 1985

A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A:Reference number: A04003; PMID:85090453; PMID:2578227

A:Accession: A03976

A:Molecule type: DNA

A:Residues: 1-855 <SAN>

A:Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly

F:1-30/Domain: signal sequence #status predicted <Sig>

F:31-509/Product: exterior membrane glycoprotein #status predicted <TM>

F:510-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,

F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.6%; Score 164; DB 1; Length 855;

Best Local Similarity 90.6%; Pred. No. 6.5e-12;

Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 641 IYTLIESONQOEKNEDELLELDKMASLWNF 672

Search completed: May 16, 2003, 11:25:08

Job time: 11.1325 secs





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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CR64;

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Query Match 100.0%; Score 179; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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OY 1 LHSLSIESQNOOEKNEDELLELDKWSLSMNF 33
DB 636 LHSLSIESQNOOEKNEDELLELDKWSLSMNF 668

```

```

RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV
OS Human immunodeficiency virus type 1 (BHD isolate) (HIV-1).
OS Viruses: Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;
RA MEDLINE=8511123; PubMed=2578615;
RA Ratter L., Haseltine W., Patarca R., Livak K.J., Starich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumesler K., Ivanoff B., Peteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Pappas T.S., Ghayab J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RA Nature 313:277-284 (1985).
RN [2]
RN DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
RT potential glycosylation sites of the type 1 recombinant human
RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells.";
RT J. Biol. Chem. 265:10373-10382 (1990).
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CC EMBL: M15654; AAA44205.1; -.
CC PIR: A03973; VCL03.
DR HIV: M15654; ENV5BH102.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Signal.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;

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FT SIGNAL 1 30
FT CHAIN 1 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
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FT DISULFID 218 247
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FT DISULFID 385 418
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FT CARBOHYD 136 136
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FT CARBOHYD 156 156
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FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931B27 CR64;

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Query Match 100.0%; Score 179; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LHSLSIESQNOOEKNEDELLELDKWSLSMNF 33
DB 641 LHSLSIESQNOOEKNEDELLELDKWSLSMNF 673

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RESULT 3
ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 97188 MW; 3373C68B84C1AFC CRC64;

Query Match 100.0%; Score 179; DB 1; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONOEKNEQELLELDKWSLIMNF 33  
 DB 641 LHSLSIESONOEKNEQELLELDKWSLIMNF 673

RESULT 5  
 ENV\_HVILW STANDARD; PRT; 856 AA.  
 AC Q70626;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 ENV.

OC Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=82834;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,  
 RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC EMBL: U12055; AAA76690.1; -  
 DR GLYcosultEDB: Q70626;  
 DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 241 241  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 289 289  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392  
 FT CARBOHYD 397 397  
 FT CARBOHYD 406 406  
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 FT CARBOHYD 463 463  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 624 624  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

Query Match 100.0%; Score 179; DB 1; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONOEKNEQELLELDKWSLIMNF 33  
 DB 641 LHSLSIESONOEKNEQELLELDKWSLIMNF 673

RESULT 6  
 ENV\_HVILW STANDARD; PRT; 861 AA.  
 AC P03377;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 ENV.

OC Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11086;  
 RN [1]



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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 853 AA: 96912 MW: 3377B93B6F22ABA CRC64:

Query Match
Best Local Similarity 98.3%: Score 176; DB 1; Length 853;
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 LHSLSIESQNOEKNEDELLEDKWASLWNMF 33
639 LHSLSIESQNOEKNEDELLEDKWASLWNMF 671

OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Outroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
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CC -----
CC EMBL: M65024; AAA5072.1; -
CC HIV; M38428; ENV56SF162.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
KW Signal.
FT FT 1 29
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 338 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.

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FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 847 AA: 96135 MW: 0A901317FD7FE2AB CRC64:

Query Match
Best Local Similarity 95.0%: Score 170; DB 1; Length 847;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 LHSLSIESQNOEKNEDELLEDKWASLWNMF 33
632 LHSLSIESQNOEKNEDELLEDKWASLWNMF 664

OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
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CC -----
CC EMBL: K02083; AAB59873.1; -
CC EMBL: X01762; CAA25903.1; ALT_SEQ.
DR PIR: A03974; VCLIVL.
DR HIV: K02083; ENVSPV22.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.

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DR Pfam: PF00517; GP41; 1.  
 KM Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 RN Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
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 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97339 MW; 5FCD81DC3C1209B3 CRC64;  
 Query Match 95.0%; Score 170; DB 1; Length 856;  
 Best Local Similarity 96.9%; Pred. No. 2.5e-13;  
 Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LIHSLIESONQOEKNEDELLEDKWASLMNW 32  
 Db 641 LIHSLIESONQOEKNEDELLEDKWASLMNW 672  
 RESULT 10  
 ENV\_HV1SC STANDARD; PRT: 856 AA.  
 AC P05878; 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).  
 OC Viruses: Retroid viruses; Retroviridae; Lentivirus.  
 OC NCBI\_TaxID=11702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88219542; PubMed=3369091;

RA Guirgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;  
 FT "Envelope sequences of two new United States HIV-1 isolates."  
 RL Virology 164:531-536(1988).  
 CC -i- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.  
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 CC -----  
 CC EMBL: M17450; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: B28922; VCLJSC.  
 DR HIV: M17450; ENVSSC.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 RN Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 510  
 FT CHAIN 511 856  
 FT SITE 760 760  
 FT DISULFID 53 73  
 FT DISULFID 118 206  
 FT DISULFID 125 197  
 FT DISULFID 130 160  
 FT DISULFID 219 247  
 FT DISULFID 228 239  
 FT DISULFID 266 330  
 FT DISULFID 296 330  
 FT DISULFID 376 439  
 FT DISULFID 383 412  
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 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;  
 Query Match 95.0%; Score 170; DB 1; Length 856;  
 Best Local Similarity 93.9%; Pred. No. 2.5e-13;







Query Match	Best Local Similarity	Matches	29; Conservative	Score 164; DB 1; Length 855; Pared No. 1,3e-12; Mismatches 0; Indels 0; Gaps 0
QY 2	INSLSIESQNOQEKNEDELLELDKWSLWNWF	33	100	100
Db 641	ITYTLLESQNOQEKNEDELLELDKWSLWNWF	672	100	100

RESULT 15

ID	ENV_HVIEL	STANDARD:	PRT:	853 AA.
AC	ENV_HVIEL			
AC	P04581:			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].			
DE	ENV.			
OS	Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).			
OC	Viruses; Retrovirdae; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11689;			
RM	[1]			
RP-	SEQUENCE FROM N.A.			
RX	MEDLINE=86245056; PubMed=2424612;			
RA	Allison M., Main-Hobson S., Montagnier L., Sonigo P.;			
RT	"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients."			
RL	Cell 46:63-74(1986).			
CC	-----			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL: K03454; AAA44329.1; -			
DR	EMBL: A07108; CAA00616.1; -			
DR	HIV: K03454; ENSESEL.			
DR	InterPro: IPR000328; ENV_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	SIGNAL	1	31	BY SIMILARITY.
FT	CHAIN	32	508	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	509	853	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	154	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	257	330	BY SIMILARITY.
FT	DISULFID	376	442	BY SIMILARITY.
FT	DISULFID	383	416	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	137	137	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	143	143	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	153	153	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	188	188	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	235	235	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	277	277	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	353	353	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	384	384	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	390	390	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	394	394	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	405	405	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	411	411	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	445	445	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAA0D07A5 CRC64;

Query Match 91.1%; Score 163; DB 1; Length 853;  
 Best Local Similarity 90.9%; Pred. No. 1.8e-12;  
 Matches 30; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQELLEDKWSLWNP 33  
 ||:||||| ||||:|||||  
 Db 638 LHSLSIESQTOEKNEKELLEDKWSLWNP 670

Search completed: May 16, 2003, 11:13:34  
 time : 6.56626 secs

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GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 24.0542 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-119  
Perfect score: 179  
Sequence: 1 LIHSLIEESONQOEKNEQELLELDKWSLWVWF 33

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mhc:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	179	100.0	645 15 0993A6	0993A6 human immun
2	179	100.0	747 15 070607	070607 human immun
3	179	100.0	748 15 070606	070606 human immun
4	179	100.0	752 15 070604	070604 human immun
5	179	100.0	752 15 070605	070605 human immun
6	179	100.0	752 15 070608	070608 human immun
7	179	100.0	851 15 078243	078243 human immun
8	179	100.0	852 15 089797	089797 human immun
9	179	100.0	854 15 085582	085582 human immun
10	179	100.0	854 15 072502	072502 human immun
11	179	100.0	856 15 092877	092877 simian-huma
12	179	100.0	856 15 074599	074599 human immun
13	179	100.0	856 15 074090	074090 human immun
14	175	97.8	854 15 090178	090178 human immun
15	175	97.8	854 15 078705	078705 human immun
16	174	97.2	856 15 0905M7	0905M7 human immun

17	173	96.6	616 15 0993B0	0993B0 human immun
18	173	96.6	618 15 0993B2	0993B2 human immun
19	173	96.6	757 15 090722	090722 human immun
20	173	96.6	848 15 069990	069990 human immun
21	171	95.5	122 15 091XK6	091XK6 human immun
22	171	95.5	122 15 09Q1W0	09Q1W0 human immun
23	171	95.5	838 15 003806	003806 human immun
24	171	95.5	854 15 078225	078225 human immun
25	171	95.5	855 15 003805	003805 human immun
26	170	95.0	42 15 069910	069910 human immun
27	170	95.0	122 15 091XK2	091XK2 human immun
28	170	95.0	122 15 09YX08	09YX08 human immun
29	170	95.0	122 15 09YX00	09YX00 human immun
30	170	95.0	122 15 091J03	091J03 human immun
31	170	95.0	122 15 091J03	091J03 human immun
32	170	95.0	122 15 091J02	091J02 human immun
33	170	95.0	357 15 078118	078118 human immun
34	170	95.0	357 15 078119	078119 human immun
35	170	95.0	443 15 080023	080023 human immun
36	170	95.0	684 15 091K06	091K06 human immun
37	170	95.0	841 15 041556	041556 human immun
38	170	95.0	843 15 070008	070008 human immun
39	170	95.0	847 15 069996	069996 human immun
40	170	95.0	849 15 077368	077368 human immun
41	170	95.0	849 15 080851	080851 human immun
42	170	95.0	850 15 041591	041591 human immun
43	170	95.0	851 15 056110	056110 human immun
44	170	95.0	851 15 080852	080852 human immun
45	170	95.0	854 15 040222	040222 human immun

## ALIGNMENTS

RESULT 1  
0993A6 PRELIMINARY; PRT; 645 AA.  
ID 0993A6  
AC 0993A6;  
DT 01-JUN-2001 (TRENBLREL 17, Created)  
DT 01-JUN-2001 (TRENBLREL 17, Last sequence update)  
DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Stobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.,  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing."  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
RL EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
KW Transmembrane.  
FT NON\_TER  
SQ  
SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;  
Query Match 100.0%; Score 179; DB 15; Length 645;  
Best Local Similarity 100.0%; Pred. No. 8.5e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LIHSLIEESONQOEKNEQELLELDKWSLWVWF 33  
DB 610 LIHSLIEESONQOEKNEQELLELDKWSLWVWF 642

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RESULT 2
ID 070607 PRELIMINARY; PRT; 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RX MEDLINE=95127297; Pubmed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
RA AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;

Query Match 100.0%; Score 179; DB 15; Length 747;
Best Local Similarity 100.0%; Pred. No. 9.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIESQNOEKNEQELLELDKWSLWNF 33
Db 636 LIHSLIESQNOEKNEQELLELDKWSLWNF 668

RESULT 3
ID 070606 PRELIMINARY; PRT; 748 AA.
AC 070606;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW81;
RX MEDLINE=95127297; Pubmed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW81;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
RA AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 179; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 9.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIESQNOEKNEQELLELDKWSLWNF 33
Db 641 LIHSLIESQNOEKNEQELLELDKWSLWNF 673

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DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEFF186C67694B CRC64;

Query Match 100.0%; Score 179; DB 15; Length 748;
Best Local Similarity 100.0%; Pred. No. 9.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIESQNOEKNEQELLELDKWSLWNF 33
Db 637 LIHSLIESQNOEKNEQELLELDKWSLWNF 669

RESULT 4
ID 070604 PRELIMINARY; PRT; 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RX MEDLINE=95127297; Pubmed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12030; AAA7666.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
RA AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 179; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 9.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIESQNOEKNEQELLELDKWSLWNF 33
Db 641 LIHSLIESQNOEKNEQELLELDKWSLWNF 673

RESULT 5
ID 070605 PRELIMINARY; PRT; 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;

```

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM852;  
RX MEDLINE-95127297; PubMed-7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HIV type IIB).";  
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RL [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM852;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12031; AAA76667.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
NON\_TER 752  
SEQUENCE 752 AA; 84894 MW; 8B30AB994013B45A CRC64;

Query Match 100.0%; Score 179; DB 15; Length 752;  
Best Local Similarity 100.0%; Pred. No. 9.9e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONOOEKNEQELLELDKASISLWNMF 33  
DB 641 LHSLSIESONOOEKNEQELLELDKASISLWNMF 673

## RESULT 6

ID 070608 PRELIMINARY: PRT; 752 AA.  
AC 070608;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM87-2;  
RX MEDLINE-95127297; PubMed-7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HIV type IIB).";  
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RL [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM87-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12035; AAA76670.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
NON\_TER 752  
SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 100.0%; Score 179; DB 15; Length 752;  
Best Local Similarity 100.0%; Pred. No. 9.9e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONOOEKNEQELLELDKASISLWNMF 33  
DB 641 LHSLSIESONOOEKNEQELLELDKASISLWNMF 673

DB 641 LHSLSIESONOOEKNEQELLELDKASISLWNMF 673

## RESULT 7

ID 078243 PRELIMINARY: PRT; 851 AA.  
AC 078243;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env polyprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
Verani P., Rossi G.B.;  
RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
chronically infected HUT-78 cellular clone.";  
RN J. Viral Diseases 1:40-55(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-89352106; PubMed-2765297;  
RA Federic M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
Masci B., Mangiano N., Verani P., Rossi G.;  
RT "Biological and molecular characterization of producer and non  
producer clones from HUT-78 infected with a patient HIV isolate.";  
RN AIDS Res. Hum. Retroviruses 5:385-396(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Titti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
Borsetti A., Saggio I., Verani P., Rossi G.;  
RT "Variability of HIV-1 virus: characteristics of an infected but not  
productive clone.";  
RN Int. J. Immunopharmacol. 3:17-23(1990).  
DR EMBL: Z11530; CAA77628.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 100.0%; Score 179; DB 15; Length 851;  
Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONOOEKNEQELLELDKASISLWNMF 33  
DB 636 LHSLSIESONOOEKNEQELLELDKASISLWNMF 668

## RESULT 8

ID 089797 PRELIMINARY: PRT; 852 AA.  
AC 089797;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM90-2;  
RX MEDLINE-95127297; PubMed-7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker

infected with HIV type 1 (HIV type IIB).";  
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RL [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM90-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12035; AAA76670.1; -  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
NON\_TER 852  
SEQUENCE 852 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Qy	1	LIHSLIESQNOQEKNEQELLELDKWSLIMNF	33
Db	639	LIHSLIESQNOQEKNEQELLELDKWSLIMNF	671

  

Matches	33;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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RESULT	10
072502	
ID	072502
AC	PRELIMINARY;
PR	PRT;
AA	854 AA.

  

DT	01-NOV-1996	(TREMBlrel. 01, Created)
DT <td>01-NOV-1996</td> <td>(TREMBlrel. 01, Last sequence update)</td>	01-NOV-1996	(TREMBlrel. 01, Last sequence update)
DT <td>01-DEC-2001</td> <td>(TREMBlrel. 19, Last annotation update)</td>	01-DEC-2001	(TREMBlrel. 19, Last annotation update)
DE	ENV	polypotein.
GN	ENV.	
OS	Human immunodeficiency virus type 1.	
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=11676;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NL4-3.	
RX	MEDLINE=96036482; PubMed=7483282;	
RA	Salmien M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,	
RT	Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;	
RT	"Recovery of virtually full-length HIV-1 provirus of diverse subtypes	
RL	from primary virus cultures using the polymerase chain reaction.";	
RL	Virology 213:80-86(1995).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NL4-3.	
RX	MEDLINE=86281827; PubMed=3016298;	
RA	Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,	
RA	Marlin M.A.;	
RT	"Production of acquired immunodeficiency syndrome-associated	
RT	retrovirus in human and nonhuman cells transfected with an infectious	
RT	molecular clone.";	
RL	J. Virol. 59:284-291(1986).	
DR	EMBL; U26942; AAB60578.1;	
DR	InterPro; IPR000328; Env-GP41.	
DR	InterPro; IPR000777; GP120.	
DR	Pfam; PF00516; GP120; 1.	
DR	Pfam; PF00517; GP41; 1.	
KW	AIDS; Coa protein; Glycoprotein; Polypotein; Transmembrane.	
FT	CONFLICT	214
FT	CONFLICT	530
FT	CONFLICT	739
SO	SEQUENCE	854 AA; 97005 MM; FF2264B3841D1220 CRC64;

  

Query Match	100.0%;	Score 179;	DB 15;	Length 854;
Best Local Similarity	100.0%;	Prod. No. 1,1e-13;		
Matches	33;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps

  

Qy	1	LIHSLIESQNOQEKNEQELLELDKWSLIMNF	33
Db <td>639<td>LIHSLIESQNOQEKNEQELLELDKWSLIMNF<td>671</td></td></td>	639 <td>LIHSLIESQNOQEKNEQELLELDKWSLIMNF<td>671</td></td>	LIHSLIESQNOQEKNEQELLELDKWSLIMNF <td>671</td>	671

  

RESULT	11
092877	
ID	092877
AC	PRELIMINARY;
PR	PRT;
AA	856 AA.

  

DT	01-NOV-1998	(TREMBlrel. 08, Created)
DT <td>01-NOV-1998</td> <td>(TREMBlrel. 08, Last sequence update)</td>	01-NOV-1998	(TREMBlrel. 08, Last sequence update)
DT <td>01-DEC-2001</td> <td>(TREMBlrel. 19, Last annotation update)</td>	01-DEC-2001	(TREMBlrel. 19, Last annotation update)
DE	Envelope	glycoprotein.
GN	ENV.	
OS	Simian-Human immunodeficiency virus.	
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.	
OX	NCBI_TaxID=57667;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	MEDLINE=9908984;	PubMed=9882298;



RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodroski J.G.: "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 RT responsible for the pathogenicity of a multiply passaged simian-human  
 RT immunodeficiency virus (SHV-HXBc2).";  
 RL J. Virol. 73:976-984(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.:  
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF041850; AAD1242.1; -  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97151 MW; C50BE038FB73659 CRC64;

Query Match 100.0%; Score 179; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-13;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLIEESQNOQEKNEDELLELDKWSLWNMF 33  
 DB 641 LHSLIEESQNOQEKNEDELLELDKWSLWNMF 673

## RESULT 12

ID 074599 PRELIMINARY; PRT; 856 AA.  
 AC 074599;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 RL Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86068; BAA12995.1; -  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;

Query Match 100.0%; Score 179; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-13;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLIEESQNOQEKNEDELLELDKWSLWNMF 33  
 DB 641 LHSLIEESQNOQEKNEDELLELDKWSLWNMF 673

## RESULT 13

074090

ID 074090 PRELIMINARY; PRT; 856 AA.  
 AC 074090;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 RL Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1; -  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 100.0%; Score 179; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-13;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLIEESQNOQEKNEDELLELDKWSLWNMF 33  
 DB 641 LHSLIEESQNOQEKNEDELLELDKWSLWNMF 673

## RESULT 14

ID 090178 PRELIMINARY; PRT; 854 AA.  
 AC 090178;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95074930; PubMed=7983770;  
 RA Fang H., Pincus S.H.;  
 RT "Unique insertion sequence and pattern of CD4 expression in variants  
 RT selected with immunotoxins from human immunodeficiency virus type 1-  
 RT infected T cells.";  
 RL J. Virol. 69:75-81(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Fang H., Pincus S.H.;  
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
 RT immunotoxin-resistant variant T cell line";  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF070521; AAC28452.1; -  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 97.8%; Score 175; DB 15; Length 854;  
 Best Local Similarity 97.0%; Pred. No. 3.5e-13;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESONQOEKNEQELLELDKWSLWNF 33  
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 Db 639 LIHSLIEESONQOEKNEQELLELDKWSLWNF 671

## RESULT 15

Q78705 PRELIMINARY; PRT; 854 AA.  
 AC Q78705;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Envelope glycoprotein gp120.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 VS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96013815; PubMed-7474132;  
 RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 RT resistant cell lines chronically infected with human immunodeficiency  
 RT virus type 1.";  
 RL J. Virol. 69:7122-7131(1995).  
 DR EMBL: I42371; AAA96326.1; -;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 854 AA; 97199 MW; 5B9512216533E256 CRC64;

Query Match 97.8%; Score 175; DB 15; Length 854;  
 Best Local Similarity 97.0%; Pred. No. 3.5e-13;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESONQOEKNEQELLELDKWSLWNF 33  
 ||||||||||||||||||||||||||||||||  
 Db 639 LIHSLIEESONQOEKNEQELLELDKWSLWNF 671

Search completed: May 16, 2003, 11:19:46  
 Time : 25.1256 secs

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 9.34337 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533a-119

Perfect score: 179

Sequence: 1 LHSLSIERSONQOEKNEQELLELDKWSILMNWF 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCRTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	179	100.0	33	1	US-08-073-028-72
2	179	100.0	33	3	US-08-484-223B-235
3	179	100.0	33	4	US-08-554-616-72
4	179	100.0	33	4	US-09-082-279B-61
5	179	100.0	33	4	US-09-082-279B-639
6	179	100.0	33	4	US-09-082-279B-801
7	179	100.0	33	4	US-08-474-349A-417
8	179	100.0	33	4	US-09-315-304B-61
9	179	100.0	33	4	US-09-315-304B-639
10	179	100.0	33	4	US-09-315-304B-801
11	179	100.0	34	1	US-08-073-028-73
12	179	100.0	34	4	US-08-554-616-73
13	179	100.0	34	4	US-09-082-279B-800
14	179	100.0	34	4	US-09-315-304B-800
15	179	100.0	35	1	US-08-073-028-74
16	179	100.0	35	4	US-08-484-223B-234
17	179	100.0	35	4	US-08-554-616-74
18	179	100.0	35	4	US-09-082-279B-638
19	179	100.0	35	4	US-09-082-279B-799
20	179	100.0	35	4	US-08-474-349A-416
21	179	100.0	35	4	US-09-315-304B-638
22	179	100.0	35	4	US-09-315-304B-799
23	179	100.0	36	1	US-08-073-028-1
24	179	100.0	36	3	US-08-486-099-1
25	179	100.0	36	3	US-09-071-877-1
26	179	100.0	36	3	US-08-360-107A-1
27	179	100.0	36	3	US-08-484-223B-1

28	179	100.0	36	3	US-08-484-223B-231	Sequence 231, App
29	179	100.0	36	3	US-08-484-223B-232	Sequence 232, App
30	179	100.0	36	3	US-08-484-223B-233	Sequence 233, App
31	179	100.0	36	3	US-08-919-597-1	Sequence 1, Appl
32	179	100.0	36	3	US-08-475-668A-1	Sequence 1, Appl
33	179	100.0	36	3	US-08-485-551A-1	Sequence 1, Appl
34	179	100.0	36	3	US-08-471-913A-1	Sequence 1, Appl
35	179	100.0	36	4	US-08-554-616-1	Sequence 1, Appl
36	179	100.0	36	4	US-08-485-264A-1	Sequence 15, Appl
37	179	100.0	36	4	US-09-082-279B-15	Sequence 497, App
38	179	100.0	36	4	US-09-082-279B-497	Sequence 498, App
39	179	100.0	36	4	US-09-082-279B-498	Sequence 559, App
40	179	100.0	36	4	US-09-082-279B-559	Sequence 560, App
41	179	100.0	36	4	US-09-082-279B-560	Sequence 561, App
42	179	100.0	36	4	US-09-082-279B-561	Sequence 603, App
43	179	100.0	36	4	US-09-082-279B-603	Sequence 630, App
44	179	100.0	36	4	US-09-082-279B-630	Sequence 631, App
45	179	100.0	36	4	US-09-082-279B-631	

## ALIGNMENTS

```
RESULT 1
US-08-073-028-72
: Sequence 72, Application US/08073028
: Patent No. 5464933
: GENERAL INFORMATION:
: APPLICANT: Bolognesi, Dani P.
: APPLICANT: Mathews, Thomas J.
: APPLICANT: Wild, Carl T.
: TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
: NUMBER OF INVENTION: TRANSMISSION
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/073,028
: FILING DATE: 07-JUN-1993
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7872-004-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 72:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 33 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
: US-08-073-028-72

Query Match      100.0%; Score 179; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.7e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      1 LHSLSIERSONQOEKNEQELLELDKWSILMNWF 33
      1 LHSLSIERSONQOEKNEQELLELDKWSILMNWF 33
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RESULT 2  
US-08-484-223B-235  
Sequence 235, Application US/08484223B  
Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 235:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
08-484-223B-235

Query Match 100.0%; Score 179; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33  
|||||  
Db 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33

RESULT 3  
US-08-554-616-72  
Sequence 72, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-72

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33  
|||||  
Db 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33

RESULT 4  
US-09-082-279B-61  
Sequence 61, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-61

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33  
|||||

DB 1 LHSLSIESONQOEKNEQELLELDKWSLWMPF 33

RESULT 5

US-09-082-279B-639

Sequence 639, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 639

LENGTH: 33

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-639

Query Match

Best Local Similarity 100.0%; Score 179; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.7e-16;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQELLELDKWSLWMPF 33

DB 1 LHSLSIESONQOEKNEQELLELDKWSLWMPF 33

RESULT 6

US-09-082-279B-801

Sequence 801, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 801

LENGTH: 33

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-801

Query Match

Best Local Similarity 100.0%; Score 179; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.7e-16;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQELLELDKWSLWMPF 33

DB 1 LHSLSIESONQOEKNEQELLELDKWSLWMPF 33

RESULT 7

US-08-474-349A-417

Sequence 417, Application US/08474349A

Patent No. 6333395

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pelleway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA

TITLE OF INVENTION: VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 517

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penite & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,349A

FILING DATE: 07-JUN-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-024

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 417:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-474-349A-417

Query Match

Best Local Similarity 100.0%; Score 179; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.7e-16;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQELLELDKWSLWMPF 33

DB 1 LHSLSIESONQOEKNEQELLELDKWSLWMPF 33

RESULT 8

US-09-315-304B-61

Sequence 61, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 61  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-61

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLIEESONOQEKNEQELLELDKWSLWNMF 33  
DB 1 LHSLIEESONOQEKNEQELLELDKWSLWNMF 33

RESULT 9  
US-09-315-304B-639

Sequence 639, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 639

LENGTH: 33

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-639

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLIEESONOQEKNEQELLELDKWSLWNMF 33  
DB 1 LHSLIEESONOQEKNEQELLELDKWSLWNMF 33

RESULT 10  
US-09-315-304B-801

Sequence 801, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 801  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-801

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLIEESONOQEKNEQELLELDKWSLWNMF 33  
DB 1 LHSLIEESONOQEKNEQELLELDKWSLWNMF 33

RESULT 11  
US-08-073-028-73

Sequence 73, Application US/08073028

Patent No. 5464933

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/073,028

FILING DATE: 07-JUN-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8664/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLBUCE TYPE: peptide

US-08-073-028-73

Query Match 100.0%; Score 179; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 7.9e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLIEESONOQEKNEQELLELDKWSLWNMF 33  
DB 2 LHSLIEESONOQEKNEQELLELDKWSLWNMF 34

RESULT 12  
US-08-554-616-73

Sequence 73, Application US/08554616

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; Patent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,616
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,028
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-554-616-73

Query Match          100.0%; Score 179; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.9e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LHSLSIESONQOEKNEQLLELDKWSLWNWF 33
  |||
2 LHSLSIESONQOEKNEQLLELDKWSLWNWF 34

RESULT 13
US-09-082-279B-800
; Sequence 800, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 800
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-800

Query Match          100.0%; Score 179; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.9e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LHSLSIESONQOEKNEQLLELDKWSLWNWF 33
  |||
2 LHSLSIESONQOEKNEQLLELDKWSLWNWF 34

RESULT 14
US-09-315-304B-800
; Sequence 800, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M. D.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 800
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Core polypeptide
; US-09-315-304B-800

Query Match          100.0%; Score 179; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.9e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LHSLSIESONQOEKNEQLLELDKWSLWNWF 33
  |||
2 LHSLSIESONQOEKNEQLLELDKWSLWNWF 34

RESULT 15
US-08-073-028-74
; Sequence 74, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/073.028  
 FILING DATE: 07-JUN-1993  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30.742  
 REFERENCE/DOCKET NUMBER: 7872-004-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 74:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 35 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-073-028-74

Query Match 100.0%; Score 179; DB 1; Length 35;  
 Local Similarity 100.0%; Pred. No. 8.2e-16;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LIHSLIESQNOQEKNEQELLELDKWSLNNF	33
DB	3	LIHSLIESQNOQEKNEQELLELDKWSLNNF	35

Search completed: May 16, 2003, 11:22:12  
 Job time : 10.3434 secs



GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 14.4458 Seconds  
(Without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-119  
Perfect score: 179  
Sequence: 1 LHSLSIESONQOEKNEQELLELDKASLWVWF 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues  
1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PC7\_NEW\_PUB pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB pep:\*  
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7: /cgn2\_6/ptodata/1/pubppaa/PC7US\_PUBCOMB pep:\*  
8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB pep:\*  
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10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB pep:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB pep:\*  
12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	179	100.0	36	US-09-874-475-16	Sequence 16, Appl
2	179	100.0	36	US-10-116-797-1	Sequence 1, Appl
3	179	100.0	36	US-09-493-346-1	Sequence 10, Appl
4	179	100.0	36	US-09-796-202-10	Sequence 5, Appl
5	179	100.0	36	US-09-779-451-5	Sequence 1, Appl
6	179	100.0	36	US-09-834-628-1	Sequence 97, Appl
7	179	100.0	36	US-09-854-816-1	Sequence 16, Appl
8	179	100.0	36	US-09-854-816-108	Sequence 17, Appl
9	179	100.0	37	US-09-848-616-176	Sequence 18, Appl
10	179	100.0	46	US-09-779-451-41	Sequence 41, Appl
11	179	100.0	56	US-09-779-451-4	Sequence 4, Appl
12	179	100.0	177	US-10-040-349B-2	Sequence 84, Appl
13	179	100.0	221	US-10-059-271-84	Sequence 84, Appl
14	179	100.0	232	US-10-059-271-81	Sequence 82, Appl
15	179	100.0	254	US-10-059-271-82	Sequence 97, Appl
16	179	100.0	256	US-10-059-271-97	Sequence 16, Appl
17	179	100.0	268	US-09-854-816-15	Sequence 17, Appl
18	179	100.0	268	US-09-854-816-17	Sequence 18, Appl
19	179	100.0	268	US-09-854-816-18	Sequence 18, Appl

20	179	100.0	344	US-10-040-349B-1	Sequence 1, Appl
21	179	100.0	345	US-10-026-741-49	Sequence 49, Appl
22	179	100.0	345	US-09-779-451-8	Sequence 8, Appl
23	179	100.0	391	US-10-059-271-93	Sequence 93, Appl
24	179	100.0	519	US-09-756-351A-8	Sequence 8, Appl
25	179	100.0	853	US-10-003-035-33	Sequence 33, Appl
26	179	100.0	856	US-09-476-242-1	Sequence 1, Appl
27	179	100.0	861	US-10-026-741-103	Sequence 103, App
28	179	100.0	1101	US-10-003-035-53	Sequence 53, Appl
29	179	100.0	1186	US-10-003-035-55	Sequence 55, Appl
30	176	98.3	36	US-09-912-824-1	Sequence 1, Appl
31	176	98.3	268	US-09-854-816-19	Sequence 19, Appl
32	173	96.6	1231	US-10-059-271-94	Sequence 94, Appl
33	171	95.5	268	US-09-854-816-13	Sequence 13, Appl
34	170	95.0	46	US-09-854-816-109	Sequence 109, App
35	170	95.0	233	US-09-854-816-50	Sequence 50, Appl
36	170	95.0	267	US-09-854-816-38	Sequence 38, Appl
37	170	95.0	268	US-09-854-816-9	Sequence 9, Appl
38	170	95.0	268	US-09-854-816-26	Sequence 26, Appl
39	170	95.0	268	US-09-854-816-41	Sequence 41, Appl
40	170	95.0	269	US-09-854-816-6	Sequence 6, Appl
41	170	95.0	269	US-09-854-816-12	Sequence 12, Appl
42	170	95.0	269	US-09-854-816-43	Sequence 43, Appl
43	170	95.0	619	US-09-891-609-4	Sequence 4, Appl
44	170	95.0	646	US-09-891-609-2	Sequence 2, Appl
45	170	95.0	847	US-09-476-242-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
Sequence 16, Application US/09874475  
Publication No. US20020182592A1  
GENERAL INFORMATION:  
APPLICANT: Petropoulos, Christos J.  
APPLICANT: Parkin, Neil T.  
APPLICANT: Whitcomb, Jeanette  
APPLICANT: Huang, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS  
FILE REFERENCE: 2793/6516  
CURRENT FILING DATE: 2001-06-04  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16

Query Match 100.0%; Score 179; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.8e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQELLELDKASLWVWF 33  
DB 4 LHSLSIESONQOEKNEQELLELDKASLWVWF 36

RESULT 2  
US-10-116-797-1  
Sequence 1, Application US/10116797  
Publication No. US2003004411A1  
GENERAL INFORMATION:  
APPLICANT: Olsen, William C.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
FILE REFERENCE: 64672-A  
CURRENT APPLICATION NUMBER: US/10/116.797  
CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match  
Best Local Similarity 100.0%; Score 179; DB 9; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 33  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Olson, William C  
APPLICANT: Maddon, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
TITLE OF INVENTION: Infection  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match  
Best Local Similarity 100.0%; Score 179; DB 9; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 33  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 36

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US2002006813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match  
Best Local Similarity 100.0%; Score 179; DB 10; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 33  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US2002009452A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.030003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match  
Best Local Similarity 100.0%; Score 179; DB 10; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 33  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 36

RESULT 6  
US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US2002011922A1  
GENERAL INFORMATION:

APPLICANT: YU, YEON GYU  
APPLICANT: KIM, BONG-SUK  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match  
Best Local Similarity 100.0%; Score 179; DB 10; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 33  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNWF 36

RESULT 7  
US-09-854-816-1  
; Sequence 1, Application US/09854816  
; Patent No. US20020151473A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew C. Braisted  
; J. Kevin Judice  
; Robert S. McDowell  
; J. Christopher Pheasant  
; Melissa A. Starovasnik  
; James A. Wells  
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/854,816  
; FILING DATE: 15-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/965,056  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, PhD., Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: P1005R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; MOLECULE TYPE: DP178  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
09-854-816-1  
Query Match 100.0%; Score 179; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5,8e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHSLSIESQNOOEKNEQELLELDKWSLWNMF 33  
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DB 4 LHSLSIESQNOOEKNEQELLELDKWSLWNMF 36  
|||||  
RESULT 8  
US-09-854-816-108  
; Sequence 108, Application US/09854816  
; Patent No. US20020151473A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew C. Braisted  
; J. Kevin Judice  
; Robert S. McDowell  
; J. Christopher Pheasant  
; Melissa A. Starovasnik  
; James A. Wells  
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/854,816  
; FILING DATE: 15-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/965,056  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, PhD., Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: P1005R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 108:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108  
Query Match 100.0%; Score 179; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5,8e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHSLSIESQNOOEKNEQELLELDKWSLWNMF 33  
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DB 4 LHSLSIESQNOOEKNEQELLELDKWSLWNMF 36  
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RESULT 9  
US-09-848-616-176  
; Sequence 176, Application US/09848616  
; Publication No. US20030054010A1  
; GENERAL INFORMATION:  
; APPLICANT: Sebbel, Peter  
; APPLICANT: Dunant, Nicolas  
; APPLICANT: Bachmann, Martin  
; APPLICANT: Tissot, Alain  
; APPLICANT: Lechner, Franziska  
; TITLE OF INVENTION: Molecular Antigen Array  
; FILE REFERENCE: 1700.0180002  
; CURRENT APPLICATION NUMBER: US/09/848,616  
; CURRENT FILING DATE: 2001-05-05  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 176  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DP178c peptide  
US-09-848-616-176  
Query Match 100.0%; Score 179; DB 9; Length 37;  
Best Local Similarity 100.0%; Pred. No. 5,9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHSLSIESQNOOEKNEQELLELDKWSLWNMF 33  
|||||

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Db      5  LHSLSIESONQOEKNEQELLELDKWSLWNMF 37

RESULT 10
US-09-779-451-41
; Sequence 41, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-41

Query Match      100.0%; Score 179; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 7,4e-15;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  LHSLSIESONQOEKNEQELLELDKWSLWNMF 33
Db      14  LHSLSIESONQOEKNEQELLELDKWSLWNMF 46

RESULT 11
US-09-779-451-4
; Sequence 4, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-4

Query Match      100.0%; Score 179; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 9,1e-15;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  LHSLSIESONQOEKNEQELLELDKWSLWNMF 33
Db      19  LHSLSIESONQOEKNEQELLELDKWSLWNMF 51

RESULT 12
US-10-040-349B-2
; Sequence 2, Application US/10040349B
; Publication No. US20030082521A1
; GENERAL INFORMATION:
; APPLICANT: Brasseur, Robert

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; APPLICANT: Charlotiaux, Benoît
; APPLICANT: Chevalier, Michel
; APPLICANT: El Habib, Raghabelle
; APPLICANT: Krell, Tino
; TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
; FILE REFERENCE: 01-078-A
; CURRENT APPLICATION NUMBER: US/10/040,349B
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(177)
; OTHER INFORMATION: polypeptide derived from gp41 LAI
US-10-040-349B-2

Query Match      100.0%; Score 179; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 2,9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  LHSLSIESONQOEKNEQELLELDKWSLWNMF 33
Db      107  LHSLSIESONQOEKNEQELLELDKWSLWNMF 139

RESULT 13
US-10-059-271-84
; Sequence 84, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDDÉ, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-84

Query Match      100.0%; Score 179; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 3,6e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  LHSLSIESONQOEKNEQELLELDKWSLWNMF 33
Db      134  LHSLSIESONQOEKNEQELLELDKWSLWNMF 166

RESULT 14
US-10-059-271-81
; Sequence 81, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDDÉ, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

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